NCBI GI	g4263507
BLAST score	197
E value	3.0e-15
Match length	120
% identity	35
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226547
Seq. ID	LIB3189-002-P1-K1-E6
Method	BLASTX
NCBI GI	g3885511
BLAST score	390
E value	7.0e-38
Match length	97
% identity	79
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	226548
Seq. ID	LIB3189-002-P1-K1-E9
Method	BLASTX
NCBI GI	g70644
BLAST score	531
E value	2.0e-54
Match length	109
% identity	19
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	226549
Seq. ID	LIB3189-002-P1-K1-F1
Method	BLASTX
NCBI GI	g4432832
BLAST score	241
E value	5.0e-31
Match length	97
% identity	73
NCBI Description	(AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.	226550
Seq. ID	LIB3189-002-P1-K1-F10
Method	BLASTX
NCBI GI	g808839
BLAST score	184
E value	1.0e-13
Match length	103
% identity	45
NCBI Description	(J04186) unknown protein [Saccharomyces cerevisiae]

Seq. No.	226551
Seq. ID	LIB3189-002-P1-K1-F11
Method	BLASTX
NCBI GI	g4530585
BLAST score	349
E value	3.0e-33
Match length	83
% identity	75
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

09504600.040501

Seq. No.	226552
Seq. ID	LIB3189-002-P1-K1-F12
Method	BLASTX
NCBI GI	g2160185
BLAST score	326
E value	2.0e-30
Match length	86
% identity	72
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	226553
Seq. ID	LIB3189-002-P1-K1-F2
Method	BLASTX
NCBI GI	g1362086
BLAST score	603
E value	7.0e-63
Match length	121
% identity	93
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	226554
Seq. ID	LIB3189-002-P1-K1-F3
Method	BLASTX
NCBI GI	g3914370
BLAST score	245
E value	7.0e-21
Match length	74
% identity	72
NCBI Description	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) >gi_419754_pir__S31083 glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis thaliana >gi_217845_dbj_BAA00575_ (D00672) glycerol-3-phosphate acyltransferase [Arabidopsis thaliana] >gi_217847_dbj_BAA00576_ (D00673) glycerol-3-phosphate acyltransferase precursor [Arabidopsis thaliana]

Seq. No.	226555
Seq. ID	LIB3189-002-P1-K1-F4
Method	BLASTX
NCBI GI	g1709761
BLAST score	466
E value	8.0e-47
Match length	100
% identity	93
NCBI Description	PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 27 KD SUBUNIT) >gi_1262146_emb_CAA65660_ (X96974) proteasome subunit [Spinacia oleracea]

Seq. No.	226556

Seq. ID	LIB3189-002-P1-K1-F7
Method	BLASTX
NCBI GI	g2829887
BLAST score	440
E value	9.0e-44
Match length	123
% identity	70
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	226557
Seq. ID	LIB3189-002-P1-K1-F8
Method	BLASTX
NCBI GI	g3927916
BLAST score	471
E value	2.0e-47
Match length	88
% identity	98
NCBI Description	(AJ130887) glycine-rich protein 2 [Fagus sylvatica]

Seq. No.	226558
Seq. ID	LIB3189-002-P1-K1-G10
Method	BLASTX
NCBI GI	g3043428
BLAST score	443
E value	4.0e-44
Match length	92
% identity	88
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	226559
Seq. ID	LIB3189-002-P1-K1-G12
Method	BLASTX
NCBI GI	g2335099
BLAST score	461
E value	3.0e-46
Match length	126
% identity	40
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	226560
Seq. ID	LIB3189-002-P1-K1-G2
Method	BLASTX
NCBI GI	g2828296
BLAST score	230
E value	5.0e-19
Match length	43
% identity	95
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	226561
Seq. ID	LIB3189-002-P1-K1-G4
Method	BLASTX
NCBI GI	g2369766
BLAST score	366
E value	4.0e-35
Match length	105
% identity	68

NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No. 226562
Seq. ID LIB3189-002-P1-K1-G5
Method BLASTX
NCBI GI g3335341
BLAST score 140
E value 1.0e-08
Match length 96
% identity 38
NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No. 226563
Seq. ID LIB3189-002-P1-K1-G7
Method BLASTX
NCBI GI g2335101
BLAST score 473
E value 1.0e-47
Match length 118
% identity 72
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 226564
Seq. ID LIB3189-002-P1-K1-G9
Method BLASTX
NCBI GI g1743354
BLAST score 264
E value 7.0e-28
Match length 80
% identity 76
NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No. 226565
Seq. ID LIB3189-002-P1-K1-H10
Method BLASTX
NCBI GI g4220528
BLAST score 335
E value 2.0e-31
Match length 125
% identity 58
NCBI Description (AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 226566
Seq. ID LIB3189-002-P1-K1-H11
Method BLASTX
NCBI GI g3021485
BLAST score 269
E value 1.0e-23
Match length 66
% identity 82
NCBI Description (AJ224932) histone H2B-3 [Lycopersicon esculentum]

Seq. No. 226567
Seq. ID LIB3189-002-P1-K1-H12
Method BLASTX
NCBI GI g132086

09604706.960604

BLAST score	213
E value	1.0e-17
Match length	75
% identity	63
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR (RUBISCO SMALL SUBUNIT 1) >gi_68053_pir__RKSYS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor SRS1 - soybean >gi_18742_emb_CAA23736_ (V00458) rubpcase [Glycine max]

Seq. No.	226568
Seq. ID	LIB3189-002-P1-K1-H3
Method	BLASTX
NCBI GI	g2772934
BLAST score	407
E value	7.0e-40
Match length	121
% identity	62
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	226569
Seq. ID	LIB3189-002-P1-K1-H6
Method	BLASTX
NCBI GI	g1055368
BLAST score	599
E value	2.0e-62
Match length	114
% identity	99
NCBI Description	(U39567) ribulose-1,5-bisphosphate carboxylase small subunit [Glycine max]

Seq. No.	226570
Seq. ID	LIB3189-002-P1-K1-H8
Method	BLASTX
NCBI GI	g4376233
BLAST score	517
E value	8.0e-53
Match length	101
% identity	93
NCBI Description	(X00798) L2 protein [Nicotiana debneyi]

Seq. No.	226571
Seq. ID	LIB3189-003-P1-K1-A10
Method	BLASTX
NCBI GI	g2088654
BLAST score	405
E value	1.0e-39
Match length	92
% identity	86
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	226572
Seq. ID	LIB3189-003-P1-K1-A11
Method	BLASTX
NCBI GI	g2980770

BLAST score 214
E value 2.0e-17
Match length 79
% identity 59
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 226573
Seq. ID LIB3189-003-P1-K1-A2
Method BLASTX
NCBI GI g2501448
BLAST score 144
E value 2.0e-09
Match length 40
% identity 78
NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923_ (X99609) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 226574
Seq. ID LIB3189-003-P1-K1-A3
Method BLASTX
NCBI GI g4455208
BLAST score 368
E value 3.0e-35
Match length 86
% identity 79
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 226575
Seq. ID LIB3189-003-P1-K1-B1
Method BLASTX
NCBI GI g2245000
BLAST score 156
E value 3.0e-10
Match length 136
% identity 30
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 226576
Seq. ID LIB3189-003-P1-K1-B6
Method BLASTX
NCBI GI g4090257
BLAST score 284
E value 9.0e-26
Match length 61
% identity 89
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No. 226577
Seq. ID LIB3189-003-P1-K1-C1
Method BLASTX
NCBI GI g2811278
BLAST score 345
E value 8.0e-33
Match length 99
% identity 67
NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No.	226578
Seq. ID	LIB3189-003-P1-K1-C11
Method	BLASTX
NCBI GI	g1718097
BLAST score	272
E value	5.0e-24
Match length	78
% identity	62
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	226579
Seq. ID	LIB3189-003-P1-K1-C2
Method	BLASTX
NCBI GI	g4539405
BLAST score	348
E value	4.0e-33
Match length	89
% identity	75
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	226580
Seq. ID	LIB3189-003-P1-K1-C3
Method	BLASTX
NCBI GI	g2832625
BLAST score	326
E value	2.0e-30
Match length	104
% identity	62
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	226581
Seq. ID	LIB3189-003-P1-K1-D1
Method	BLASTX
NCBI GI	g3126967
BLAST score	544
E value	6.0e-56
Match length	113
% identity	17
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No.	226582
Seq. ID	LIB3189-003-P1-K1-D12
Method	BLASTX
NCBI GI	g1076316
BLAST score	260
E value	2.0e-22
Match length	71
% identity	58
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	226583
Seq. ID	LIB3189-003-P1-K1-D4
Method	BLASTX
NCBI GI	g1172874
BLAST score	559
E value	2.0e-57
Match length	150
% identity	70
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	226584
Seq. ID	LIB3189-003-P1-K1-D6
Method	BLASTX
NCBI GI	g3004565
BLAST score	217
E value	1.0e-17
Match length	70
% identity	77
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	226585
Seq. ID	LIB3189-003-P1-K1-D8
Method	BLASTX
NCBI GI	g478753
BLAST score	137
E value	9.0e-09
Match length	26
% identity	92
NCBI Description	tubulin alpha-4 chain - maize (fragment)

Seq. No.	226586
Seq. ID	LIB3189-003-P1-K1-E1
Method	BLASTX
NCBI GI	g2286153
BLAST score	523
E value	2.0e-53
Match length	106
% identity	98
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	226587
Seq. ID	LIB3189-003-P1-K1-E10
Method	BLASTX
NCBI GI	g3122572
BLAST score	287
E value	2.0e-26
Match length	72
% identity	72
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No.	226588
Seq. ID	LIB3189-003-P1-K1-E7
Method	BLASTX
NCBI GI	g119350
BLAST score	489
E value	2.0e-49
Match length	117
% identity	83
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana]

Seq. No.	226589
Seq. ID	LIB3189-003-P1-K1-F10
Method	BLASTX
NCBI GI	g3236237
BLAST score	458
E value	1.0e-45
Match length	146
% identity	60
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	226590
Seq. ID	LIB3189-003-P1-K1-F11
Method	BLASTX
NCBI GI	g1518540
BLAST score	359
E value	2.0e-34
Match length	79
% identity	87
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	226591
Seq. ID	LIB3189-003-P1-K1-F2
Method	BLASTX
NCBI GI	g4432825
BLAST score	479
E value	3.0e-48
Match length	132
% identity	70
NCBI Description	(AC006593) putative SOP2p protein [Arabidopsis thaliana]

Seq. No.	226592
Seq. ID	LIB3189-003-P1-K1-F4
Method	BLASTX
NCBI GI	g4567249
BLAST score	433
E value	7.0e-43
Match length	117
% identity	66
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226593
Seq. ID	LIB3189-003-P1-K1-F6
Method	BLASTX
NCBI GI	g2852640
BLAST score	219
E value	9.0e-18
Match length	101
% identity	45
NCBI Description	(AF007157) unknown [Homo sapiens]

Seq. No.	226594
Seq. ID	LIB3189-003-P1-K1-F8
Method	BLASTX
NCBI GI	g2129581
BLAST score	666
E value	4.0e-70
Match length	141
% identity	93
NCBI Description	envelope Ca2+-ATPase precursor - Arabidopsis thaliana >gi_471089_dbj_BAA03091_ (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana] >gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	226595
Seq. ID	LIB3189-003-P1-K1-F9
Method	BLASTX
NCBI GI	g3335060
BLAST score	178
E value	2.0e-13
Match length	44
% identity	89
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	226596
Seq. ID	LIB3189-003-P1-K1-G10
Method	BLASTX
NCBI GI	g267069
BLAST score	341
E value	3.0e-32
Match length	74
% identity	86
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	226597
Seq. ID	LIB3189-003-P1-K1-G11
Method	BLASTX
NCBI GI	g126894
BLAST score	285
E value	2.0e-25
Match length	79
% identity	76

NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_319832_pir__DEPUGW malate dehydrogenase (EC 1.1.1.37) precursor, glyoxysomal - watermelon >gi_167284 (M33148) glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37) [Citrullus vulgaris]
Seq. No.	226598
Seq. ID	LIB3189-003-P1-K1-G6
Method	BLASTX
NCBI GI	g2253384
BLAST score	613
E value	5.0e-64
Match length	136
% identity	85
NCBI Description	(AF007100) biotin carboxylase precursor [Glycine max]
Seq. No.	226599
Seq. ID	LIB3189-003-P1-K1-H1
Method	BLASTX
NCBI GI	g1076678
BLAST score	392
E value	3.0e-38
Match length	91
% identity	91
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.	226600
Seq. ID	LIB3189-003-P1-K1-H3
Method	BLASTX
NCBI GI	g267082
BLAST score	490
E value	1.0e-49
Match length	95
% identity	94
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]
Seq. No.	226601
Seq. ID	LIB3189-003-P1-K1-H6
Method	BLASTX
NCBI GI	g1632822
BLAST score	558
E value	2.0e-57
Match length	138
% identity	81
NCBI Description	(Y08962) transmembrane protein [Oryza sativa] >gi_1667594 (U77297) transmembrane protein [Oryza sativa]
Seq. No.	226602
Seq. ID	LIB3189-003-P1-K1-H9
Method	BLASTX
NCBI GI	g4508073
BLAST score	176
E value	5.0e-13
Match length	62
% identity	56

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 226603
Seq. ID LIB3189-004-P1-K1-A10
Method BLASTX
NCBI GI g445613
BLAST score 667
E value 3.0e-70
Match length 155
% identity 79
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 226604
Seq. ID LIB3189-004-P1-K1-A12
Method BLASTX
NCBI GI g82209
BLAST score 148
E value 1.0e-09
Match length 66
% identity 47
NCBI Description hypothetical protein 228 - common tobacco chloroplast >gi_225265_prf__1211235DA ORF 228 [Nicotiana tabacum]

Seq. No. 226605
Seq. ID LIB3189-004-P1-K1-A4
Method BLASTX
NCBI GI g3269288
BLAST score 471
E value 3.0e-47
Match length 114
% identity 81
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 226606
Seq. ID LIB3189-004-P1-K1-B11
Method BLASTX
NCBI GI g2982320
BLAST score 228
E value 9.0e-19
Match length 116
% identity 43
NCBI Description (AF051245) hypothetical protein [Picea mariana]

Seq. No. 226607
Seq. ID LIB3189-004-P1-K1-C1
Method BLASTX
NCBI GI g585963
BLAST score 262
E value 6.0e-23
Match length 69
% identity 78
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 226608
Seq. ID LIB3189-004-P1-K1-C12
Method BLASTX
NCBI GI g2244740

BLAST score	616
E value	3.0e-64
Match length	138
% identity	87
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	226609
Seq. ID	LIB3189-004-P1-K1-C4
Method	BLASTX
NCBI GI	g730449
BLAST score	545
E value	6.0e-56
Match length	131
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi_480647_pir__S37132 ribosomal protein L13.A - rape >gi_398918_emb_CAA80341_ (Z22618) cold induced protein (BnC24A) [Brassica napus]

Seq. No.	226610
Seq. ID	LIB3189-004-P1-K1-C6
Method	BLASTX
NCBI GI	g122781
BLAST score	268
E value	2.0e-23
Match length	60
% identity	80
NCBI Description	POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) >gi_82210_pir__A05198 hypothetical protein 229 - common tobacco chloroplast >gi_11844_emb_CAA77364_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]

Seq. No.	226611
Seq. ID	LIB3189-004-P1-K1-C8
Method	BLASTX
NCBI GI	g2501850
BLAST score	330
E value	5.0e-31
Match length	65
% identity	94
NCBI Description	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No.	226612
Seq. ID	LIB3189-004-P1-K1-D1
Method	BLASTX
NCBI GI	g4206765
BLAST score	228
E value	7.0e-19
Match length	89
% identity	55
NCBI Description	(AF104329) putative type 1 membrane protein [Arabidopsis thaliana]

Seq. No.	226613
Seq. ID	LIB3189-004-P1-K1-D12
Method	BLASTX

NCBI GI	g3128176
BLAST score	376
E value	4.0e-36
Match length	139
% identity	53
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	226614
Seq. ID	LIB3189-004-P1-K1-D2
Method	BLASTX
NCBI GI	g2829893
BLAST score	639
E value	5.0e-67
Match length	143
% identity	87
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	226615
Seq. ID	LIB3189-004-P1-K1-D6
Method	BLASTX
NCBI GI	g3269283
BLAST score	155
E value	3.0e-10
Match length	146
% identity	22
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	226616
Seq. ID	LIB3189-004-P1-K1-D8
Method	BLASTX
NCBI GI	g4580394
BLAST score	238
E value	3.0e-20
Match length	68
% identity	65
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	226617
Seq. ID	LIB3189-004-P1-K1-E1
Method	BLASTX
NCBI GI	g2370312
BLAST score	536
E value	5.0e-55
Match length	123
% identity	80
NCBI Description	(AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020 (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No.	226618
Seq. ID	LIB3189-004-P1-K1-E12
Method	BLASTX
NCBI GI	g3551031
BLAST score	517
E value	7.0e-53
Match length	107
% identity	95

NCBI Description	(AB011467) chalcone synthase [Hydrangea macrophylla]
Seq. No.	226619
Seq. ID	LIB3189-004-P1-K1-E5
Method	BLASTX
NCBI GI	g3123614
BLAST score	594
E value	9.0e-62
Match length	123
% identity	93
NCBI Description	(Y17225) cyclin-dependent protein kinase p34cdc2 [Lycopersicon esculentum]
Seq. No.	226620
Seq. ID	LIB3189-004-P1-K1-E9
Method	BLASTX
NCBI GI	g3892713
BLAST score	191
E value	2.0e-23
Match length	71
% identity	76
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]
Seq. No.	226621
Seq. ID	LIB3189-004-P1-K1-F10
Method	BLASTX
NCBI GI	g267069
BLAST score	331
E value	4.0e-31
Match length	72
% identity	85
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	226622
Seq. ID	LIB3189-004-P1-K1-F11
Method	BLASTX
NCBI GI	g2129473
BLAST score	269
E value	1.0e-23
Match length	105
% identity	50
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.	226623
Seq. ID	LIB3189-004-P1-K1-F4
Method	BLASTX
NCBI GI	g116923
BLAST score	355
E value	1.0e-33
Match length	156
% identity	54
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat

	>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]
Seq. No.	226624
Seq. ID	LIB3189-004-P1-K1-F6
Method	BLASTX
NCBI GI	g3876865
BLAST score	161
E value	5.0e-11
Match length	73
% identity	40
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
Seq. No.	226625
Seq. ID	LIB3189-004-P1-K1-G11
Method	BLASTX
NCBI GI	g1169228
BLAST score	212
E value	7.0e-17
Match length	70
% identity	60
NCBI Description	RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639 helicase-like protein - Wood tobacco >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris]
Seq. No.	226626
Seq. ID	LIB3189-004-P1-K1-G12
Method	BLASTX
NCBI GI	g1172874
BLAST score	302
E value	8.0e-28
Match length	91
% identity	68
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]
Seq. No.	226627
Seq. ID	LIB3189-004-P1-K1-G2
Method	BLASTX
NCBI GI	g2580499
BLAST score	320
E value	9.0e-30
Match length	79
% identity	75
NCBI Description	(U67186) NADPH:ferrihemoprotein oxidoreductase [Eschscholzia californica]
Seq. No.	226628
Seq. ID	LIB3189-004-P1-K1-G4
Method	BLASTX

NCBI GI	g2995384
BLAST score	141
E value	3.0e-09
Match length	50
% identity	56
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	226629
Seq. ID	LIB3189-004-P1-K1-G5
Method	BLASTX
NCBI GI	g441457
BLAST score	734
E value	4.0e-78
Match length	143
% identity	96
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	226630
Seq. ID	LIB3189-004-P1-K1-G9
Method	BLASTX
NCBI GI	g4220535
BLAST score	246
E value	2.0e-24
Match length	97
% identity	61
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	226631
Seq. ID	LIB3189-004-P1-K1-H5
Method	BLASTX
NCBI GI	g3876865
BLAST score	173
E value	3.0e-12
Match length	113
% identity	35
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	226632
Seq. ID	LIB3189-004-P1-K1-H6
Method	BLASTX
NCBI GI	g3914435
BLAST score	408
E value	5.0e-40
Match length	83
% identity	89
NCBI Description	PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin [Glycine max]

Seq. No.	226633
Seq. ID	LIB3189-005-P1-K1-A10
Method	BLASTX
NCBI GI	g2062167

BLAST score	217
E value	7.0e-18
Match length	50
% identity	76
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	226634
Seq. ID	LIB3189-005-P1-K1-A11
Method	BLASTX
NCBI GI	g3914437
BLAST score	440
E value	2.0e-49
Match length	120
% identity	81
NCBI Description	PROFILIN >gi_3183706_emb_CAA75312_ (Y15042) profilin [Hevea brasiliensis]

Seq. No.	226635
Seq. ID	LIB3189-005-P1-K1-A12
Method	BLASTX
NCBI GI	g1076621
BLAST score	323
E value	3.0e-30
Match length	66
% identity	89
NCBI Description	cytochrome b5 - common tobacco >gi_296386_emb_CAA50575_ (X71441) cytochrome b5 [Nicotiana tabacum]

Seq. No.	226636
Seq. ID	LIB3189-005-P1-K1-A3
Method	BLASTX
NCBI GI	g2765316
BLAST score	276
E value	1.0e-24
Match length	55
% identity	93
NCBI Description	(Y13321) asparagine synthetase 1 [Pisum sativum]

Seq. No.	226637
Seq. ID	LIB3189-005-P1-K1-A5
Method	BLASTX
NCBI GI	g2829902
BLAST score	353
E value	1.0e-33
Match length	87
% identity	79
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	226638
Seq. ID	LIB3189-005-P1-K1-A6
Method	BLASTX
NCBI GI	g3962377
BLAST score	762
E value	2.0e-81
Match length	156

% identity	94
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	226639
Seq. ID	LIB3189-005-P1-K1-B1
Method	BLASTX
NCBI GI	g3334113
BLAST score	466
E value	1.0e-46
Match length	89
% identity	100
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	226640
Seq. ID	LIB3189-005-P1-K1-B2
Method	BLASTX
NCBI GI	g3367520
BLAST score	622
E value	5.0e-65
Match length	148
% identity	78
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	226641
Seq. ID	LIB3189-005-P1-K1-B3
Method	BLASTX
NCBI GI	g1710780
BLAST score	502
E value	7.0e-51
Match length	132
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	226642
Seq. ID	LIB3189-005-P1-K1-B5
Method	BLASTX
NCBI GI	g3096947
BLAST score	371
E value	2.0e-35
Match length	115
% identity	63
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	226643
Seq. ID	LIB3189-005-P1-K1-B7
Method	BLASTX
NCBI GI	g1263291
BLAST score	411
E value	2.0e-40
Match length	83
% identity	95

NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	226644
Seq. ID	LIB3189-005-P1-K1-B8
Method	BLASTX
NCBI GI	g2244754
BLAST score	406
E value	1.0e-39
Match length	93
% identity	78
NCBI Description	(Z97335) heat shock transcription factor homolog [Arabidopsis thaliana]

Seq. No.	226645
Seq. ID	LIB3189-005-P1-K1-C1
Method	BLASTX
NCBI GI	g322750
BLAST score	654
E value	1.0e-68
Match length	128
% identity	98
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	226646
Seq. ID	LIB3189-005-P1-K1-C12
Method	BLASTX
NCBI GI	g4263704
BLAST score	234
E value	2.0e-19
Match length	79
% identity	53
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	226647
Seq. ID	LIB3189-005-P1-K1-C2
Method	BLASTX
NCBI GI	g2618698
BLAST score	543
E value	1.0e-55
Match length	156
% identity	70
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	226648
Seq. ID	LIB3189-005-P1-K1-C3
Method	BLASTX
NCBI GI	g133438
BLAST score	622
E value	6.0e-65
Match length	157
% identity	79
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA' CHAIN >gi_81504_pir__B29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - spinach chloroplast >gi_295120

(M55297) RNA polymerase [Spinacia oleracea]

Seq. No.	226649
Seq. ID	LIB3189-005-P1-K1-C4
Method	BLASTX
NCBI GI	g3402279
BLAST score	720
E value	2.0e-76
Match length	154
% identity	87
NCBI Description	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

Seq. No.	226650
Seq. ID	LIB3189-005-P1-K1-C8
Method	BLASTX
NCBI GI	g2244732
BLAST score	351
E value	3.0e-33
Match length	73
% identity	95
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	226651
Seq. ID	LIB3189-005-P1-K1-D12
Method	BLASTX
NCBI GI	g3335337
BLAST score	432
E value	1.0e-42
Match length	132
% identity	70
NCBI Description	(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene

Seq. No.	226652
Seq. ID	LIB3189-005-P1-K1-D6
Method	BLASTX
NCBI GI	g3212877
BLAST score	516
E value	1.0e-52
Match length	115
% identity	82
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	226653
Seq. ID	LIB3189-005-P1-K1-D8
Method	BLASTX
NCBI GI	g3122673
BLAST score	284
E value	9.0e-28
Match length	70
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	226654
Seq. ID	LIB3189-005-P1-K1-E1
Method	BLASTX
NCBI GI	g870726
BLAST score	301
E value	3.0e-27
Match length	78
% identity	78
NCBI Description	(L38260) biotin carboxylase subunit [Nicotiana tabacum] >gi_1582354_prf__2118337A Ac-CoA carboxylase:SUBUNIT=biotin carboxylase [Nicotiana tabacum]

Seq. No.	226655
Seq. ID	LIB3189-005-P1-K1-E2
Method	BLASTX
NCBI GI	g3168840
BLAST score	330
E value	7.0e-31
Match length	97
% identity	67
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	226656
Seq. ID	LIB3189-005-P1-K1-E7
Method	BLASTX
NCBI GI	g1174592
BLAST score	477
E value	4.0e-48
Match length	117
% identity	84
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	226657
Seq. ID	LIB3189-005-P1-K1-E9
Method	BLASTX
NCBI GI	g2129753
BLAST score	730
E value	1.0e-77
Match length	149
% identity	93
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	226658
Seq. ID	LIB3189-005-P1-K1-F1
Method	BLASTX
NCBI GI	g3885341
BLAST score	337
E value	1.0e-31
Match length	151
% identity	46
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	226659
Seq. ID	LIB3189-005-P1-K1-F3
Method	BLASTX
NCBI GI	g4558678
BLAST score	213
E value	5.0e-17
Match length	67
% identity	55
NCBI Description	(AC006586) unknown protein [Arabidopsis thaliana]

Seq. No.	226660
Seq. ID	LIB3189-005-P1-K1-F6
Method	BLASTX
NCBI GI	g3928142
BLAST score	710
E value	3.0e-75
Match length	154
% identity	88
NCBI Description	(AJ131045) protein phosphatase [Cicer arietinum]

Seq. No.	226661
Seq. ID	LIB3189-005-P1-K1-F8
Method	BLASTX
NCBI GI	g2129575
BLAST score	513
E value	3.0e-52
Match length	110
% identity	89
NCBI Description	DNA repair protein homolog XPBara - Arabidopsis thaliana

Seq. No.	226662
Seq. ID	LIB3189-005-P1-K1-F9
Method	BLASTX
NCBI GI	g2995198
BLAST score	189
E value	3.0e-14
Match length	103
% identity	36
NCBI Description	(Y11588) apoptosis specific protein [Homo sapiens]

Seq. No.	226663
Seq. ID	LIB3189-005-P1-K1-G10
Method	BLASTX
NCBI GI	g3540197
BLAST score	327
E value	2.0e-30
Match length	135
% identity	58
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	226664
Seq. ID	LIB3189-005-P1-K1-G2
Method	BLASTX
NCBI GI	g2335053
BLAST score	170
E value	6.0e-12
Match length	86

% identity	43
NCBI Description	(D88825) ORF3 [Aeromonas caviae]

Seq. No.	226665
Seq. ID	LIB3189-005-P1-K1-G6
Method	BLASTX
NCBI GI	g2924520
BLAST score	501
E value	6.0e-51
Match length	106
% identity	92
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	226666
Seq. ID	LIB3189-005-P1-K1-G7
Method	BLASTX
NCBI GI	g1850546
BLAST score	445
E value	2.0e-44
Match length	113
% identity	79
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	226667
Seq. ID	LIB3189-005-P1-K1-G8
Method	BLASTX
NCBI GI	g4454466
BLAST score	244
E value	9.0e-21
Match length	74
% identity	59
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	226668
Seq. ID	LIB3189-005-P1-K1-G9
Method	BLASTX
NCBI GI	g2583123
BLAST score	646
E value	1.0e-68
Match length	150
% identity	86
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	226669
Seq. ID	LIB3189-005-P1-K1-H10
Method	BLASTX
NCBI GI	g3600043
BLAST score	209
E value	1.0e-16
Match length	75
% identity	51
NCBI Description	(AF080119) No definition line found [Arabidopsis thaliana]

Seq. No. 226670

Seq. ID	LIB3189-005-P1-K1-H11
Method	BLASTX
NCBI GI	g1332579
BLAST score	497
E value	2.0e-50
Match length	101
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	226671
Seq. ID	LIB3189-005-P1-K1-H6
Method	BLASTX
NCBI GI	g2829204
BLAST score	481
E value	2.0e-48
Match length	115
% identity	85
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	226672
Seq. ID	LIB3189-005-P1-K1-H8
Method	BLASTX
NCBI GI	g1703108
BLAST score	572
E value	4.0e-59
Match length	105
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	226673
Seq. ID	LIB3189-005-P1-K1-H9
Method	BLASTX
NCBI GI	g421757
BLAST score	567
E value	9.0e-59
Match length	104
% identity	96
NCBI Description	tubulin alpha chain - Euglena gracilis

Seq. No.	226674
Seq. ID	LIB3189-006-P1-K1-A11
Method	BLASTX
NCBI GI	g3668089
BLAST score	211
E value	3.0e-17
Match length	83
% identity	51
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	226675
Seq. ID	LIB3189-006-P1-K1-A12
Method	BLASTX

NCBI GI	g3169028
BLAST score	297
E value	6.0e-27
Match length	134
% identity	49
NCBI Description	(AL023702) putative cationic amino acid transporter [Streptomyces coelicolor]

Seq. No.	226676
Seq. ID	LIB3189-006-P1-K1-A2
Method	BLASTX
NCBI GI	g1854386
BLAST score	591
E value	2.0e-61
Match length	148
% identity	76
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	226677
Seq. ID	LIB3189-006-P1-K1-A3
Method	BLASTX
NCBI GI	g1854386
BLAST score	205
E value	2.0e-17
Match length	91
% identity	57
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	226678
Seq. ID	LIB3189-006-P1-K1-A4
Method	BLASTX
NCBI GI	g232024
BLAST score	628
E value	1.0e-65
Match length	131
% identity	90
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	226679
Seq. ID	LIB3189-006-P1-K1-B1
Method	BLASTX
NCBI GI	g232024
BLAST score	262
E value	2.0e-24
Match length	80
% identity	69
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	226680
Seq. ID	LIB3189-006-P1-K1-B12
Method	BLASTX
NCBI GI	g2498982
BLAST score	226
E value	9.0e-19
Match length	83
% identity	49
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT (TAFII-31) (TAFII-32) (TAFII32) (NEURONAL CELL DEATH RELATED GENE IN NEURON -7) (DN-7) >gi_1103900 (U40188) induced upon programmed cell death in neuronally differentiated PC12 cells [Rattus norvegicus]

Seq. No.	226681
Seq. ID	LIB3189-006-P1-K1-C1
Method	BLASTX
NCBI GI	g232024
BLAST score	601
E value	1.0e-62
Match length	117
% identity	97
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	226682
Seq. ID	LIB3189-006-P1-K1-D10
Method	BLASTX
NCBI GI	g461498
BLAST score	338
E value	5.0e-32
Match length	93
% identity	72
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]

Seq. No.	226683
Seq. ID	LIB3189-006-P1-K1-D12
Method	BLASTX
NCBI GI	g4406781
BLAST score	197
E value	4.0e-15
Match length	132
% identity	45
NCBI Description	(AC006532) putative Na+/H+ antiporter [Arabidopsis thaliana]

Seq. No.	226684
Seq. ID	LIB3189-006-P1-K1-D3
Method	BLASTX

NCBI GI	g1706326
BLAST score	559
E value	1.0e-57
Match length	121
% identity	88
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_2146786_pir__S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_ (Z66543) pyruvate decarboxylase [Pisum sativum]

Seq. No.	226685
Seq. ID	LIB3189-006-P1-K1-E1
Method	BLASTX
NCBI GI	g84373
BLAST score	275
E value	1.0e-24
Match length	56
% identity	93
NCBI Description	tubulin alpha chain - Stylonychia lemnae (SGC5)

Seq. No.	226686
Seq. ID	LIB3189-006-P1-K1-E11
Method	BLASTX
NCBI GI	g2114046
BLAST score	263
E value	2.0e-23
Match length	58
% identity	86
NCBI Description	(AB002147) water channel protein [Nicotiana excelsior]

Seq. No.	226687
Seq. ID	LIB3189-006-P1-K1-E12
Method	BLASTX
NCBI GI	g3163946
BLAST score	307
E value	1.0e-28
Match length	67
% identity	85
NCBI Description	(AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No.	226688
Seq. ID	LIB3189-006-P1-K1-F1
Method	BLASTX
NCBI GI	g4335763
BLAST score	246
E value	6.0e-21
Match length	87
% identity	51
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	226689
Seq. ID	LIB3189-006-P1-K1-F10
Method	BLASTX
NCBI GI	g267069
BLAST score	170
E value	8.0e-13
Match length	49

% identity	82
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	226690
Seq. ID	LIB3189-006-P1-K1-F12
Method	BLASTX
NCBI GI	g4432841
BLAST score	341
E value	4.0e-32
Match length	138
% identity	49
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.	226691
Seq. ID	LIB3189-006-P1-K1-F6
Method	BLASTX
NCBI GI	g2911801
BLAST score	276
E value	9.0e-25
Match length	73
% identity	75
NCBI Description	(AF009565) alpha-tubulin [Gossypium hirsutum]
Seq. No.	226692
Seq. ID	LIB3189-006-P1-K1-G1
Method	BLASTX
NCBI GI	g2894612
BLAST score	391
E value	6.0e-38
Match length	110
% identity	67
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	226693
Seq. ID	LIB3189-006-P1-K1-G12
Method	BLASTX
NCBI GI	g2497743
BLAST score	153
E value	3.0e-10
Match length	56
% identity	59
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]
Seq. No.	226694
Seq. ID	LIB3189-006-P1-K1-H1
Method	BLASTX
NCBI GI	g3283409
BLAST score	147
E value	3.0e-09
Match length	60
% identity	48

NCBI Description	(AF068754) heat shock factor binding protein 1 HSBP1 [Homo sapiens] >gi_4557647_ref_NP_001528.1_pHSBP1_ heat shock factor binding protein
Seq. No.	226695
Seq. ID	LIB3189-006-P1-K1-H10
Method	BLASTX
NCBI GI	g3036804
BLAST score	195
E value	7.0e-15
Match length	67
% identity	57
NCBI Description	(AL022373) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.	226696
Seq. ID	LIB3189-006-P1-K1-H11
Method	BLASTX
NCBI GI	g755150
BLAST score	290
E value	3.0e-26
Match length	88
% identity	70
NCBI Description	(U13670) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum]
Seq. No.	226697
Seq. ID	LIB3189-006-P1-K1-H2
Method	BLASTX
NCBI GI	g3687251
BLAST score	440
E value	1.0e-43
Match length	115
% identity	74
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.	226698
Seq. ID	LIB3189-006-P1-K1-H5
Method	BLASTX
NCBI GI	g2129495
BLAST score	291
E value	1.0e-26
Match length	60
% identity	95
NCBI Description	fiber protein E6 (clone SIE6-2A) - sea-island cotton >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090 (U30508) E6 [Gossypium barbadense]
Seq. No.	226699
Seq. ID	LIB3189-006-P1-K1-H7
Method	BLASTX
NCBI GI	g1709002
BLAST score	361
E value	2.0e-34
Match length	86
% identity	81
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_1033190

(U38186) S-adenosyl methionine synthetase [Pinus banksiana]

Seq. No.	226700
Seq. ID	LIB3189-006-P1-K1-H8
Method	BLASTX
NCBI GI	g3327868
BLAST score	128
E value	2.0e-13
Match length	71
% identity	61
NCBI Description	(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana]

Seq. No.	226701
Seq. ID	LIB3189-006-P1-K1-H9
Method	BLASTX
NCBI GI	g3169182
BLAST score	212
E value	5.0e-17
Match length	42
% identity	86
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	226702
Seq. ID	LIB3189-007-P1-K1-A1
Method	BLASTX
NCBI GI	g1174592
BLAST score	441
E value	6.0e-44
Match length	82
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	226703
Seq. ID	LIB3189-007-P1-K1-A11
Method	BLASTX
NCBI GI	g4098129
BLAST score	639
E value	5.0e-67
Match length	127
% identity	95
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	226704
Seq. ID	LIB3189-007-P1-K1-A2
Method	BLASTX
NCBI GI	g2245012
BLAST score	166
E value	2.0e-11
Match length	92
% identity	40
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226705
Seq. ID	LIB3189-007-P1-K1-A6

Method	BLASTX
NCBI GI	g3420239
BLAST score	264
E value	1.0e-23
Match length	57
% identity	89
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	226706
Seq. ID	LIB3189-007-P1-K1-A7
Method	BLASTX
NCBI GI	g2995384
BLAST score	145
E value	4.0e-09
Match length	40
% identity	75
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	226707
Seq. ID	LIB3189-007-P1-K1-B1
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	8.0e-20
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	226708
Seq. ID	LIB3189-007-P1-K1-B10
Method	BLASTX
NCBI GI	g2244750
BLAST score	635
E value	1.0e-66
Match length	124
% identity	97
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	226709
Seq. ID	LIB3189-007-P1-K1-B11
Method	BLASTX
NCBI GI	g1710838
BLAST score	376
E value	3.0e-36
Match length	79
% identity	89
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_535584 (L36119) adenosylhomocysteinase [Medicago sativa]

Seq. No.	226710
Seq. ID	LIB3189-007-P1-K1-B12
Method	BLASTX
NCBI GI	g3122389

BLAST score	496
E value	3.0e-50
Match length	123
% identity	70
NCBI Description	WD-40 REPEAT PROTEIN MSI3 >gi_2394233 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	226711
Seq. ID	LIB3189-007-P1-K1-B4
Method	BLASTX
NCBI GI	g586076
BLAST score	633
E value	3.0e-66
Match length	119
% identity	97
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	226712
Seq. ID	LIB3189-007-P1-K1-B7
Method	BLASTX
NCBI GI	g481818
BLAST score	179
E value	4.0e-13
Match length	77
% identity	56
NCBI Description	coproporphyrinogen oxidase - soybean

Seq. No.	226713
Seq. ID	LIB3189-007-P1-K1-C1
Method	BLASTX
NCBI GI	g1203832
BLAST score	534
E value	1.0e-54
Match length	143
% identity	71
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	226714
Seq. ID	LIB3189-007-P1-K1-C10
Method	BLASTX
NCBI GI	g629858
BLAST score	483
E value	9.0e-49
Match length	115
% identity	81
NCBI Description	protein kinase C inhibitor - maize

Seq. No.	226715
Seq. ID	LIB3189-007-P1-K1-C2
Method	BLASTX
NCBI GI	g2244749
BLAST score	489
E value	1.0e-49

Match length	116
% identity	79
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	226716
Seq. ID	LIB3189-007-P1-K1-C3
Method	BLASTX
NCBI GI	g2564253
BLAST score	369
E value	2.0e-35
Match length	112
% identity	59
NCBI Description	(Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Hordeum vulgare]

Seq. No.	226717
Seq. ID	LIB3189-007-P1-K1-C5
Method	BLASTX
NCBI GI	g4102859
BLAST score	465
E value	9.0e-47
Match length	109
% identity	77
NCBI Description	(AF016892) cytoplasmic superoxide dismutase 1 [Populus tremuloides]

Seq. No.	226718
Seq. ID	LIB3189-007-P1-K1-C7
Method	BLASTX
NCBI GI	g2880049
BLAST score	184
E value	5.0e-15
Match length	84
% identity	58
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226719
Seq. ID	LIB3189-007-P1-K1-D9
Method	BLASTX
NCBI GI	g2129499
BLAST score	575
E value	1.0e-59
Match length	129
% identity	86
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	226720
Seq. ID	LIB3189-007-P1-K1-E10
Method	BLASTX
NCBI GI	g2244732
BLAST score	551
E value	1.0e-56
Match length	105
% identity	100
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	226721
Seq. ID	LIB3189-007-P1-K1-E11
Method	BLASTX
NCBI GI	g2673913
BLAST score	441
E value	9.0e-44
Match length	108
% identity	76
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226722
Seq. ID	LIB3189-007-P1-K1-E12
Method	BLASTX
NCBI GI	g629838
BLAST score	678
E value	2.0e-71
Match length	162
% identity	73
NCBI Description	tubulin beta-4 chain - maize >gi_416145 (L10635) beta-4 tubulin [Zea mays]

Seq. No.	226723
Seq. ID	LIB3189-007-P1-K1-E2
Method	BLASTX
NCBI GI	g4371290
BLAST score	354
E value	2.0e-33
Match length	127
% identity	54
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	226724
Seq. ID	LIB3189-007-P1-K1-E5
Method	BLASTX
NCBI GI	g3702327
BLAST score	158
E value	1.0e-10
Match length	105
% identity	46
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	226725
Seq. ID	LIB3189-007-P1-K1-E6
Method	BLASTX
NCBI GI	g3775997
BLAST score	361
E value	1.0e-34
Match length	95
% identity	76
NCBI Description	(AJ010462) RNA helicase [Arabidopsis thaliana]

Seq. No.	226726
Seq. ID	LIB3189-007-P1-K1-E8
Method	BLASTX
NCBI GI	g3334261
BLAST score	206
E value	3.0e-16

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Match length	54
% identity	63
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1655851 (U61973) metallothionein-like protein [Malus domestica]

Seq. No.	226727
Seq. ID	LIB3189-007-P1-K1-E9
Method	BLASTX
NCBI GI	g4544399
BLAST score	248
E value	3.0e-21
Match length	99
% identity	44
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	226728
Seq. ID	LIB3189-007-P1-K1-F12
Method	BLASTX
NCBI GI	g2961384
BLAST score	215
E value	3.0e-17
Match length	95
% identity	46
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	226729
Seq. ID	LIB3189-007-P1-K1-F2
Method	BLASTX
NCBI GI	g3320379
BLAST score	511
E value	5.0e-52
Match length	135
% identity	76
NCBI Description	(AF014375) putative JUN kinase activation domain binding protein [Medicago sativa]

Seq. No.	226730
Seq. ID	LIB3189-007-P1-K1-F4
Method	BLASTX
NCBI GI	g4249382
BLAST score	267
E value	2.0e-23
Match length	66
% identity	76
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	226731
Seq. ID	LIB3189-007-P1-K1-G12
Method	BLASTX
NCBI GI	g4191784
BLAST score	400
E value	6.0e-39
Match length	119

% identity	64
NCBI Description	(AC005917) putative WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	226732
Seq. ID	LIB3189-007-P1-K1-G2
Method	BLASTX
NCBI GI	g3876865
BLAST score	152
E value	6.0e-10
Match length	68
% identity	41
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	226733
Seq. ID	LIB3189-007-P1-K1-H10
Method	BLASTX
NCBI GI	g3953457
BLAST score	162
E value	5.0e-11
Match length	68
% identity	50
NCBI Description	(AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No.	226734
Seq. ID	LIB3189-007-P1-K1-H11
Method	BLASTX
NCBI GI	g3953457
BLAST score	155
E value	3.0e-10
Match length	60
% identity	58
NCBI Description	(AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No.	226735
Seq. ID	LIB3189-007-P1-K1-H12
Method	BLASTX
NCBI GI	g1346422
BLAST score	239
E value	1.0e-22
Match length	145
% identity	41
NCBI Description	SERINE PALMITOYLTRANSFERASE 2 (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2) >gi_2130481_pir__JC5183 serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) >gi_1001947 (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] >gi_2414613_emb_CAB16362_ (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe]

Seq. No.	226736
Seq. ID	LIB3189-007-P1-K1-H5
Method	BLASTX
NCBI GI	g3914368

BLAST score	158
E value	3.0e-17
Match length	78
% identity	63
NCBI Description	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) >gi_167519 (M80571) glycerol-3-phosphate acyltransferase [Cucumis sativus] >gi_444331_prf__1906380A glycerol phosphate acyltransferase [Cucumis sativus]

Seq. No.	226737
Seq. ID	LIB3189-007-P1-K1-H7
Method	BLASTX
NCBI GI	g3334115
BLAST score	550
E value	1.0e-56
Match length	119
% identity	51
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	226738
Seq. ID	LIB3189-007-P1-K1-H9
Method	BLASTX
NCBI GI	g2662343
BLAST score	395
E value	1.0e-38
Match length	82
% identity	95
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	226739
Seq. ID	LIB3189-008-P1-K1-A1
Method	BLASTX
NCBI GI	g3915847
BLAST score	204
E value	4.0e-16
Match length	71
% identity	70
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	226740
Seq. ID	LIB3189-008-P1-K1-A10
Method	BLASTX
NCBI GI	g1916807
BLAST score	284
E value	2.0e-25
Match length	106
% identity	65
NCBI Description	(U81162) auxin-binding protein [Prunus persica]

Seq. No.	226741
Seq. ID	LIB3189-008-P1-K1-A12
Method	BLASTX
NCBI GI	g4490332

BLAST score	208
E value	1.0e-16
Match length	79
% identity	56
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	226742
Seq. ID	LIB3189-008-P1-K1-A3
Method	BLASTX
NCBI GI	g3273828
BLAST score	304
E value	1.0e-27
Match length	118
% identity	58
NCBI Description	(AF068686) nodule-enhanced malate dehydrogenase [Glycine max]

Seq. No.	226743
Seq. ID	LIB3189-008-P1-K1-A6
Method	BLASTX
NCBI GI	g3420239
BLAST score	208
E value	4.0e-17
Match length	50
% identity	80
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	226744
Seq. ID	LIB3189-008-P1-K1-A8
Method	BLASTX
NCBI GI	g4467146
BLAST score	365
E value	5.0e-35
Match length	107
% identity	62
NCBI Description	(AL035540) galactosidase like protein [Arabidopsis thaliana]

Seq. No.	226745
Seq. ID	LIB3189-008-P1-K1-B1
Method	BLASTX
NCBI GI	g3128176
BLAST score	310
E value	2.0e-28
Match length	101
% identity	59
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	226746
Seq. ID	LIB3189-008-P1-K1-B3
Method	BLASTX
NCBI GI	g4204300
BLAST score	160
E value	7.0e-11
Match length	62
% identity	56
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	226747
Seq. ID	LIB3189-008-P1-K1-B5
Method	BLASTX
NCBI GI	g4406819
BLAST score	190
E value	2.0e-14
Match length	98
% identity	48
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	226748
Seq. ID	LIB3189-008-P1-K1-B6
Method	BLASTX
NCBI GI	g1518540
BLAST score	519
E value	7.0e-65
Match length	143
% identity	93
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	226749
Seq. ID	LIB3189-008-P1-K1-B8
Method	BLASTX
NCBI GI	g3551131
BLAST score	153
E value	2.0e-12
Match length	56
% identity	64
NCBI Description	(AB012044) plasma membrane aquaporin (PAQ1) [Raphanus sativus]

Seq. No.	226750
Seq. ID	LIB3189-008-P1-K1-C1
Method	BLASTX
NCBI GI	g2529665
BLAST score	646
E value	8.0e-68
Match length	136
% identity	93
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	226751
Seq. ID	LIB3189-008-P1-K1-C10
Method	BLASTX
NCBI GI	g4455208
BLAST score	199
E value	1.0e-15
Match length	71
% identity	54
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	226752
Seq. ID	LIB3189-008-P1-K1-C11
Method	BLASTX
NCBI GI	g2088649

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BLAST score	342
E value	3.0e-32
Match length	107
% identity	63
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	226753
Seq. ID	LIB3189-008-P1-K1-C2
Method	BLASTX
NCBI GI	g2078350
BLAST score	157
E value	1.0e-10
Match length	35
% identity	83
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	226754
Seq. ID	LIB3189-008-P1-K1-C3
Method	BLASTX
NCBI GI	g1421730
BLAST score	540
E value	2.0e-55
Match length	138
% identity	78
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	226755
Seq. ID	LIB3189-008-P1-K1-C4
Method	BLASTX
NCBI GI	g4580460
BLAST score	311
E value	1.0e-28
Match length	93
% identity	72
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	226756
Seq. ID	LIB3189-008-P1-K1-C6
Method	BLASTX
NCBI GI	g3004564
BLAST score	239
E value	5.0e-20
Match length	88
% identity	56
NCBI Description	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	226757
Seq. ID	LIB3189-008-P1-K1-C9
Method	BLASTX
NCBI GI	g4467133
BLAST score	398
E value	1.0e-38
Match length	120
% identity	66
NCBI Description	(AL035540) geranylgeranyl pyrophosphate synthase-related

protein [Arabidopsis thaliana]

Seq. No.	226758
Seq. ID	LIB3189-008-P1-K1-D1
Method	BLASTX
NCBI GI	g3080428
BLAST score	341
E value	5.0e-32
Match length	94
% identity	68
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	226759
Seq. ID	LIB3189-008-P1-K1-D2
Method	BLASTX
NCBI GI	g3080428
BLAST score	144
E value	4.0e-09
Match length	66
% identity	48
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	226760
Seq. ID	LIB3189-008-P1-K1-D5
Method	BLASTX
NCBI GI	g3746069
BLAST score	222
E value	4.0e-18
Match length	129
% identity	37
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	226761
Seq. ID	LIB3189-008-P1-K1-D7
Method	BLASTX
NCBI GI	g541951
BLAST score	437
E value	3.0e-43
Match length	133
% identity	65
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	226762
Seq. ID	LIB3189-008-P1-K1-D8
Method	BLASTX
NCBI GI	g1345882
BLAST score	141
E value	3.0e-09
Match length	30
% identity	87
NCBI Description	CYTOCHROME B5

Seq. No.	226763
Seq. ID	LIB3189-008-P1-K1-D9
Method	BLASTX

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NCBI GI	g3150402
BLAST score	677
E value	2.0e-71
Match length	147
% identity	92
NCBI Description	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]

Seq. No.	226764
Seq. ID	LIB3189-008-P1-K1-E1
Method	BLASTX
NCBI GI	g1173055
BLAST score	509
E value	9.0e-52
Match length	105
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No.	226765
Seq. ID	LIB3189-008-P1-K1-E10
Method	BLASTX
NCBI GI	g3355480
BLAST score	328
E value	1.0e-30
Match length	97
% identity	64
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	226766
Seq. ID	LIB3189-008-P1-K1-E4
Method	BLASTX
NCBI GI	g2129499
BLAST score	457
E value	1.0e-45
Match length	98
% identity	84
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	226767
Seq. ID	LIB3189-008-P1-K1-E8
Method	BLASTX
NCBI GI	g1449179
BLAST score	327
E value	8.0e-33
Match length	87
% identity	83
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	226768
Seq. ID	LIB3189-008-P1-K1-F1
Method	BLASTX

NCBI GI	g121953
BLAST score	175
E value	1.0e-12
Match length	43
% identity	81
NCBI Description	HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >gi_20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum]

Seq. No.	226769
Seq. ID	LIB3189-008-P1-K1-F10
Method	BLASTX
NCBI GI	g3608171
BLAST score	367
E value	3.0e-35
Match length	93
% identity	78
NCBI Description	(D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Seq. No.	226770
Seq. ID	LIB3189-008-P1-K1-F11
Method	BLASTX
NCBI GI	g2661840
BLAST score	424
E value	7.0e-42
Match length	124
% identity	64
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	226771
Seq. ID	LIB3189-008-P1-K1-F12
Method	BLASTX
NCBI GI	g3420055
BLAST score	560
E value	9.0e-58
Match length	138
% identity	80
NCBI Description	(AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No.	226772
Seq. ID	LIB3189-008-P1-K1-F2
Method	BLASTX
NCBI GI	g3355470
BLAST score	255
E value	1.0e-34
Match length	98
% identity	73
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	226773
Seq. ID	LIB3189-008-P1-K1-F4
Method	BLASTX
NCBI GI	g267069
BLAST score	586
E value	9.0e-61

Match length	110
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	226774
Seq. ID	LIB3189-008-P1-K1-G1
Method	BLASTX
NCBI GI	g2829204
BLAST score	375
E value	3.0e-36
Match length	94
% identity	83
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	226775
Seq. ID	LIB3189-008-P1-K1-G12
Method	BLASTX
NCBI GI	g2062167
BLAST score	452
E value	4.0e-45
Match length	97
% identity	86
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	226776
Seq. ID	LIB3189-008-P1-K1-G3
Method	BLASTX
NCBI GI	g1223922
BLAST score	496
E value	3.0e-50
Match length	117
% identity	74
NCBI Description	(U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata]

Seq. No.	226777
Seq. ID	LIB3189-008-P1-K1-G4
Method	BLASTX
NCBI GI	g3914437
BLAST score	176
E value	3.0e-13
Match length	50
% identity	66
NCBI Description	PROFILIN >gi_3183706_emb_CAA75312_ (Y15042) profilin [Hevea brasiliensis]

Seq. No.	226778
Seq. ID	LIB3189-008-P1-K1-G6
Method	BLASTX
NCBI GI	g2062167
BLAST score	213
E value	2.0e-17

Match length	44
% identity	86
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	226779
Seq. ID	LIB3189-008-P1-K1-G7
Method	BLASTX
NCBI GI	g3360289
BLAST score	161
E value	3.0e-11
Match length	64
% identity	45
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	226780
Seq. ID	LIB3189-008-P1-K1-H1
Method	BLASTX
NCBI GI	g4539417
BLAST score	475
E value	7.0e-48
Match length	107
% identity	80
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	226781
Seq. ID	LIB3189-008-P1-K1-H3
Method	BLASTX
NCBI GI	g3986110
BLAST score	367
E value	1.0e-35
Match length	78
% identity	90
NCBI Description	(AB012716) heat shock protein 70 cognate [Salix gilgiana]

Seq. No.	226782
Seq. ID	LIB3189-008-P1-K1-H7
Method	BLASTX
NCBI GI	g3915873
BLAST score	497
E value	1.0e-50
Match length	99
% identity	93
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) (NODULIN-100) >gi_2606081 (AF030231) sucrose synthase [Glycine max]

Seq. No.	226783
Seq. ID	LIB3189-008-P1-K1-H8
Method	BLASTX
NCBI GI	g4098129
BLAST score	403
E value	2.0e-39
Match length	86
% identity	88
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	226784
Seq. ID	LIB3189-008-P1-K1-H9
Method	BLASTX
NCBI GI	g4262226
BLAST score	139
E value	1.0e-08
Match length	92
% identity	45
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	226785
Seq. ID	LIB3189-010-P1-K1-A7
Method	BLASTX
NCBI GI	g4314378
BLAST score	147
E value	3.0e-09
Match length	81
% identity	47
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	226786
Seq. ID	LIB3189-010-P1-K1-B11
Method	BLASTX
NCBI GI	g3786005
BLAST score	255
E value	3.0e-22
Match length	73
% identity	42
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	226787
Seq. ID	LIB3189-010-P1-K1-B12
Method	BLASTX
NCBI GI	g4126399
BLAST score	456
E value	1.0e-45
Match length	111
% identity	81
NCBI Description	(AB011794) chalcone isomerase [Citrus sinensis]

Seq. No.	226788
Seq. ID	LIB3189-010-P1-K1-B9
Method	BLASTX
NCBI GI	g3786005
BLAST score	374
E value	5.0e-36
Match length	100
% identity	42
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	226789
Seq. ID	LIB3189-010-P1-K1-C10
Method	BLASTX
NCBI GI	g3176098

BLAST score 356
E value 7.0e-34
Match length 123
% identity 60
NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No. 226790
Seq. ID LIB3189-010-P1-K1-C12
Method BLASTX
NCBI GI g2129473
BLAST score 250
E value 2.0e-21
Match length 91
% identity 52
NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 226791
Seq. ID LIB3189-010-P1-K1-C2
Method BLASTX
NCBI GI g3023847
BLAST score 489
E value 1.0e-60
Match length 131
% identity 34
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No. 226792
Seq. ID LIB3189-010-P1-K1-C7
Method BLASTX
NCBI GI g2506139
BLAST score 501
E value 9.0e-51
Match length 120
% identity 83
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No. 226793
Seq. ID LIB3189-010-P1-K1-C9
Method BLASTX
NCBI GI g3023847
BLAST score 247
E value 1.0e-21
Match length 62
% identity 81
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No. 226794
Seq. ID LIB3189-010-P1-K1-D2
Method BLASTX
NCBI GI g1619602

BLAST score	327
E value	1.0e-30
Match length	95
% identity	36
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	226795
Seq. ID	LIB3189-010-P1-K1-D3
Method	BLASTX
NCBI GI	g2651310
BLAST score	202
E value	2.0e-16
Match length	57
% identity	61
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	226796
Seq. ID	LIB3189-010-P1-K1-D5
Method	BLASTX
NCBI GI	g3970652
BLAST score	513
E value	3.0e-52
Match length	129
% identity	76
NCBI Description	(X77499) amino acid permease [Arabidopsis thaliana]

Seq. No.	226797
Seq. ID	LIB3189-010-P1-K1-D8
Method	BLASTX
NCBI GI	g4335774
BLAST score	193
E value	1.0e-14
Match length	116
% identity	42
NCBI Description	(AC006284) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	226798
Seq. ID	LIB3189-010-P1-K1-E10
Method	BLASTX
NCBI GI	g2811278
BLAST score	183
E value	4.0e-14
Match length	44
% identity	77
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	226799
Seq. ID	LIB3189-010-P1-K1-E11
Method	BLASTX
NCBI GI	g3063396
BLAST score	605
E value	5.0e-63
Match length	132
% identity	85
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	226800
Seq. ID	LIB3189-010-P1-K1-E12
Method	BLASTX
NCBI GI	g100225
BLAST score	381
E value	1.0e-36
Match length	101
% identity	66
NCBI Description	heat shock transcription factor 8 - tomato >gi_19260_emb_CAA47868_ (X67599) heat stress transcription factor 8 [Lycopersicon esculentum]

Seq. No.	226801
Seq. ID	LIB3189-010-P1-K1-E2
Method	BLASTX
NCBI GI	g70639
BLAST score	381
E value	6.0e-37
Match length	95
% identity	21
NCBI Description	ubiquitin precursor - Neurospora crassa >gi_295930_emb_CAA31530_ (X13140) ubiquitin [Neurospora crassa]

Seq. No.	226802
Seq. ID	LIB3189-010-P1-K1-E7
Method	BLASTX
NCBI GI	g2369714
BLAST score	715
E value	7.0e-76
Match length	152
% identity	93
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	226803
Seq. ID	LIB3189-010-P1-K1-E8
Method	BLASTX
NCBI GI	g115492
BLAST score	640
E value	4.0e-67
Match length	125
% identity	56
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	226804
Seq. ID	LIB3189-010-P1-K1-F10
Method	BLASTX
NCBI GI	g1353352
BLAST score	191
E value	4.0e-15
Match length	62
% identity	65
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	226805
Seq. ID	LIB3189-010-P1-K1-F11
Method	BLASTX
NCBI GI	g4510430
BLAST score	589
E value	4.0e-61
Match length	122
% identity	88
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	226806
Seq. ID	LIB3189-010-P1-K1-F2
Method	BLASTX
NCBI GI	g2760320
BLAST score	200
E value	1.0e-18
Match length	86
% identity	66
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.	226807
Seq. ID	LIB3189-010-P1-K1-F6
Method	BLASTX
NCBI GI	g3075394
BLAST score	456
E value	4.0e-50
Match length	150
% identity	71
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	226808
Seq. ID	LIB3189-010-P1-K1-F8
Method	BLASTX
NCBI GI	g4139264
BLAST score	391
E value	5.0e-38
Match length	88
% identity	85
NCBI Description	(AF111812) actin [Brassica napus]

Seq. No.	226809
Seq. ID	LIB3189-010-P1-K1-F9
Method	BLASTX
NCBI GI	g2791900
BLAST score	557
E value	2.0e-57
Match length	140
% identity	71
NCBI Description	(AJ000057) PP7 [Arabidopsis thaliana]

Seq. No.	226810
Seq. ID	LIB3189-010-P1-K1-G1
Method	BLASTX
NCBI GI	g3033380

BLAST score	415
E value	6.0e-43
Match length	127
% identity	66
NCBI Description	(AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No.	226811
Seq. ID	LIB3189-010-P1-K1-G11
Method	BLASTX
NCBI GI	g3309269
BLAST score	496
E value	3.0e-50
Match length	106
% identity	90
NCBI Description	(AF074940) ferric leghemoglobin reductase-2 precursor [Glycine max]

Seq. No.	226812
Seq. ID	LIB3189-010-P1-K1-G12
Method	BLASTX
NCBI GI	g3928150
BLAST score	212
E value	5.0e-17
Match length	66
% identity	61
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	226813
Seq. ID	LIB3189-010-P1-K1-G2
Method	BLASTX
NCBI GI	g2464905
BLAST score	298
E value	5.0e-27
Match length	116
% identity	54
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	226814
Seq. ID	LIB3189-010-P1-K1-G3
Method	BLASTX
NCBI GI	g464846
BLAST score	507
E value	2.0e-51
Match length	102
% identity	91
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	226815
Seq. ID	LIB3189-010-P1-K1-G5
Method	BLASTX
NCBI GI	g2244792
BLAST score	235
E value	9.0e-20
Match length	68

% identity	71
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	226816
Seq. ID	LIB3189-010-P1-K1-G6
Method	BLASTX
NCBI GI	g2760326
BLAST score	320
E value	1.0e-29
Match length	151
% identity	50
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	226817
Seq. ID	LIB3189-010-P1-K1-G8
Method	BLASTX
NCBI GI	g4262250
BLAST score	381
E value	1.0e-36
Match length	85
% identity	85
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	226818
Seq. ID	LIB3189-010-P1-K1-G9
Method	BLASTX
NCBI GI	g1173218
BLAST score	387
E value	1.0e-37
Match length	77
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	226819
Seq. ID	LIB3189-010-P1-K1-H1
Method	BLASTX
NCBI GI	g2688839
BLAST score	373
E value	9.0e-36
Match length	88
% identity	80
NCBI Description	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]

Seq. No.	226820
Seq. ID	LIB3189-010-P1-K1-H10
Method	BLASTX
NCBI GI	g4468979
BLAST score	500
E value	1.0e-50
Match length	123
% identity	79
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 226821

Seq. ID	LIB3189-010-P1-K1-H2
Method	BLASTX
NCBI GI	g4416307
BLAST score	179
E value	1.0e-18
Match length	91
% identity	55
NCBI Description	(AF105716) hypothetical protein [Zea mays]

Seq. No.	226822
Seq. ID	LIB3189-010-P1-K1-H3
Method	BLASTX
NCBI GI	g4204300
BLAST score	214
E value	4.0e-17
Match length	81
% identity	52
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	226823
Seq. ID	LIB3189-010-P1-K1-H4
Method	BLASTX
NCBI GI	g3757522
BLAST score	291
E value	3.0e-26
Match length	129
% identity	53
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	226824
Seq. ID	LIB3189-010-P1-K1-H8
Method	BLASTX
NCBI GI	g3618214
BLAST score	171
E value	4.0e-12
Match length	136
% identity	34
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	226825
Seq. ID	LIB3189-011-P1-K1-A1
Method	BLASTX
NCBI GI	g4191789
BLAST score	197
E value	2.0e-15
Match length	106
% identity	45
NCBI Description	(AC005917) putative transmembrane transport protein [Arabidopsis thaliana]

Seq. No.	226826
Seq. ID	LIB3189-011-P1-K1-A10
Method	BLASTX
NCBI GI	g3047085
BLAST score	154
E value	2.0e-10

Match length	53
% identity	55
NCBI Description	(AF058914) No definition line found [Arabidopsis thaliana]

Seq. No.	226827
Seq. ID	LIB3189-011-P1-K1-A11
Method	BLASTX
NCBI GI	g267069
BLAST score	329
E value	5.0e-31
Match length	61
% identity	95
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	226828
Seq. ID	LIB3189-011-P1-K1-A12
Method	BLASTX
NCBI GI	g3914394
BLAST score	720
E value	2.0e-76
Match length	150
% identity	90
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	226829
Seq. ID	LIB3189-011-P1-K1-A2
Method	BLASTX
NCBI GI	g2829893
BLAST score	311
E value	8.0e-29
Match length	71
% identity	87
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	226830
Seq. ID	LIB3189-011-P1-K1-A3
Method	BLASTX
NCBI GI	g4530585
BLAST score	357
E value	7.0e-34
Match length	85
% identity	74
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	226831
Seq. ID	LIB3189-011-P1-K1-A5
Method	BLASTX
NCBI GI	g4455129
BLAST score	194
E value	9.0e-15

Match length	85
% identity	42
NCBI Description	(AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]

Seq. No.	226832
Seq. ID	LIB3189-011-P1-K1-A6
Method	BLASTX
NCBI GI	g2245012
BLAST score	179
E value	5.0e-13
Match length	62
% identity	58
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226833
Seq. ID	LIB3189-011-P1-K1-A7
Method	BLASTX
NCBI GI	g2130073
BLAST score	252
E value	5.0e-22
Match length	65
% identity	78
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	226834
Seq. ID	LIB3189-011-P1-K1-A8
Method	BLASTX
NCBI GI	g4490317
BLAST score	172
E value	2.0e-12
Match length	62
% identity	52
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	226835
Seq. ID	LIB3189-011-P1-K1-A9
Method	BLASTX
NCBI GI	g2244841
BLAST score	255
E value	4.0e-22
Match length	92
% identity	53
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226836
Seq. ID	LIB3189-011-P1-K1-B1
Method	BLASTX
NCBI GI	g228316
BLAST score	185
E value	2.0e-14
Match length	57
% identity	58
NCBI Description	albumin [Theobroma cacao]

Seq. No.	226837
Seq. ID	LIB3189-011-P1-K1-B10
Method	BLASTX
NCBI GI	g3914832
BLAST score	214
E value	3.0e-17
Match length	59
% identity	66
NCBI Description	DNA-DIRECTED RNA POLYMERASE MITOCHONDRIAL PRECURSOR >gi_1742971_emb_CAA70583_ (Y09432) mitochondrial singel subunit DNA-directed RNA polymerase [Arabidopsis thaliana] >gi_2330566_emb_CAA70210_ (Y09006) mitochondrial single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No.	226838
Seq. ID	LIB3189-011-P1-K1-B12
Method	BLASTX
NCBI GI	g2129840
BLAST score	378
E value	2.0e-36
Match length	113
% identity	65
NCBI Description	nucleosome assembly protein 1 - soybean >gi_1161252 (L38856) nucleosome assembly protein 1 [Glycine max]

Seq. No.	226839
Seq. ID	LIB3189-011-P1-K1-B2
Method	BLASTX
NCBI GI	g4006878
BLAST score	391
E value	4.0e-38
Match length	97
% identity	70
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	226840
Seq. ID	LIB3189-011-P1-K1-B6
Method	BLASTX
NCBI GI	g4406816
BLAST score	589
E value	3.0e-61
Match length	119
% identity	91
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	226841
Seq. ID	LIB3189-011-P1-K1-B7
Method	BLASTX
NCBI GI	g1199806
BLAST score	176
E value	5.0e-13
Match length	52
% identity	65
NCBI Description	(X95663) elongation factor 1 alpha [Brugia pahangi]

Seq. No. 226842

Seq. ID	LIB3189-011-P1-K1-C3
Method	BLASTX
NCBI GI	g4098129
BLAST score	383
E value	4.0e-37
Match length	89
% identity	82
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	226843
Seq. ID	LIB3189-011-P1-K1-C4
Method	BLASTX
NCBI GI	g2827715
BLAST score	498
E value	2.0e-50
Match length	144
% identity	7
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	226844
Seq. ID	LIB3189-011-P1-K1-C5
Method	BLASTX
NCBI GI	g1351408
BLAST score	339
E value	8.0e-32
Match length	106
% identity	67
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	226845
Seq. ID	LIB3189-011-P1-K1-C6
Method	BLASTX
NCBI GI	g2911073
BLAST score	347
E value	3.0e-33
Match length	82
% identity	84
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	226846
Seq. ID	LIB3189-011-P1-K1-D1
Method	BLASTX
NCBI GI	g3142289
BLAST score	151
E value	5.0e-10
Match length	44
% identity	68
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	226847
Seq. ID	LIB3189-011-P1-K1-D2

Method	BLASTX
NCBI GI	g3914685
BLAST score	292
E value	6.0e-27
Match length	68
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No.	226848
Seq. ID	LIB3189-011-P1-K1-D4
Method	BLASTX
NCBI GI	g126770
BLAST score	466
E value	1.0e-48
Match length	105
% identity	84
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate synthase (EC 4.1.3.2) - upland cotton >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567) [Gossypium hirsutum]

Seq. No.	226849
Seq. ID	LIB3189-011-P1-K1-E10
Method	BLASTX
NCBI GI	g2935298
BLAST score	653
E value	2.0e-68
Match length	145
% identity	94
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	226850
Seq. ID	LIB3189-011-P1-K1-E2
Method	BLASTX
NCBI GI	g2244838
BLAST score	145
E value	5.0e-09
Match length	37
% identity	73
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226851
Seq. ID	LIB3189-011-P1-K1-E5
Method	BLASTX
NCBI GI	g3808101
BLAST score	430
E value	2.0e-42
Match length	128
% identity	68
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	226852
Seq. ID	LIB3189-011-P1-K1-E6
Method	BLASTX
NCBI GI	g4539305

BLAST score	403
E value	8.0e-45
Match length	135
% identity	62
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	226853
Seq. ID	LIB3189-011-P1-K1-E7
Method	BLASTX
NCBI GI	g2980781
BLAST score	184
E value	1.0e-13
Match length	53
% identity	58
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	226854
Seq. ID	LIB3189-011-P1-K1-F3
Method	BLASTX
NCBI GI	g730645
BLAST score	592
E value	2.0e-61
Match length	133
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	226855
Seq. ID	LIB3189-011-P1-K1-F8
Method	BLASTX
NCBI GI	g3461845
BLAST score	195
E value	6.0e-15
Match length	74
% identity	54
NCBI Description	(AC005315) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226856
Seq. ID	LIB3189-011-P1-K1-F9
Method	BLASTX
NCBI GI	g4322940
BLAST score	350
E value	4.0e-33
Match length	109
% identity	37
NCBI Description	(AF096299) DNA-binding protein 2 [Nicotiana tabacum]

Seq. No.	226857
Seq. ID	LIB3189-011-P1-K1-G1
Method	BLASTX
NCBI GI	g3687243

BLAST score	124
E value	1.0e-12
Match length	55
% identity	78
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	226858
Seq. ID	LIB3189-011-P1-K1-G10
Method	BLASTX
NCBI GI	g1703091
BLAST score	197
E value	2.0e-15
Match length	50
% identity	80
NCBI Description	ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP) (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1) >gi_903689 (L23574) acyl carrier protein precursor [Arabidopsis thaliana] >gi_3341682 (AC003672) acyl carrier protein [Arabidopsis thaliana]

Seq. No.	226859
Seq. ID	LIB3189-011-P1-K1-G12
Method	BLASTX
NCBI GI	g3928083
BLAST score	627
E value	1.0e-65
Match length	151
% identity	76
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	226860
Seq. ID	LIB3189-011-P1-K1-G2
Method	BLASTX
NCBI GI	g3894099
BLAST score	538
E value	4.0e-55
Match length	118
% identity	89
NCBI Description	(AJ012750) MCM3 protein [Pisum sativum]

Seq. No.	226861
Seq. ID	LIB3189-011-P1-K1-G3
Method	BLASTX
NCBI GI	g529353
BLAST score	169
E value	9.0e-12
Match length	94
% identity	45
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	226862
Seq. ID	LIB3189-011-P1-K1-G4
Method	BLASTX
NCBI GI	g2078350
BLAST score	223
E value	3.0e-18

Match length	50
% identity	82
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	226863
Seq. ID	LIB3189-011-P1-K1-G5
Method	BLASTX
NCBI GI	g2829204
BLAST score	512
E value	4.0e-52
Match length	120
% identity	86
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	226864
Seq. ID	LIB3189-011-P1-K1-G7
Method	BLASTX
NCBI GI	g167367
BLAST score	328
E value	9.0e-31
Match length	87
% identity	75
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	226865
Seq. ID	LIB3189-011-P1-K1-G8
Method	BLASTX
NCBI GI	g730536
BLAST score	103
E value	2.0e-11
Match length	72
% identity	64
NCBI Description	60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal protein subunit L17 [Nicotiana tabacum]

Seq. No.	226866
Seq. ID	LIB3189-011-P1-K1-G9
Method	BLASTX
NCBI GI	g2764806
BLAST score	189
E value	1.0e-14
Match length	45
% identity	71
NCBI Description	(X78548) epoxide hydrolase [Glycine max]

Seq. No.	226867
Seq. ID	LIB3189-011-P1-K1-H2
Method	BLASTX
NCBI GI	g2497743
BLAST score	174
E value	1.0e-12
Match length	57
% identity	60
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]

[Gossypium hirsutum]

Seq. No.	226868
Seq. ID	LIB3189-011-P1-K1-H4
Method	BLASTX
NCBI GI	g3694811
BLAST score	175
E value	7.0e-13
Match length	36
% identity	86
NCBI Description	(AF060481) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]

Seq. No.	226869
Seq. ID	LIB3189-011-P1-K1-H6
Method	BLASTX
NCBI GI	g4432839
BLAST score	296
E value	5.0e-27
Match length	59
% identity	52
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	226870
Seq. ID	LIB3189-012-P1-K1-A6
Method	BLASTX
NCBI GI	g2388885
BLAST score	137
E value	1.0e-08
Match length	51
% identity	57
NCBI Description	(Y14762) glutathione peroxidase [Lycopersicon esculentum]

Seq. No.	226871
Seq. ID	LIB3189-012-P1-K1-A7
Method	BLASTX
NCBI GI	g3559814
BLAST score	185
E value	8.0e-14
Match length	90
% identity	50
NCBI Description	(Y15781) transketolase 1 [Capsicum annuum]

Seq. No.	226872
Seq. ID	LIB3189-012-P1-K1-A9
Method	BLASTX
NCBI GI	g4406780
BLAST score	249
E value	1.0e-21
Match length	73
% identity	66
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	226873
Seq. ID	LIB3189-012-P1-K1-B1
Method	BLASTX

NCBI GI	g2149640
BLAST score	477
E value	5.0e-48
Match length	114
% identity	83
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	226874
Seq. ID	LIB3189-012-P1-K1-B2
Method	BLASTX
NCBI GI	g1171035
BLAST score	161
E value	4.0e-11
Match length	43
% identity	60
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504 >gi_1086021_pir__S48038 metallothionein-like protein - kiwi fruit >gi_450245 (L27813) metallothionein-like protein [Actinidia deliciosa]

Seq. No.	226875
Seq. ID	LIB3189-012-P1-K1-C8
Method	BLASTX
NCBI GI	g543905
BLAST score	503
E value	3.0e-51
Match length	94
% identity	94
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	226876
Seq. ID	LIB3189-012-P1-K1-C9
Method	BLASTX
NCBI GI	g312179
BLAST score	570
E value	7.0e-59
Match length	135
% identity	81
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	226877
Seq. ID	LIB3189-012-P1-K1-D1
Method	BLASTX
NCBI GI	g2435511
BLAST score	255
E value	5.0e-22
Match length	93
% identity	56
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	226878

Seq. ID	LIB3189-012-P1-K1-D12
Method	BLASTX
NCBI GI	g3894183
BLAST score	256
E value	5.0e-22
Match length	141
% identity	30
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	226879
Seq. ID	LIB3189-012-P1-K1-D4
Method	BLASTX
NCBI GI	g3059131
BLAST score	260
E value	8.0e-27
Match length	118
% identity	53
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	226880
Seq. ID	LIB3189-012-P1-K1-D7
Method	BLASTX
NCBI GI	g126896
BLAST score	191
E value	5.0e-15
Match length	43
% identity	91
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - watermelon >gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27 to 320) [Citrullus lanatus]

Seq. No.	226881
Seq. ID	LIB3189-012-P1-K1-D8
Method	BLASTX
NCBI GI	g120669
BLAST score	363
E value	4.0e-35
Match length	70
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	226882
Seq. ID	LIB3189-012-P1-K1-D9
Method	BLASTX
NCBI GI	g462013
BLAST score	468
E value	6.0e-47
Match length	135
% identity	73
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar

periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	226883
Seq. ID	LIB3189-012-P1-K1-E11
Method	BLASTX
NCBI GI	g3643603
BLAST score	555
E value	3.0e-57
Match length	127
% identity	84
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	226884
Seq. ID	LIB3189-012-P1-K1-E3
Method	BLASTX
NCBI GI	g3023713
BLAST score	207
E value	7.0e-17
Match length	52
% identity	85
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372 (U09450) enolase [Oryza sativa]

Seq. No.	226885
Seq. ID	LIB3189-012-P1-K1-E4
Method	BLASTX
NCBI GI	g136057
BLAST score	185
E value	2.0e-14
Match length	38
% identity	89
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	226886
Seq. ID	LIB3189-012-P1-K1-E6
Method	BLASTX
NCBI GI	g4204300
BLAST score	354
E value	1.0e-33
Match length	104
% identity	63
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	226887
Seq. ID	LIB3189-012-P1-K1-E7
Method	BLASTX
NCBI GI	g4105696
BLAST score	523
E value	9.0e-54
Match length	127
% identity	86
NCBI Description	(AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No.	226888
Seq. ID	LIB3189-012-P1-K1-F1
Method	BLASTX
NCBI GI	g3024629
BLAST score	189
E value	3.0e-14
Match length	134
% identity	31
NCBI Description	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA) >gi_423252_pir__S32369 gamma-SNAP protein - bovine >gi_298669_bbs_127528 gamma soluble NSF attachment protein, gamma SNAP=N-ethyl-maleimide-sensitive fusion protein attachment protein [cattle, brain, Peptide, 328 aa] >gi_445846_prf__1910317C NSF attachment protein (SNAP):ISOTYPE=gamma [Bos taurus]

Seq. No.	226889
Seq. ID	LIB3189-012-P1-K1-F10
Method	BLASTX
NCBI GI	g2780365
BLAST score	138
E value	1.0e-09
Match length	79
% identity	51
NCBI Description	(AB007693) Elongin C [Drosophila melanogaster]

Seq. No.	226890
Seq. ID	LIB3189-012-P1-K1-F12
Method	BLASTX
NCBI GI	g1346675
BLAST score	628
E value	1.0e-65
Match length	132
% identity	89
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) >gi_499112 (U10283) nucleoside diphosphate kinase [Flaveria bidentis]

Seq. No.	226891
Seq. ID	LIB3189-012-P1-K1-F4
Method	BLASTX
NCBI GI	g3128228
BLAST score	307
E value	3.0e-28
Match length	69
% identity	86
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	226892
Seq. ID	LIB3189-012-P1-K1-F5
Method	BLASTX
NCBI GI	g3024629
BLAST score	188
E value	5.0e-14

Match length	133
% identity	32
NCBI Description	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA) >gi_423252_pir__S32369 gamma-SNAP protein - bovine >gi_298669_bbs_127528 gamma soluble NSF attachment protein, gamma SNAP=N-ethyl-maleimide-sensitive fusion protein attachment protein [cattle, brain, Peptide, 328 aa] >gi_445846_prf__1910317C NSF attachment protein (SNAP):ISOTYPE=gamma [Bos taurus]

Seq. No.	226893
Seq. ID	LIB3189-012-P1-K1-F6
Method	BLASTX
NCBI GI	g3980396
BLAST score	460
E value	4.0e-46
Match length	111
% identity	77
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	226894
Seq. ID	LIB3189-012-P1-K1-G1
Method	BLASTX
NCBI GI	g2507455
BLAST score	435
E value	4.0e-43
Match length	102
% identity	86
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	226895
Seq. ID	LIB3189-012-P1-K1-G11
Method	BLASTX
NCBI GI	g1915974
BLAST score	631
E value	5.0e-66
Match length	149
% identity	81
NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi_2102693 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No.	226896
Seq. ID	LIB3189-012-P1-K1-G2
Method	BLASTX
NCBI GI	g2662343
BLAST score	614
E value	5.0e-64
Match length	122
% identity	97
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	226897

Seq. ID	LIB3189-012-P1-K1-G3
Method	BLASTX
NCBI GI	g130720
BLAST score	279
E value	9.0e-25
Match length	126
% identity	44
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi_500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	226898
Seq. ID	LIB3189-012-P1-K1-G8
Method	BLASTX
NCBI GI	g2583123
BLAST score	423
E value	2.0e-42
Match length	128
% identity	80
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	226899
Seq. ID	LIB3189-012-P1-K1-H10
Method	BLASTX
NCBI GI	g2829204
BLAST score	369
E value	2.0e-35
Match length	70
% identity	99
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	226900
Seq. ID	LIB3189-012-P1-K1-H11
Method	BLASTX
NCBI GI	g2500443
BLAST score	159
E value	7.0e-11
Match length	32
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_1762931 (U66262) ribosomal protein S14 [Nicotiana tabacum]

Seq. No.	226901
Seq. ID	LIB3189-012-P1-K1-H2
Method	BLASTX
NCBI GI	g3080402
BLAST score	262
E value	3.0e-23
Match length	76
% identity	71
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_

	(AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]
Seq. No.	226902
Seq. ID	LIB3189-012-P1-K1-H5
Method	BLASTX
NCBI GI	g3860259
BLAST score	190
E value	2.0e-14
Match length	90
% identity	49
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.	226903
Seq. ID	LIB3189-012-P1-K1-H6
Method	BLASTX
NCBI GI	g1402833
BLAST score	166
E value	4.0e-12
Match length	41
% identity	83
NCBI Description	(U60147) plasma membrane major intrinsic protein 1 [Beta vulgaris]
Seq. No.	226904
Seq. ID	LIB3189-012-P1-K1-H7
Method	BLASTX
NCBI GI	g4191255
BLAST score	385
E value	2.0e-37
Match length	81
% identity	89
NCBI Description	(AJ132323) chalcone synthase [Casuarina glauca]
Seq. No.	226905
Seq. ID	LIB3189-012-P1-K1-H8
Method	BLASTX
NCBI GI	g2267567
BLAST score	419
E value	2.0e-41
Match length	92
% identity	87
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]
Seq. No.	226906
Seq. ID	LIB3189-013-P1-K1-A1
Method	BLASTX
NCBI GI	g2130017
BLAST score	391
E value	7.0e-38
Match length	122
% identity	58
NCBI Description	hypothetical protein - common sunflower >gi_1040729_emb_CAA60621_ (X87143) cytochrome b5 containing fusion protein [Helianthus annuus]

Seq. No.	226907
Seq. ID	LIB3189-013-P1-K1-A4
Method	BLASTX
NCBI GI	g1280611
BLAST score	468
E value	6.0e-47
Match length	129
% identity	64
NCBI Description	(U53860) steroid reductase DET2 [Arabidopsis thaliana]

Seq. No.	226908
Seq. ID	LIB3189-013-P1-K1-A6
Method	BLASTX
NCBI GI	g2924520
BLAST score	503
E value	4.0e-51
Match length	108
% identity	91
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	226909
Seq. ID	LIB3189-013-P1-K1-A7
Method	BLASTX
NCBI GI	g1694976
BLAST score	170
E value	2.0e-12
Match length	61
% identity	52
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	226910
Seq. ID	LIB3189-013-P1-K1-A8
Method	BLASTX
NCBI GI	g2065531
BLAST score	478
E value	2.0e-48
Match length	93
% identity	89
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	226911
Seq. ID	LIB3189-013-P1-K1-A9
Method	BLASTX
NCBI GI	g2129921
BLAST score	194
E value	8.0e-15
Match length	51
% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	226912
Seq. ID	LIB3189-013-P1-K1-B1

Method	BLASTX
NCBI GI	g4455800
BLAST score	190
E value	2.0e-14
Match length	65
% identity	51
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	226913
Seq. ID	LIB3189-013-P1-K1-B11
Method	BLASTX
NCBI GI	g1174600
BLAST score	658
E value	3.0e-69
Match length	130
% identity	92
NCBI Description	TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717) beta-tubulin [Oryza sativa]

Seq. No.	226914
Seq. ID	LIB3189-013-P1-K1-B12
Method	BLASTX
NCBI GI	g2982322
BLAST score	711
E value	2.0e-75
Match length	149
% identity	89
NCBI Description	(AF051246) probable proteasome subunit [Picea mariana]

Seq. No.	226915
Seq. ID	LIB3189-013-P1-K1-B3
Method	BLASTX
NCBI GI	g1703375
BLAST score	288
E value	4.0e-26
Match length	64
% identity	94
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	226916
Seq. ID	LIB3189-013-P1-K1-B4
Method	BLASTX
NCBI GI	g4006867
BLAST score	153
E value	2.0e-10
Match length	55
% identity	62
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	226917
Seq. ID	LIB3189-013-P1-K1-B5
Method	BLASTX
NCBI GI	g1175016
BLAST score	176
E value	2.0e-13
Match length	63

% identity	48
NCBI Description	WHITE PROTEIN HOMOLOG >gi_1160186_emb_CAA62631_ (X91249) white [Homo sapiens]

Seq. No.	226918
Seq. ID	LIB3189-013-P1-K1-B7
Method	BLASTX
NCBI GI	g951427
BLAST score	287
E value	8.0e-26
Match length	99
% identity	60
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No.	226919
Seq. ID	LIB3189-013-P1-K1-B9
Method	BLASTX
NCBI GI	g1545805
BLAST score	235
E value	1.0e-19
Match length	93
% identity	54
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	226920
Seq. ID	LIB3189-013-P1-K1-C10
Method	BLASTX
NCBI GI	g2811278
BLAST score	243
E value	5.0e-21
Match length	63
% identity	76
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	226921
Seq. ID	LIB3189-013-P1-K1-C12
Method	BLASTX
NCBI GI	g218157
BLAST score	608
E value	2.0e-63
Match length	133
% identity	90
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	226922
Seq. ID	LIB3189-013-P1-K1-C2
Method	BLASTX
NCBI GI	g730583
BLAST score	275
E value	2.0e-24
Match length	76
% identity	75
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	226923
Seq. ID	LIB3189-013-P1-K1-D1
Method	BLASTX
NCBI GI	g3915031
BLAST score	759
E value	5.0e-81
Match length	145
% identity	99
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	226924
Seq. ID	LIB3189-013-P1-K1-D12
Method	BLASTX
NCBI GI	g4454014
BLAST score	259
E value	2.0e-22
Match length	123
% identity	44
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	226925
Seq. ID	LIB3189-013-P1-K1-E1
Method	BLASTX
NCBI GI	g3702327
BLAST score	290
E value	5.0e-26
Match length	96
% identity	62
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	226926
Seq. ID	LIB3189-013-P1-K1-E10
Method	BLASTX
NCBI GI	g1703375
BLAST score	488
E value	2.0e-49
Match length	96
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	226927
Seq. ID	LIB3189-013-P1-K1-E12
Method	BLASTX
NCBI GI	g2497543
BLAST score	500
E value	1.0e-50
Match length	122
% identity	83
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	226928

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Seq. ID	LIB3189-013-P1-K1-E8
Method	BLASTX
NCBI GI	g730583
BLAST score	219
E value	4.0e-18
Match length	56
% identity	79
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	226929
Seq. ID	LIB3189-013-P1-K1-F1
Method	BLASTX
NCBI GI	g1362086
BLAST score	150
E value	4.0e-10
Match length	29
% identity	97
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	226930
Seq. ID	LIB3189-013-P1-K1-F10
Method	BLASTX
NCBI GI	g3785983
BLAST score	247
E value	3.0e-21
Match length	84
% identity	55
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226931
Seq. ID	LIB3189-013-P1-K1-F12
Method	BLASTX
NCBI GI	g1703375
BLAST score	680
E value	9.0e-72
Match length	134
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	226932
Seq. ID	LIB3189-013-P1-K1-F2
Method	BLASTX
NCBI GI	g3879754
BLAST score	218
E value	1.0e-17
Match length	107
% identity	42
NCBI Description	(Z72514) Similarity to Rabbit glycogenin (SW:GLYG_RABIT)

[Caenorhabditis elegans]

Seq. No.	226933
Seq. ID	LIB3189-013-P1-K1-F4
Method	BLASTX
NCBI GI	g2369714
BLAST score	295
E value	9.0e-27
Match length	111
% identity	58
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	226934
Seq. ID	LIB3189-013-P1-K1-F6
Method	BLASTX
NCBI GI	g2267567
BLAST score	273
E value	1.0e-24
Match length	73
% identity	74
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	226935
Seq. ID	LIB3189-013-P1-K1-G10
Method	BLASTX
NCBI GI	g4193382
BLAST score	379
E value	2.0e-36
Match length	85
% identity	82
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	226936
Seq. ID	LIB3189-013-P1-K1-G4
Method	BLASTX
NCBI GI	g4115377
BLAST score	428
E value	3.0e-42
Match length	122
% identity	72
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	226937
Seq. ID	LIB3189-013-P1-K1-G5
Method	BLASTX
NCBI GI	g862640
BLAST score	398
E value	8.0e-39
Match length	92
% identity	85
NCBI Description	(U20182) MADS-box protein AGL11 [Arabidopsis thaliana] >gi_4538999_emb_CAB39620.1_ (AL049481) MADS-box protein AGL11 [Arabidopsis thaliana]

Seq. No.	226938
Seq. ID	LIB3189-013-P1-K1-G9
Method	BLASTX
NCBI GI	g3880625
BLAST score	158
E value	8.0e-11
Match length	60
% identity	50
NCBI Description	(Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge

Seq. No.	226939
Seq. ID	LIB3189-013-P1-K1-H5
Method	BLASTX
NCBI GI	g1362086
BLAST score	330
E value	5.0e-31
Match length	78
% identity	85
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	226940
Seq. ID	LIB3189-014-P1-K1-A1
Method	BLASTX
NCBI GI	g4512671
BLAST score	297
E value	4.0e-27
Match length	84
% identity	68
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	226941
Seq. ID	LIB3189-014-P1-K1-A11
Method	BLASTX
NCBI GI	g2492953
BLAST score	147
E value	7.0e-10
Match length	66
% identity	52
NCBI Description	CHORISMATE SYNTHASE 2 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 2) >gi_542027_pir__S40409 chorismate synthase (EC 4.6.1.4) 2 precursor - tomato >gi_410484_emb_CAA79854_ (Z21791) chorismate synthase 2 [Lycopersicon esculentum]

Seq. No.	226942
Seq. ID	LIB3189-014-P1-K1-A12

Method	BLASTX
NCBI GI	g2506139
BLAST score	452
E value	5.0e-45
Match length	106
% identity	85
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	226943
Seq. ID	LIB3189-014-P1-K1-A2
Method	BLASTX
NCBI GI	g3075398
BLAST score	354
E value	1.0e-33
Match length	114
% identity	56
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	226944
Seq. ID	LIB3189-014-P1-K1-A4
Method	BLASTX
NCBI GI	g2119719
BLAST score	250
E value	5.0e-22
Match length	56
% identity	89
NCBI Description	heat-shock cognate protein 70-3 - tomato >gi_762844 (L41253) Hsc70 [Lycopersicon esculentum]

Seq. No.	226945
Seq. ID	LIB3189-014-P1-K1-A5
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	226946
Seq. ID	LIB3189-014-P1-K1-A6
Method	BLASTX
NCBI GI	g543905
BLAST score	778
E value	3.0e-83
Match length	146
% identity	95
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	226947
Seq. ID	LIB3189-014-P1-K1-B1
Method	BLASTX
NCBI GI	g4567203

BLAST score	261
E value	1.0e-22
Match length	52
% identity	94
NCBI Description	(AC007168) putative beta-hydroxyacyl-ACP dehydratase [Arabidopsis thaliana]

Seq. No.	226948
Seq. ID	LIB3189-014-P1-K1-B11
Method	BLASTX
NCBI GI	g4467157
BLAST score	346
E value	1.0e-32
Match length	113
% identity	60
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	226949
Seq. ID	LIB3189-014-P1-K1-B3
Method	BLASTX
NCBI GI	g2959767
BLAST score	398
E value	5.0e-39
Match length	101
% identity	50
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	226950
Seq. ID	LIB3189-014-P1-K1-B7
Method	BLASTX
NCBI GI	g2832664
BLAST score	183
E value	1.0e-13
Match length	91
% identity	42
NCBI Description	(AL021710) pollen-specific protein - like [Arabidopsis thaliana]

Seq. No.	226951
Seq. ID	LIB3189-014-P1-K1-B9
Method	BLASTX
NCBI GI	g3980380
BLAST score	200
E value	1.0e-15
Match length	44
% identity	91
NCBI Description	(AC004561) putative enolase [Arabidopsis thaliana]

Seq. No.	226952
Seq. ID	LIB3189-014-P1-K1-C11
Method	BLASTX
NCBI GI	g2213628
BLAST score	136
E value	1.0e-09

Match length	109
% identity	45
NCBI Description	(AC000103) F21J9.20 [Arabidopsis thaliana]

Seq. No.	226953
Seq. ID	LIB3189-014-P1-K1-C3
Method	BLASTX
NCBI GI	g3738320
BLAST score	201
E value	1.0e-15
Match length	115
% identity	40
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	226954
Seq. ID	LIB3189-014-P1-K1-C6
Method	BLASTX
NCBI GI	g1703375
BLAST score	332
E value	2.0e-33
Match length	89
% identity	91
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	226955
Seq. ID	LIB3189-014-P1-K1-C9
Method	BLASTX
NCBI GI	g3175990
BLAST score	270
E value	5.0e-24
Match length	59
% identity	90
NCBI Description	(AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No.	226956
Seq. ID	LIB3189-014-P1-K1-D1
Method	BLASTX
NCBI GI	g121631
BLAST score	305
E value	7.0e-28
Match length	97
% identity	62
NCBI Description	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco >gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana sylvestris]

Seq. No.	226957
Seq. ID	LIB3189-014-P1-K1-D2
Method	BLASTX
NCBI GI	g3025205
BLAST score	177
E value	5.0e-13
Match length	73
% identity	51

NCBI Description	HYPOTHETICAL 65.1 KD PROTEIN SLR1919 >gi_1652223_dbj_BAA17147_ (D90903) ABC1-like [Synechocystis sp.]
Seq. No.	226958
Seq. ID	LIB3189-014-P1-K1-D5
Method	BLASTX
NCBI GI	g2815493
BLAST score	316
E value	4.0e-29
Match length	80
% identity	70
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) (CP-MI) >gi_1731988_emb_CAA70816_ (Y09603) serine carboxypeptidase I, CP-MI [Hordeum vulgare]
Seq. No.	226959
Seq. ID	LIB3189-014-P1-K1-E1
Method	BLASTX
NCBI GI	g1928981
BLAST score	526
E value	8.0e-54
Match length	112
% identity	93
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]
Seq. No.	226960
Seq. ID	LIB3189-014-P1-K1-E12
Method	BLASTX
NCBI GI	g1888357
BLAST score	443
E value	5.0e-44
Match length	146
% identity	59
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
Seq. No.	226961
Seq. ID	LIB3189-014-P1-K1-E6
Method	BLASTX
NCBI GI	g1888357
BLAST score	151
E value	6.0e-10
Match length	58
% identity	47
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
Seq. No.	226962
Seq. ID	LIB3189-014-P1-K1-E8
Method	BLASTX
NCBI GI	g2935298
BLAST score	288
E value	5.0e-26

Match length	79
% identity	70
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	226963
Seq. ID	LIB3189-014-P1-K1-F10
Method	BLASTX
NCBI GI	g2662341
BLAST score	647
E value	5.0e-68
Match length	128
% identity	95
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	226964
Seq. ID	LIB3189-014-P1-K1-F12
Method	BLASTX
NCBI GI	g4105696
BLAST score	577
E value	1.0e-59
Match length	113
% identity	94
NCBI Description	(AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No.	226965
Seq. ID	LIB3189-014-P1-K1-F6
Method	BLASTX
NCBI GI	g3776082
BLAST score	244
E value	1.0e-20
Match length	66
% identity	71
NCBI Description	(Y18250) MtN30 [Medicago truncatula]

Seq. No.	226966
Seq. ID	LIB3189-014-P1-K1-F8
Method	BLASTX
NCBI GI	g3860258
BLAST score	283
E value	2.0e-25
Match length	90
% identity	60
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	226967
Seq. ID	LIB3189-014-P1-K1-G10
Method	BLASTX
NCBI GI	g1843527
BLAST score	443
E value	4.0e-44
Match length	115
% identity	77
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	226968
Seq. ID	LIB3189-014-P1-K1-G11
Method	BLASTX
NCBI GI	g1085384
BLAST score	318
E value	2.0e-29
Match length	74
% identity	74
NCBI Description	Sm protein F - human >gi_806564_emb_CAA59688_ (X85372) Sm protein F [Homo sapiens] >gi_4507131_ref_NP_003086.1_pSNRPF_ small nuclear ribonucleoprotein polypeptide F

Seq. No.	226969
Seq. ID	LIB3189-014-P1-K1-G12
Method	BLASTX
NCBI GI	g2494162
BLAST score	316
E value	4.0e-29
Match length	141
% identity	44
NCBI Description	HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR >gi_3879803_emb_CAA87414_ (Z47356) similar to DNAJ [Caenorhabditis elegans]

Seq. No.	226970
Seq. ID	LIB3189-014-P1-K1-G2
Method	BLASTX
NCBI GI	g3915826
BLAST score	506
E value	2.0e-51
Match length	116
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	226971
Seq. ID	LIB3189-014-P1-K1-G4
Method	BLASTX
NCBI GI	g416758
BLAST score	254
E value	7.0e-22
Match length	95
% identity	54
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	226972
Seq. ID	LIB3189-014-P1-K1-G6
Method	BLASTX
NCBI GI	g3721926
BLAST score	278
E value	2.0e-30
Match length	139
% identity	52

NCBI Description (AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	226973
Seq. ID	LIB3189-014-P1-K1-H10
Method	BLASTX
NCBI GI	g266972
BLAST score	196
E value	3.0e-15
Match length	54
% identity	63
NCBI Description	40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens] >gi_4506717_ref_NP_001023.1_pRPS29_ ribosomal protein S29

Seq. No.	226974
Seq. ID	LIB3189-014-P1-K1-H4
Method	BLASTX
NCBI GI	g2494162
BLAST score	179
E value	3.0e-13
Match length	105
% identity	34
NCBI Description	HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR >gi_3879803_emb_CAA87414_ (Z47356) similar to DNAJ [Caenorhabditis elegans]

Seq. No.	226975
Seq. ID	LIB3189-014-P1-K1-H6
Method	BLASTX
NCBI GI	g464985
BLAST score	313
E value	2.0e-29
Match length	67
% identity	90
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	226976
Seq. ID	LIB3189-014-P1-K1-H8
Method	BLASTX
NCBI GI	g2511590
BLAST score	377
E value	2.0e-36
Match length	102
% identity	75
NCBI Description	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111

(AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No.	226977
Seq. ID	LIB3189-014-P1-K1-H9
Method	BLASTX
NCBI GI	g2369766
BLAST score	403
E value	2.0e-39
Match length	107
% identity	70
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	226978
Seq. ID	LIB3189-015-P1-K1-A3
Method	BLASTX
NCBI GI	g218157
BLAST score	198
E value	2.0e-15
Match length	56
% identity	73
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	226979
Seq. ID	LIB3189-015-P1-K1-A4
Method	BLASTX
NCBI GI	g1117780
BLAST score	362
E value	1.0e-34
Match length	106
% identity	68
NCBI Description	(D49367) 4-coumarate:CoA ligase [Lithospermum erythrorhizon]

Seq. No.	226980
Seq. ID	LIB3189-015-P1-K1-A5
Method	BLASTX
NCBI GI	g1669601
BLAST score	414
E value	8.0e-41
Match length	93
% identity	81
NCBI Description	(D88747) AR401 [Arabidopsis thaliana]

Seq. No.	226981
Seq. ID	LIB3189-015-P1-K1-B11
Method	BLASTX
NCBI GI	g1881378
BLAST score	478
E value	3.0e-48
Match length	106
% identity	90
NCBI Description	(AB001582) QM family protein [Solanum melongena]

Seq. No.	226982
Seq. ID	LIB3189-015-P1-K1-B2
Method	BLASTX

NCBI GI	g3023187
BLAST score	359
E value	1.0e-34
Match length	83
% identity	87
NCBI Description	14-3-3-LIKE PROTEIN (G-BOX BINDING FACTOR) >gi_1773328 (U80070) 14-3-3-like protein [Mesembryanthemum crystallinum]

Seq. No.	226983
Seq. ID	LIB3189-015-P1-K1-B3
Method	BLASTX
NCBI GI	g2499489
BLAST score	154
E value	9.0e-11
Match length	53
% identity	62
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483536_emb_CAA83683_ (Z32850) pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis]

Seq. No.	226984
Seq. ID	LIB3189-015-P1-K1-B5
Method	BLASTX
NCBI GI	g2129559
BLAST score	452
E value	3.0e-45
Match length	107
% identity	80
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	226985
Seq. ID	LIB3189-015-P1-K1-B6
Method	BLASTX
NCBI GI	g3023187
BLAST score	196
E value	3.0e-15
Match length	69
% identity	65
NCBI Description	14-3-3-LIKE PROTEIN (G-BOX BINDING FACTOR) >gi_1773328 (U80070) 14-3-3-like protein [Mesembryanthemum crystallinum]

Seq. No.	226986
Seq. ID	LIB3189-015-P1-K1-B7
Method	BLASTX
NCBI GI	g2262173
BLAST score	238
E value	3.0e-20

Match length	73
% identity	73
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	226987
Seq. ID	LIB3189-015-P1-K1-C1
Method	BLASTX
NCBI GI	g3080414
BLAST score	244
E value	1.0e-27
Match length	74
% identity	72
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	226988
Seq. ID	LIB3189-015-P1-K1-C12
Method	BLASTX
NCBI GI	g2642158
BLAST score	472
E value	1.0e-47
Match length	110
% identity	77
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226989
Seq. ID	LIB3189-015-P1-K1-C4
Method	BLASTX
NCBI GI	g1657948
BLAST score	243
E value	8.0e-30
Match length	98
% identity	71
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	226990
Seq. ID	LIB3189-015-P1-K1-C6
Method	BLASTX
NCBI GI	g1518540
BLAST score	225
E value	2.0e-26
Match length	73
% identity	88
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	226991
Seq. ID	LIB3189-015-P1-K1-D1
Method	BLASTX
NCBI GI	g2500354
BLAST score	589
E value	5.0e-65
Match length	135
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No.	226992

Seq. ID	LIB3189-015-P1-K1-D10
Method	BLASTX
NCBI GI	g2245021
BLAST score	325
E value	1.0e-35
Match length	120
% identity	68
NCBI Description	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]

Seq. No.	226993
Seq. ID	LIB3189-015-P1-K1-D11
Method	BLASTX
NCBI GI	g2497753
BLAST score	196
E value	4.0e-15
Match length	50
% identity	64
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	226994
Seq. ID	LIB3189-015-P1-K1-D3
Method	BLASTX
NCBI GI	g586004
BLAST score	276
E value	1.0e-24
Match length	64
% identity	84
NCBI Description	SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139) superoxide dismutase [Ipomoea batatas]

Seq. No.	226995
Seq. ID	LIB3189-015-P1-K1-D4
Method	BLASTX
NCBI GI	g1771162
BLAST score	159
E value	1.0e-20
Match length	115
% identity	49
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	226996
Seq. ID	LIB3189-015-P1-K1-D5
Method	BLASTX
NCBI GI	g710626
BLAST score	287
E value	8.0e-26
Match length	86
% identity	65
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	226997
Seq. ID	LIB3189-015-P1-K1-D6
Method	BLASTX
NCBI GI	g4567283
BLAST score	160
E value	3.0e-11
Match length	80
% identity	49
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	226998
Seq. ID	LIB3189-015-P1-K1-D9
Method	BLASTX
NCBI GI	g3860274
BLAST score	196
E value	3.0e-15
Match length	53
% identity	68
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	226999
Seq. ID	LIB3189-015-P1-K1-E10
Method	BLASTX
NCBI GI	g508304
BLAST score	152
E value	4.0e-10
Match length	38
% identity	79
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	227000
Seq. ID	LIB3189-015-P1-K1-E3
Method	BLASTX
NCBI GI	g3819164
BLAST score	183
E value	9.0e-14
Match length	57
% identity	68
NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No.	227001
Seq. ID	LIB3189-015-P1-K1-E9
Method	BLASTX
NCBI GI	g2961346
BLAST score	382
E value	4.0e-37
Match length	104
% identity	64
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	227002
Seq. ID	LIB3189-015-P1-K1-F10
Method	BLASTX
NCBI GI	g1351303
BLAST score	312
E value	7.0e-29
Match length	103
% identity	65
NCBI Description	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS) >gi_619732 (U18770) indole-3-glycerol phosphate synthase [Arabidopsis thaliana]

Seq. No.	227003
Seq. ID	LIB3189-015-P1-K1-F2
Method	BLASTX
NCBI GI	g1771162
BLAST score	341
E value	5.0e-32
Match length	131
% identity	53
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	227004
Seq. ID	LIB3189-015-P1-K1-F7
Method	BLASTX
NCBI GI	g3063637
BLAST score	203
E value	7.0e-16
Match length	58
% identity	66
NCBI Description	(AF056204) thioesterase homolog [Gossypium hirsutum]

Seq. No.	227005
Seq. ID	LIB3189-015-P1-K1-G11
Method	BLASTX
NCBI GI	g1703375
BLAST score	252
E value	5.0e-22
Match length	52
% identity	98
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	227006
Seq. ID	LIB3189-015-P1-K1-G2
Method	BLASTX
NCBI GI	g3834310
BLAST score	290
E value	3.0e-26
Match length	81
% identity	60
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

Seq. No.	227007
Seq. ID	LIB3189-015-P1-K1-G3
Method	BLASTX
NCBI GI	g3493172
BLAST score	256
E value	2.0e-31
Match length	85
% identity	89
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	227008
Seq. ID	LIB3189-015-P1-K1-G5
Method	BLASTX
NCBI GI	g2462748
BLAST score	442
E value	6.0e-44
Match length	94
% identity	91
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	227009
Seq. ID	LIB3189-015-P1-K1-G6
Method	BLASTX
NCBI GI	g1173055
BLAST score	611
E value	9.0e-66
Match length	153
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No.	227010
Seq. ID	LIB3189-015-P1-K1-G8
Method	BLASTX
NCBI GI	g4337025
BLAST score	372
E value	7.0e-36
Match length	106
% identity	68
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	227011
Seq. ID	LIB3189-015-P1-K1-G9
Method	BLASTX
NCBI GI	g2062167
BLAST score	386
E value	2.0e-37
Match length	79
% identity	89
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	227012
Seq. ID	LIB3189-015-P1-K1-H1
Method	BLASTX
NCBI GI	g2149380
BLAST score	518
E value	7.0e-53
Match length	139
% identity	76
NCBI Description	(U85036) syntaxin homolog [Arabidopsis thaliana]

Seq. No.	227013
Seq. ID	LIB3189-015-P1-K1-H3
Method	BLASTX
NCBI GI	g4558665
BLAST score	556
E value	3.0e-57
Match length	143
% identity	81
NCBI Description	(AC007063) putative white protein [Arabidopsis thaliana]

Seq. No.	227014
Seq. ID	LIB3189-015-P1-K1-H5
Method	BLASTX
NCBI GI	g2500517
BLAST score	151
E value	3.0e-11
Match length	53
% identity	61
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-9 (EIF-4A-9) >gi_485951_emb_CAA55736_ (X79135) NeIF-4A9 [Nicotiana tabacum]

Seq. No.	227015
Seq. ID	LIB3189-015-P1-K1-H7
Method	BLASTX
NCBI GI	g3269284
BLAST score	334
E value	3.0e-31
Match length	88
% identity	77
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	227016
Seq. ID	LIB3189-016-P1-K1-A1
Method	BLASTX
NCBI GI	g729623
BLAST score	454
E value	2.0e-45
Match length	106
% identity	85
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP 78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 5) (BIP 5) >gi_100340_pir__S21880 heat shock protein BiP homolog blp5 - common tobacco >gi_19813_emb_CAA42660_ (X60058) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	227017

Seq. ID	LIB3189-016-P1-K1-A4
Method	BLASTX
NCBI GI	g2244847
BLAST score	304
E value	1.0e-27
Match length	103
% identity	57
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	227018
Seq. ID	LIB3189-016-P1-K1-A5
Method	BLASTX
NCBI GI	g2244835
BLAST score	212
E value	5.0e-17
Match length	58
% identity	74
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	227019
Seq. ID	LIB3189-016-P1-K1-A7
Method	BLASTX
NCBI GI	g267069
BLAST score	524
E value	1.0e-53
Match length	97
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227020
Seq. ID	LIB3189-016-P1-K1-A8
Method	BLASTX
NCBI GI	g2541876
BLAST score	291
E value	4.0e-26
Match length	128
% identity	42
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	227021
Seq. ID	LIB3189-016-P1-K1-B11
Method	BLASTX
NCBI GI	g2791834
BLAST score	641
E value	1.0e-78
Match length	149
% identity	89
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	227022
Seq. ID	LIB3189-016-P1-K1-B12
Method	BLASTX

NCBI GI g3650032
BLAST score 229
E value 7.0e-19
Match length 49
% identity 69
NCBI Description (AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No. 227023
Seq. ID LIB3189-016-P1-K1-B3
Method BLASTX
NCBI GI g484656
BLAST score 451
E value 3.0e-45
Match length 105
% identity 84
NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi_452165_dbj_BAA05408_ (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No. 227024
Seq. ID LIB3189-016-P1-K1-B4
Method BLASTX
NCBI GI g2213595
BLAST score 353
E value 1.0e-33
Match length 113
% identity 63
NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No. 227025
Seq. ID LIB3189-016-P1-K1-B7
Method BLASTX
NCBI GI g542157
BLAST score 531
E value 2.0e-54
Match length 120
% identity 82
NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 227026
Seq. ID LIB3189-016-P1-K1-B9
Method BLASTX
NCBI GI g267069
BLAST score 635
E value 2.0e-66
Match length 119
% identity 98
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 227027
Seq. ID LIB3189-016-P1-K1-C10
Method BLASTX
NCBI GI g495725

BLAST score	374
E value	2.0e-36
Match length	80
% identity	86
NCBI Description	(L25042) acetyl-CoA carboxylase [Medicago sativa]

Seq. No.	227028
Seq. ID	LIB3189-016-P1-K1-C2
Method	BLASTX
NCBI GI	g1684851
BLAST score	235
E value	1.0e-19
Match length	83
% identity	58
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	227029
Seq. ID	LIB3189-016-P1-K1-C3
Method	BLASTX
NCBI GI	g3386598
BLAST score	513
E value	3.0e-52
Match length	146
% identity	69
NCBI Description	(AC004665) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	227030
Seq. ID	LIB3189-016-P1-K1-C5
Method	BLASTX
NCBI GI	g4105772
BLAST score	388
E value	2.0e-37
Match length	86
% identity	43
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	227031
Seq. ID	LIB3189-016-P1-K1-C6
Method	BLASTX
NCBI GI	g2493144
BLAST score	484
E value	9.0e-49
Match length	135
% identity	55
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	227032
Seq. ID	LIB3189-016-P1-K1-C8
Method	BLASTX
NCBI GI	g2244736
BLAST score	808
E value	9.0e-87

Match length	151
% identity	97
NCBI Description	(D88415) expansin [Gossypium hirsutum]

Seq. No.	227033
Seq. ID	LIB3189-016-P1-K1-C9
Method	BLASTX
NCBI GI	g4050007
BLAST score	153
E value	2.0e-14
Match length	52
% identity	61
NCBI Description	(AF082027) alpha tubulin [Notothenia coriiceps]

Seq. No.	227034
Seq. ID	LIB3189-016-P1-K1-D2
Method	BLASTX
NCBI GI	g3915847
BLAST score	364
E value	7.0e-35
Match length	89
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	227035
Seq. ID	LIB3189-016-P1-K1-D3
Method	BLASTX
NCBI GI	g3024526
BLAST score	232
E value	2.0e-19
Match length	79
% identity	61
NCBI Description	RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi_451860 (L18883) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	227036
Seq. ID	LIB3189-016-P1-K1-D6
Method	BLASTX
NCBI GI	g3668089
BLAST score	140
E value	1.0e-08
Match length	59
% identity	41
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	227037
Seq. ID	LIB3189-016-P1-K1-E11
Method	BLASTX
NCBI GI	g2811278
BLAST score	561
E value	7.0e-58
Match length	123
% identity	85
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227038
Seq. ID	LIB3189-016-P1-K1-E12
Method	BLASTX
NCBI GI	g1246823
BLAST score	579
E value	6.0e-60
Match length	125
% identity	84
NCBI Description	(X89865) unknown [Phoenix dactylifera]

Seq. No.	227039
Seq. ID	LIB3189-016-P1-K1-E2
Method	BLASTX
NCBI GI	g232031
BLAST score	220
E value	8.0e-18
Match length	67
% identity	60
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	227040
Seq. ID	LIB3189-016-P1-K1-E4
Method	BLASTX
NCBI GI	g3643609
BLAST score	316
E value	6.0e-31
Match length	132
% identity	61
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	227041
Seq. ID	LIB3189-016-P1-K1-F10
Method	BLASTX
NCBI GI	g267069
BLAST score	712
E value	1.0e-75
Match length	133
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227042
Seq. ID	LIB3189-016-P1-K1-F11
Method	BLASTX
NCBI GI	g3757520
BLAST score	169
E value	3.0e-12
Match length	65
% identity	57
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	227043
Seq. ID	LIB3189-016-P1-K1-F12
Method	BLASTX
NCBI GI	g3176098
BLAST score	450
E value	8.0e-45
Match length	133
% identity	39
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	227044
Seq. ID	LIB3189-016-P1-K1-F2
Method	BLASTX
NCBI GI	g2129473
BLAST score	253
E value	7.0e-22
Match length	90
% identity	54
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	227045
Seq. ID	LIB3189-016-P1-K1-F6
Method	BLASTX
NCBI GI	g2811278
BLAST score	712
E value	2.0e-75
Match length	144
% identity	90
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227046
Seq. ID	LIB3189-016-P1-K1-F7
Method	BLASTX
NCBI GI	g4539371
BLAST score	260
E value	2.0e-22
Match length	94
% identity	55
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	227047
Seq. ID	LIB3189-016-P1-K1-F8
Method	BLASTX
NCBI GI	g2804278
BLAST score	506
E value	2.0e-51
Match length	145
% identity	70
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	227048
Seq. ID	LIB3189-016-P1-K1-F9
Method	BLASTX
NCBI GI	g2244749
BLAST score	220
E value	2.0e-18

Match length	57
% identity	75
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	227049
Seq. ID	LIB3189-016-P1-K1-G10
Method	BLASTX
NCBI GI	g4432845
BLAST score	236
E value	1.0e-19
Match length	107
% identity	50
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	227050
Seq. ID	LIB3189-016-P1-K1-G12
Method	BLASTX
NCBI GI	g4539301
BLAST score	275
E value	3.0e-24
Match length	110
% identity	47
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	227051
Seq. ID	LIB3189-016-P1-K1-G2
Method	BLASTX
NCBI GI	g1350680
BLAST score	486
E value	5.0e-49
Match length	142
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	227052
Seq. ID	LIB3189-016-P1-K1-G6
Method	BLASTX
NCBI GI	g3434986
BLAST score	451
E value	7.0e-45
Match length	126
% identity	25
NCBI Description	(AB016895) Pop3 [Schizosaccharomyces pombe]

Seq. No.	227053
Seq. ID	LIB3189-016-P1-K1-G9
Method	BLASTX
NCBI GI	g2811278
BLAST score	176
E value	8.0e-15
Match length	44
% identity	95
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227054
Seq. ID	LIB3189-016-P1-K1-H11

Method	BLASTX
NCBI GI	g129881
BLAST score	668
E value	2.0e-70
Match length	146
% identity	89
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_482294_pir__A36094 pyrophosphate--fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - potato (cv. Kennebec) >gi_169538 (M55190) pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No.	227055
Seq. ID	LIB3189-016-P1-K1-H12
Method	BLASTX
NCBI GI	g2088651
BLAST score	180
E value	2.0e-13
Match length	89
% identity	44
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	227056
Seq. ID	LIB3189-016-P1-K1-H2
Method	BLASTX
NCBI GI	g2497753
BLAST score	364
E value	1.0e-34
Match length	117
% identity	54
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	227057
Seq. ID	LIB3189-016-P1-K1-H4
Method	BLASTX
NCBI GI	g2673868
BLAST score	334
E value	3.0e-31
Match length	93
% identity	75
NCBI Description	(Y14856) fimbriata-associated protein [Antirrhinum majus]

Seq. No.	227058
Seq. ID	LIB3189-016-P1-K1-H9
Method	BLASTX
NCBI GI	g4138722
BLAST score	274
E value	3.0e-24
Match length	99
% identity	61
NCBI Description	(Y09590) hexose transporter [Vitis vinifera]

Seq. No.	227059
Seq. ID	LIB3189-017-P1-K1-A10
Method	BLASTX
NCBI GI	g3650032
BLAST score	267
E value	2.0e-23
Match length	60
% identity	67
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	227060
Seq. ID	LIB3189-017-P1-K1-A2
Method	BLASTX
NCBI GI	g3126969
BLAST score	169
E value	4.0e-12
Match length	92
% identity	46
NCBI Description	(AF061808) chalcone isomerase [Elaeagnus umbellata]

Seq. No.	227061
Seq. ID	LIB3189-017-P1-K1-A4
Method	BLASTX
NCBI GI	g267069
BLAST score	531
E value	2.0e-54
Match length	98
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227062
Seq. ID	LIB3189-017-P1-K1-A5
Method	BLASTX
NCBI GI	g4185819
BLAST score	192
E value	1.0e-14
Match length	47
% identity	68
NCBI Description	(AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No.	227063
Seq. ID	LIB3189-017-P1-K1-A7
Method	BLASTX
NCBI GI	g3786001
BLAST score	638
E value	7.0e-67
Match length	144
% identity	81
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	227064

Seq. ID	LIB3189-017-P1-K1-A8
Method	BLASTX
NCBI GI	g2811278
BLAST score	447
E value	1.0e-44
Match length	118
% identity	72
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227065
Seq. ID	LIB3189-017-P1-K1-A9
Method	BLASTX
NCBI GI	g3869088
BLAST score	570
E value	6.0e-59
Match length	111
% identity	98
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	227066
Seq. ID	LIB3189-017-P1-K1-B3
Method	BLASTX
NCBI GI	g1350720
BLAST score	455
E value	2.0e-45
Match length	111
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	227067
Seq. ID	LIB3189-017-P1-K1-B6
Method	BLASTX
NCBI GI	g2497753
BLAST score	324
E value	5.0e-30
Match length	97
% identity	57
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRE P 3) >gi_1321915_emb_CAA65477_ (X96716) protein [Prunus dulcis]

Seq. No.	227068
Seq. ID	LIB3189-017-P1-K1-C12
Method	BLASTX
NCBI GI	g1914683
BLAST score	339
E value	7.0e-32
Match length	122
% identity	60
NCBI Description	(Y12013) RAD23, m I [Daucus carota]

Seq. No.	227069
Seq. ID	LIB3189-017-P1-K1-C2
Method	BLASTX
NCBI GI	g3860247
BLAST score	412
E value	1.0e-40

Match length	87
% identity	84
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	227070
Seq. ID	LIB3189-017-P1-K1-C5
Method	BLASTX
NCBI GI	g401322
BLAST score	582
E value	2.0e-60
Match length	112
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	227071
Seq. ID	LIB3189-017-P1-K1-C7
Method	BLASTX
NCBI GI	g730512
BLAST score	504
E value	3.0e-51
Match length	117
% identity	88
NCBI Description	RAS-RELATED PROTEIN RIC2 >gi_481506_pir__S38741 GTP-binding protein ric2 - rice >gi_218228_dbj_BAA02904_ (D13758) ras-related GTP binding protein [Oryza sativa]

Seq. No.	227072
Seq. ID	LIB3189-017-P1-K1-C9
Method	BLASTX
NCBI GI	g1174592
BLAST score	514
E value	1.0e-52
Match length	101
% identity	97
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	227073
Seq. ID	LIB3189-017-P1-K1-D1
Method	BLASTX
NCBI GI	g1928981
BLAST score	347
E value	5.0e-33
Match length	77
% identity	91
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	227074
Seq. ID	LIB3189-017-P1-K1-D10
Method	BLASTX
NCBI GI	g4454051
BLAST score	531
E value	2.0e-54

Match length	115
% identity	84
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	227075
Seq. ID	LIB3189-017-P1-K1-D11
Method	BLASTX
NCBI GI	g3603473
BLAST score	345
E value	8.0e-33
Match length	91
% identity	68
NCBI Description	(AF090698) elicitor-responsive gene-3 [Oryza sativa]

Seq. No.	227076
Seq. ID	LIB3189-017-P1-K1-D12
Method	BLASTX
NCBI GI	g1172811
BLAST score	368
E value	2.0e-35
Match length	84
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34) >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor suppresser [Oryza sativa]

Seq. No.	227077
Seq. ID	LIB3189-017-P1-K1-D3
Method	BLASTX
NCBI GI	g4006890
BLAST score	282
E value	2.0e-25
Match length	93
% identity	67
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	227078
Seq. ID	LIB3189-017-P1-K1-D6
Method	BLASTX
NCBI GI	g3860247
BLAST score	430
E value	1.0e-52
Match length	115
% identity	85
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	227079
Seq. ID	LIB3189-017-P1-K1-E10
Method	BLASTX
NCBI GI	g3219761
BLAST score	427
E value	6.0e-43
Match length	97
% identity	96

NCBI Description	ACTIN 66 >gi_1498351 (U60491) actin [Nicotiana tabacum]
Seq. No.	227080
Seq. ID	LIB3189-017-P1-K1-E2
Method	BLASTX
NCBI GI	g1346675
BLAST score	501
E value	6.0e-51
Match length	107
% identity	90
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) >gi_499112 (U10283) nucleoside diphosphate kinase [Flaveria bidentis]
Seq. No.	227081
Seq. ID	LIB3189-017-P1-K1-E8
Method	BLASTX
NCBI GI	g2281338
BLAST score	320
E value	1.0e-29
Match length	79
% identity	77
NCBI Description	(U83621) putative pectate lyase [Arabidopsis thaliana]
Seq. No.	227082
Seq. ID	LIB3189-017-P1-K1-F11
Method	BLASTX
NCBI GI	g3123515
BLAST score	534
E value	9.0e-55
Match length	114
% identity	91
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]
Seq. No.	227083
Seq. ID	LIB3189-017-P1-K1-F12
Method	BLASTX
NCBI GI	g3687251
BLAST score	228
E value	3.0e-28
Match length	95
% identity	63
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.	227084
Seq. ID	LIB3189-017-P1-K1-F4
Method	BLASTX
NCBI GI	g2979559
BLAST score	174
E value	1.0e-12
Match length	65
% identity	63
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]
Seq. No.	227085
Seq. ID	LIB3189-017-P1-K1-F5

Method	BLASTX
NCBI GI	g2507281
BLAST score	357
E value	3.0e-34
Match length	73
% identity	90
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	227086
Seq. ID	LIB3189-017-P1-K1-F6
Method	BLASTX
NCBI GI	g1168196
BLAST score	368
E value	2.0e-35
Match length	102
% identity	78
NCBI Description	14-3-3-LIKE PROTEIN >gi_555974 (U15036) 14-3-3-like protein [Pisum sativum]

Seq. No.	227087
Seq. ID	LIB3189-017-P1-K1-G1
Method	BLASTX
NCBI GI	g728882
BLAST score	226
E value	1.0e-33
Match length	92
% identity	83
NCBI Description	ADP-RIBOSYLATION FACTOR 3 >gi_541846_pir__S41938 ADP-ribosylation factor 3 - Arabidopsis thaliana >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3 [Arabidopsis thaliana]

Seq. No.	227088
Seq. ID	LIB3189-017-P1-K1-G10
Method	BLASTX
NCBI GI	g2815905
BLAST score	277
E value	1.0e-24
Match length	95
% identity	61
NCBI Description	(AF043734) Pros45 proteosome subunit homolog [Drosophila melanogaster]

Seq. No.	227089
Seq. ID	LIB3189-017-P1-K1-G7
Method	BLASTX
NCBI GI	g2661840
BLAST score	305
E value	5.0e-28
Match length	75
% identity	75
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	227090
Seq. ID	LIB3189-017-P1-K1-H1
Method	BLASTX

NCBI GI g4510428
BLAST score 269
E value 2.0e-31
Match length 120
% identity 62
NCBI Description (AC006929) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 227091
Seq. ID LIB3189-018-P1-K1-A1
Method BLASTX
NCBI GI g1076678
BLAST score 269
E value 3.0e-24
Match length 66
% identity 82
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 227092
Seq. ID LIB3189-018-P1-K1-A12
Method BLASTX
NCBI GI g3785971
BLAST score 406
E value 1.0e-39
Match length 141
% identity 60
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana] >gi_4262248_gb_AAD14541_ (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No. 227093
Seq. ID LIB3189-018-P1-K1-A3
Method BLASTX
NCBI GI g4544399
BLAST score 564
E value 3.0e-58
Match length 147
% identity 72
NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 227094
Seq. ID LIB3189-018-P1-K1-A5
Method BLASTX
NCBI GI g549063
BLAST score 455
E value 2.0e-45
Match length 125
% identity 74
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No. 227095
Seq. ID LIB3189-018-P1-K1-B11
Method BLASTX

NCBI GI	g4559384
BLAST score	592
E value	2.0e-61
Match length	167
% identity	69
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	227096
Seq. ID	LIB3189-018-P1-K1-B12
Method	BLASTX
NCBI GI	g4539301
BLAST score	158
E value	2.0e-10
Match length	94
% identity	38
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	227097
Seq. ID	LIB3189-018-P1-K1-B6
Method	BLASTX
NCBI GI	g3212877
BLAST score	232
E value	2.0e-32
Match length	106
% identity	72
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	227098
Seq. ID	LIB3189-018-P1-K1-B7
Method	BLASTX
NCBI GI	g3169182
BLAST score	360
E value	3.0e-34
Match length	78
% identity	85
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	227099
Seq. ID	LIB3189-018-P1-K1-B8
Method	BLASTX
NCBI GI	g3759177
BLAST score	323
E value	7.0e-30
Match length	92
% identity	73
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	227100
Seq. ID	LIB3189-018-P1-K1-C1
Method	BLASTX
NCBI GI	g2995384
BLAST score	178
E value	2.0e-13
Match length	46

% identity	76
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	227101
Seq. ID	LIB3189-018-P1-K1-C10
Method	BLASTX
NCBI GI	g3912950
BLAST score	456
E value	1.0e-45
Match length	109
% identity	83
NCBI Description	14-3-3-LIKE PROTEIN E >gi_2689479 (U91726) 14-3-3 isoform e [Nicotiana tabacum]

Seq. No.	227102
Seq. ID	LIB3189-018-P1-K1-C11
Method	BLASTX
NCBI GI	g1346802
BLAST score	318
E value	1.0e-29
Match length	87
% identity	68
NCBI Description	PROFILIN 1 >gi_1076516_pir__S49351 profilin - kidney bean >gi_556836_emb_CAA57508_ (X81982) profilin [Phaseolus vulgaris]

Seq. No.	227103
Seq. ID	LIB3189-018-P1-K1-C2
Method	BLASTX
NCBI GI	g4538913
BLAST score	348
E value	9.0e-33
Match length	79
% identity	84
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	227104
Seq. ID	LIB3189-018-P1-K1-C4
Method	BLASTX
NCBI GI	g2829204
BLAST score	251
E value	6.0e-22
Match length	59
% identity	88
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	227105
Seq. ID	LIB3189-018-P1-K1-C5
Method	BLASTX
NCBI GI	g312179
BLAST score	265
E value	1.0e-23
Match length	57
% identity	89
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic

glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	227106
Seq. ID	LIB3189-018-P1-K1-C7
Method	BLASTX
NCBI GI	g3128176
BLAST score	325
E value	3.0e-30
Match length	111
% identity	57
NCBI Description	(AC004521) unknown pr[illegible]n [Arabidopsis thaliana]

Seq. No.	227107
Seq. ID	LIB3189-018-P1-K1-C9
Method	BLASTX
NCBI GI	g3738304
BLAST score	163
E value	4.0e-11
Match length	124
% identity	31
NCBI Description	(AC005309) hypothetical protein [Arabi[illegible]iana]

Seq. No.	227108
Seq. ID	LIB3189-018-P1-K1-D11
Method	BLASTX
NCBI GI	g3237190
BLAST score	214
E value	4.0e-17
Match length	86
% identity	49
NCBI Description	(AB014760) cystein proteinase inhibitor [Cucumis sativus]

Seq. No.	227109
Seq. ID	LIB3189-018-P1-K1-D2
Method	BLASTX
NCBI GI	g4220512
BLAST score	398
E value	6.0e-39
Match length	98
% identity	76
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	227110
Seq. ID	LIB3189-018-P1-K1-D4
Method	BLASTX
NCBI GI	g3219271
BLAST score	432
E value	1.0e-42
Match length	161
% identity	57
NCBI Description	(AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

Seq. No.	227111
Seq. ID	LIB3189-018-P1-K1-D8
Method	BLASTX

NCBI GI	g4204312
BLAST score	325
E value	2.0e-30
Match length	102
% identity	69
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	227112
Seq. ID	LIB3189-018-P1-K1-E12
Method	BLASTX
NCBI GI	g729480
BLAST score	440
E value	1.0e-43
Match length	126
% identity	71
NCBI Description	FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR) >gi_435647_dbj_BAA04232_ (D17410) ferredoxin-NADP+ reductase [Oryza sativa] >gi_902936_dbj_BAA07479_ (D38445) root ferredoxin-NADP+ reductase [Oryza sativa] >gi_1096932_prf__2113196A ferredoxin-NADP oxidoreductase [Oryza sativa]

Seq. No.	227113
Seq. ID	LIB3189-018-P1-K1-E4
Method	BLASTX
NCBI GI	g4454466
BLAST score	197
E value	4.0e-15
Match length	52
% identity	69
NCBI Description	(AC006234) unknown protein [Arabidopsis]

Seq. No.	227114
Seq. ID	LIB3189-018-P1-K1-E9
Method	BLASTX
NCBI GI	g2894378
BLAST score	211
E value	7.0e-17
Match length	88
% identity	52
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	227115
Seq. ID	LIB3189-018-P1-K1-F10
Method	BLASTX
NCBI GI	g3075398
BLAST score	450
E value	9.0e-45
Match length	162
% identity	58
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	227116
Seq. ID	LIB3189-018-P1-K1-F11
Method	BLASTX
NCBI GI	g1362086

BLAST score	638
E value	8.0e-67
Match length	130
% identity	92
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	227117
Seq. ID	LIB3189-018-P1-K1-F12
Method	BLASTX
NCBI GI	g4539301
BLAST score	179
E value	4.0e-13
Match length	96
% identity	42
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	227118
Seq. ID	LIB3189-018-P1-K1-F4
Method	BLASTX
NCBI GI	g1168470
BLAST score	140
E value	1.0e-08
Match length	75
% identity	41
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	227119
Seq. ID	LIB3189-018-P1-K1-F8
Method	BLASTX
NCBI GI	g3876865
BLAST score	188
E value	4.0e-14
Match length	150
% identity	35
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227120
Seq. ID	LIB3189-018-P1-K1-G1
Method	BLASTX
NCBI GI	g3915847
BLAST score	534
E value	1.0e-54
Match length	117

% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	227121
Seq. ID	LIB3189-018-P1-K1-G11
Method	BLASTX
NCBI GI	g1619297
BLAST score	616
E value	3.0e-64
Match length	115
% identity	99
NCBI Description	(Y08490) alpha-tubulin 2 [Hordeum vulgare]

Seq. No.	227122
Seq. ID	LIB3189-018-P1-K1-G12
Method	BLASTX
NCBI GI	g3695023
BLAST score	166
E value	1.0e-11
Match length	50
% identity	58
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	227123
Seq. ID	LIB3189-018-P1-K1-G2
Method	BLASTX
NCBI GI	g538213
BLAST score	519
E value	6.0e-53
Match length	123
% identity	79
NCBI Description	(L36229) cytosolic copper/zinc-superoxide dismutase [Ipomoea batatas] >gi_1582361_prf__2118341A Cu/Zn-superoxide dismutase [Ipomoea batatas]

Seq. No.	227124
Seq. ID	LIB3189-018-P1-K1-G3
Method	BLASTX
NCBI GI	g4006858
BLAST score	345
E value	2.0e-32
Match length	107
% identity	63
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	227125
Seq. ID	LIB3189-018-P1-K1-G7
Method	BLASTX
NCBI GI	g3650037
BLAST score	474
E value	1.0e-47
Match length	116
% identity	81
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	227126
Seq. ID	LIB3189-018-P1-K1-G9
Method	BLASTX
NCBI GI	g266972
BLAST score	195
E value	5.0e-15
Match length	54
% identity	63
NCBI Description	40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens] >gi_4506717_ref_NP_001023.1_pRPS29_ ribosomal protein S29

Seq. No.	227127
Seq. ID	LIB3189-018-P1-K1-H10
Method	BLASTX
NCBI GI	g1350720
BLAST score	241
E value	3.0e-22
Match length	71
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	227128
Seq. ID	LIB3189-018-P1-K1-H4
Method	BLASTX
NCBI GI	g3695023
BLAST score	287
E value	9.0e-26
Match length	117
% identity	52
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	227129
Seq. ID	LIB3189-018-P1-K1-H6
Method	BLASTX
NCBI GI	g4490331
BLAST score	234
E value	6.0e-20
Match length	60
% identity	77
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227130
Seq. ID	LIB3189-018-P1-K1-H8
Method	BLASTX
NCBI GI	g3334405
BLAST score	645
E value	1.0e-67

Match length	134
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]
Seq. No.	227131
Seq. ID	LIB3189-021-P1-K1-A11
Method	BLASTX
NCBI GI	g82665
BLAST score	157
E value	4.0e-11
Match length	35
% identity	86
NCBI Description	ADP,ATP carrier protein G1 - maize
Seq. No.	227132
Seq. ID	LIB3189-021-P1-K1-A12
Method	BLASTX
NCBI GI	g2497753
BLAST score	240
E value	4.0e-31
Match length	124
% identity	55
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]
Seq. No.	227133
Seq. ID	LIB3189-021-P1-K1-A4
Method	BLASTX
NCBI GI	g3759184
BLAST score	249
E value	3.0e-21
Match length	95
% identity	55
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]
Seq. No.	227134
Seq. ID	LIB3189-021-P1-K1-A6
Method	BLASTX
NCBI GI	g133728
BLAST score	575
E value	2.0e-59
Match length	124
% identity	90
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi_81525_pir__B23525 ribosomal protein S11 - spinach chloroplast >gi_12264_emb_CAA27213_ (X03496) pot. ribosomal protein S11 (aa 1-138) [Spinacia oleracea]
Seq. No.	227135
Seq. ID	LIB3189-021-P1-K1-A7
Method	BLASTX
NCBI GI	g2392769
BLAST score	139
E value	9.0e-14

Match length	74
% identity	64
NCBI Description	(AC002534) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	227136
Seq. ID	LIB3189-021-P1-K1-A8
Method	BLASTX
NCBI GI	g3450889
BLAST score	223
E value	9.0e-25
Match length	90
% identity	70
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	227137
Seq. ID	LIB3189-021-P1-K1-B12
Method	BLASTX
NCBI GI	g2497743
BLAST score	168
E value	4.0e-12
Match length	31
% identity	100
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	227138
Seq. ID	LIB3189-021-P1-K1-B9
Method	BLASTX
NCBI GI	g2947060
BLAST score	461
E value	4.0e-46
Match length	99
% identity	83
NCBI Description	(AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No.	227139
Seq. ID	LIB3189-021-P1-K1-C11
Method	BLASTX
NCBI GI	g1871192
BLAST score	264
E value	3.0e-23
Match length	72
% identity	75
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	227140
Seq. ID	LIB3189-021-P1-K1-C12
Method	BLASTX
NCBI GI	g294668
BLAST score	481
E value	2.0e-48
Match length	130
% identity	80

NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	227141
Seq. ID	LIB3189-021-P1-K1-C2
Method	BLASTX
NCBI GI	g730456
BLAST score	254
E value	3.0e-22
Match length	67
% identity	69
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	227142
Seq. ID	LIB3189-021-P1-K1-C4
Method	BLASTX
NCBI GI	g310317
BLAST score	146
E value	9.0e-10
Match length	37
% identity	76
NCBI Description	(L19598) beta-tubulin [Oryza sativa]

Seq. No.	227143
Seq. ID	LIB3189-021-P1-K1-D1
Method	BLASTX
NCBI GI	g4218120
BLAST score	526
E value	1.0e-53
Match length	138
% identity	74
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	227144
Seq. ID	LIB3189-021-P1-K1-D10
Method	BLASTX
NCBI GI	g120669
BLAST score	189
E value	8.0e-15
Match length	41
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	227145
Seq. ID	LIB3189-021-P1-K1-D11
Method	BLASTX
NCBI GI	g3859944
BLAST score	413
E value	1.0e-40
Match length	102
% identity	83
NCBI Description	(AF084570) FKBP12 interacting protein [Arabidopsis thaliana]

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Seq. No.	227146
Seq. ID	LIB3189-021-P1-K1-D12
Method	BLASTX
NCBI GI	g1172817
BLAST score	251
E value	1.0e-21
Match length	69
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_ (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]

Seq. No.	227147
Seq. ID	LIB3189-021-P1-K1-E1
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	8.0e-20
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	227148
Seq. ID	LIB3189-021-P1-K1-E11
Method	BLASTX
NCBI GI	g1279206
BLAST score	270
E value	2.0e-24
Match length	59
% identity	90
NCBI Description	(X97446) alpha-tubulin [Avena sativa]

Seq. No.	227149
Seq. ID	LIB3189-021-P1-K1-E3
Method	BLASTX
NCBI GI	g133409
BLAST score	398
E value	1.0e-38
Match length	87
% identity	86
NCBI Description	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi_66962_pir__RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast >gi_11860_emb_CAA77376_ (Z00044) RNA polymerase alpha subunit [Nicotiana tabacum] >gi_225228_prf__1211235BK RNA polymerase alpha [Nicotiana tabacum]

Seq. No.	227150
Seq. ID	LIB3189-021-P1-K1-E4
Method	BLASTX
NCBI GI	g1172817
BLAST score	182
E value	2.0e-13
Match length	57

% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_ (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]

Seq. No.	227151
Seq. ID	LIB3189-021-P1-K1-F11
Method	BLASTX
NCBI GI	g2624326
BLAST score	142
E value	2.0e-09
Match length	36
% identity	75
NCBI Description	(AJ002893) OsGRP1 [Oryza sativa]

Seq. No.	227152
Seq. ID	LIB3189-021-P1-K1-F7
Method	BLASTX
NCBI GI	g3152606
BLAST score	154
E value	3.0e-10
Match length	41
% identity	61
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	227153
Seq. ID	LIB3189-021-P1-K1-G1
Method	BLASTX
NCBI GI	g1703108
BLAST score	568
E value	1.0e-58
Match length	104
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	227154
Seq. ID	LIB3189-021-P1-K1-G7
Method	BLASTX
NCBI GI	g548774
BLAST score	539
E value	3.0e-55
Match length	138
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	227155
Seq. ID	LIB3189-021-P1-K1-G8
Method	BLASTX
NCBI GI	g132944

BLAST score	584
E value	1.0e-60
Match length	116
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	227156
Seq. ID	LIB3189-021-P1-K1-H11
Method	BLASTX
NCBI GI	g1771162
BLAST score	339
E value	7.0e-32
Match length	84
% identity	73
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	227157
Seq. ID	LIB3189-021-P1-K1-H3
Method	BLASTX
NCBI GI	g1495251
BLAST score	428
E value	3.0e-42
Match length	129
% identity	66
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	227158
Seq. ID	LIB3189-021-P1-K1-H5
Method	BLASTX
NCBI GI	g4204300
BLAST score	199
E value	9.0e-16
Match length	76
% identity	53
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	227159
Seq. ID	LIB3189-021-P1-K1-H6
Method	BLASTX
NCBI GI	g4325369
BLAST score	150
E value	5.0e-10
Match length	75
% identity	51
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	227160
Seq. ID	LIB3189-022-P1-K1-A12
Method	BLASTX
NCBI GI	g2341034
BLAST score	222
E value	1.0e-18
Match length	50

% identity	90
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	227161
Seq. ID	LIB3189-022-P1-K1-A3
Method	BLASTX
NCBI GI	g3915823
BLAST score	200
E value	4.0e-16
Match length	46
% identity	80
NCBI Description	[Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No.	227162
Seq. ID	LIB3189-022-P1-K1-A5
Method	BLASTX
NCBI GI	g3377797
BLAST score	154
E value	2.0e-10
Match length	47
% identity	70
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	227163
Seq. ID	LIB3189-022-P1-K1-B4
Method	BLASTX
NCBI GI	g924951
BLAST score	352
E value	3.0e-33
Match length	148
% identity	45
NCBI Description	(U30324) class I chitinase [Theobroma cacao]

Seq. No.	227164
Seq. ID	LIB3189-022-P1-K1-B7
Method	BLASTX
NCBI GI	g4454026
BLAST score	416
E value	8.0e-41
Match length	129
% identity	64
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	227165
Seq. ID	LIB3189-022-P1-K1-B8
Method	BLASTX
NCBI GI	g4454026
BLAST score	194
E value	3.0e-15
Match length	72
% identity	57
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	227166
Seq. ID	LIB3189-022-P1-K1-C8
Method	BLASTX
NCBI GI	g4510395
BLAST score	276
E value	7.0e-25
Match length	73
% identity	73
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	227167
Seq. ID	LIB3189-022-P1-K1-D11
Method	BLASTX
NCBI GI	g2435395
BLAST score	254
E value	4.0e-22
Match length	51
% identity	88
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	227168
Seq. ID	LIB3189-022-P1-K1-D12
Method	BLASTX
NCBI GI	g3694872
BLAST score	497
E value	2.0e-50
Match length	110
% identity	83
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	227169
Seq. ID	LIB3189-022-P1-K1-D2
Method	BLASTX
NCBI GI	g3377797
BLAST score	284
E value	1.0e-25
Match length	82
% identity	69
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	227170
Seq. ID	LIB3189-022-P1-K1-D3
Method	BLASTX
NCBI GI	g3650032
BLAST score	233
E value	2.0e-19
Match length	49
% identity	71
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	227171

Seq. ID	LIB3189-022-P1-K1-D4
Method	BLASTX
NCBI GI	g586076
BLAST score	570
E value	6.0e-59
Match length	114
% identity	93
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	227172
Seq. ID	LIB3189-022-P1-K1-E6
Method	BLASTX
NCBI GI	g3924612
BLAST score	442
E value	7.0e-44
Match length	125
% identity	71
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	227173
Seq. ID	LIB3189-022-P1-K1-E7
Method	BLASTX
NCBI GI	g1129145
BLAST score	183
E value	4.0e-14
Match length	62
% identity	65
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	227174
Seq. ID	LIB3189-022-P1-K1-E9
Method	BLASTX
NCBI GI	g3860272
BLAST score	228
E value	5.0e-19
Match length	51
% identity	88
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	227175
Seq. ID	LIB3189-022-P1-K1-F12
Method	BLASTX
NCBI GI	g115515
BLAST score	235
E value	3.0e-20
Match length	48
% identity	52
NCBI Description	CALMODULIN >gi_71683_pir__MCAA calmodulin - alfalfa >gi_19579_emb_CAA36644_ (X52398) calmodulin (AA 1-149) [Medicago sativa] >gi_170070 (L01430) calmodulin [Glycine max] >gi_170074 (L01432) calmodulin [Glycine max]

	>gi_506852 (L20507) calmodulin [Vigna radiata] >gi_4103957 (AF030032) calmodulin [Phaseolus vulgaris] >gi_1583767_prf__2121384A calmodulin [Glycine max] >gi_1583769_prf__2121384C calmodulin [Glycine max]
Seq. No.	227176
Seq. ID	LIB3189-022-P1-K1-F3
Method	BLASTX
NCBI GI	g1617036
BLAST score	302
E value	1.0e-27
Match length	67
% identity	79
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]
Seq. No.	227177
Seq. ID	LIB3189-022-P1-K1-F5
Method	BLASTX
NCBI GI	g3334115
BLAST score	539
E value	2.0e-55
Match length	113
% identity	57
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]
Seq. No.	227178
Seq. ID	LIB3189-022-P1-K1-F6
Method	BLASTX
NCBI GI	g3334115
BLAST score	306
E value	1.0e-28
Match length	62
% identity	41
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]
Seq. No.	227179
Seq. ID	LIB3189-022-P1-K1-F8
Method	BLASTX
NCBI GI	g120669
BLAST score	245
E value	2.0e-21
Match length	54
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	227180
Seq. ID	LIB3189-022-P1-K1-F9

Method	BLASTX
NCBI GI	g2244750
BLAST score	535
E value	8.0e-61
Match length	127
% identity	94
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	227181
Seq. ID	LIB3189-022-P1-K1-H1
Method	BLASTX
NCBI GI	g1703375
BLAST score	580
E value	5.0e-60
Match length	117
% identity	97
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	227182
Seq. ID	LIB3189-022-P1-K1-H12
Method	BLASTX
NCBI GI	g1658197
BLAST score	619
E value	5.0e-67
Match length	146
% identity	86
NCBI Description	(U74630) calreticulin [Ricinus communis] >gi_1763297 (U74631) calreticulin [Ricinus communis]

Seq. No.	227183
Seq. ID	LIB3189-022-P1-K1-H3
Method	BLASTX
NCBI GI	g586076
BLAST score	538
E value	3.0e-55
Match length	101
% identity	96
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	227184
Seq. ID	LIB3189-022-P1-K1-H4
Method	BLASTX
NCBI GI	g3202042
BLAST score	197
E value	3.0e-15
Match length	126
% identity	45
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	227185
Seq. ID	LIB3189-022-P1-K1-H7

Method	BLASTX
NCBI GI	g2129499
BLAST score	551
E value	1.0e-56
Match length	120
% identity	87
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227186
Seq. ID	LIB3189-023-P1-K1-A10
Method	BLASTX
NCBI GI	g3450842
BLAST score	290
E value	4.0e-26
Match length	121
% identity	46
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	227187
Seq. ID	LIB3189-023-P1-K1-A11
Method	BLASTX
NCBI GI	g3334322
BLAST score	363
E value	1.0e-34
Match length	103
% identity	57
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_2108347 (U55036) small GTP-binding protein Bsar1b [Brassica rapa]

Seq. No.	227188
Seq. ID	LIB3189-023-P1-K1-A12
Method	BLASTX
NCBI GI	g4204285
BLAST score	243
E value	4.0e-22
Match length	90
% identity	63
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	227189
Seq. ID	LIB3189-023-P1-K1-A2
Method	BLASTX
NCBI GI	g2244736
BLAST score	712
E value	2.0e-75
Match length	134
% identity	97
NCBI Description	(D88415) expansin [Gossypium hirsutum]

Seq. No.	227190
Seq. ID	LIB3189-023-P1-K1-A3
Method	BLASTX
NCBI GI	g120669
BLAST score	407

E value	7.0e-40
Match length	100
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	227191
Seq. ID	LIB3189-023-P1-K1-A5
Method	BLASTX
NCBI GI	g2288986
BLAST score	149
E value	4.0e-10
Match length	47
% identity	62
NCBI Description	(AC002335) glyoxalase II isolog [Arabidopsis thaliana]

Seq. No.	227192
Seq. ID	LIB3189-023-P1-K1-A7
Method	BLASTX
NCBI GI	g1922278
BLAST score	246
E value	2.0e-21
Match length	49
% identity	90
NCBI Description	(Z86091) TCTP protein [Fragaria x ananassa]

Seq. No.	227193
Seq. ID	LIB3189-023-P1-K1-A8
Method	BLASTX
NCBI GI	g2244736
BLAST score	654
E value	1.0e-68
Match length	124
% identity	96
NCBI Description	(D88415) expansin [Gossypium hirsutum]

Seq. No.	227194
Seq. ID	LIB3189-023-P1-K1-A9
Method	BLASTX
NCBI GI	g2160174
BLAST score	203
E value	8.0e-16
Match length	91
% identity	49
NCBI Description	(AC000132) Identical to A. thaliana PUR2 (gb_X74766). ESTs gb_ATTS3927,gb_N96446 come from this gene. [Arabidopsis thaliana]

Seq. No.	227195
Seq. ID	LIB3189-023-P1-K1-B10
Method	BLASTX
NCBI GI	g4185511
BLAST score	420
E value	2.0e-41

Match length	92
% identity	83
NCBI Description	(AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No.	227196
Seq. ID	LIB3189-023-P1-K1-B12
Method	BLASTX
NCBI GI	g4455225
BLAST score	330
E value	1.0e-30
Match length	101
% identity	55
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	227197
Seq. ID	LIB3189-023-P1-K1-B2
Method	BLASTX
NCBI GI	g3876865
BLAST score	161
E value	5.0e-11
Match length	73
% identity	40
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227198
Seq. ID	LIB3189-023-P1-K1-B9
Method	BLASTX
NCBI GI	g1170168
BLAST score	151
E value	6.0e-10
Match length	80
% identity	49
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1) >gi_549883 (U09332) homeobox protein [Arabidopsis thaliana] >gi_549884 (U09333) homeobox protein [Arabidopsis thaliana] >gi_2245105_emb_CAB10527_ (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	227199
Seq. ID	LIB3189-023-P1-K1-C1
Method	BLASTX
NCBI GI	g2894558
BLAST score	331
E value	7.0e-31
Match length	81
% identity	79
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	227200
Seq. ID	LIB3189-023-P1-K1-C10
Method	BLASTX
NCBI GI	g4530585
BLAST score	357

E value 7.0e-34
Match length 85
% identity 74
NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 227201
Seq. ID LIB3189-023-P1-K1-C12
Method BLASTX
NCBI GI g4544428
BLAST score 341
E value 4.0e-32
Match length 102
% identity 64
NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 227202
Seq. ID LIB3189-023-P1-K1-C2
Method BLASTX
NCBI GI g3650032
BLAST score 256
E value 4.0e-22
Match length 56
% identity 70
NCBI Description (AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No. 227203
Seq. ID LIB3189-023-P1-K1-C4
Method BLASTX
NCBI GI g3641836
BLAST score 216
E value 2.0e-22
Match length 105
% identity 50
NCBI Description (AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 227204
Seq. ID LIB3189-023-P1-K1-D11
Method BLASTX
NCBI GI g4206112
BLAST score 321
E value 9.0e-30
Match length 62
% identity 100
NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]

Seq. No. 227205
Seq. ID LIB3189-023-P1-K1-D2
Method BLASTX
NCBI GI g3135264
BLAST score 457
E value 1.0e-45
Match length 105
% identity 81
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	227206
Seq. ID	LIB3189-023-P1-K1-D6
Method	BLASTX
NCBI GI	g2811278
BLAST score	187
E value	1.0e-14
Match length	43
% identity	84
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227207
Seq. ID	LIB3189-023-P1-K1-D9
Method	BLASTX
NCBI GI	g2811278
BLAST score	523
E value	2.0e-53
Match length	128
% identity	76
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227208
Seq. ID	LIB3189-023-P1-K1-E11
Method	BLASTX
NCBI GI	g4337175
BLAST score	448
E value	1.0e-44
Match length	126
% identity	68
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	227209
Seq. ID	LIB3189-023-P1-K1-E2
Method	BLASTX
NCBI GI	g1350956
BLAST score	483
E value	9.0e-49
Match length	100
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	227210
Seq. ID	LIB3189-023-P1-K1-E5
Method	BLASTX
NCBI GI	g3021513
BLAST score	348
E value	5.0e-33
Match length	108
% identity	64
NCBI Description	(X96728) isocitrate dehydrogenase (NADP+) [Nicotiana tabacum]

Seq. No.	227211
Seq. ID	LIB3189-023-P1-K1-E7
Method	BLASTX

NCBI GI g2464905
BLAST score 139
E value 8.0e-09
Match length 74
% identity 43
NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]

Seq. No. 227212
Seq. ID LIB3189-023-P1-K1-F1
Method BLASTX
NCBI GI g2924258
BLAST score 378
E value 2.0e-36
Match length 116
% identity 66
NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No. 227213
Seq. ID LIB3189-023-P1-K1-F2
Method BLASTX
NCBI GI g4098129
BLAST score 581
E value 4.0e-60
Match length 115
% identity 91
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 227214
Seq. ID LIB3189-023-P1-K1-F4
Method BLASTX
NCBI GI g3687237
BLAST score 611
E value 1.0e-63
Match length 137
% identity 77
NCBI Description (AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No. 227215
Seq. ID LIB3189-023-P1-K1-F6
Method BLASTX
NCBI GI g3687237
BLAST score 437
E value 1.0e-43
Match length 87
% identity 80
NCBI Description (AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No. 227216
Seq. ID LIB3189-023-P1-K1-F7
Method BLASTX
NCBI GI g3319882
BLAST score 643
E value 2.0e-67
Match length 150
% identity 83

NCBI Description	(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]
Seq. No.	227217
Seq. ID	LIB3189-023-P1-K1-G1
Method	BLASTX
NCBI GI	g3759184
BLAST score	269
E value	1.0e-23
Match length	123
% identity	53
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]
Seq. No.	227218
Seq. ID	LIB3189-023-P1-K1-G10
Method	BLASTX
NCBI GI	g3319774
BLAST score	201
E value	1.0e-15
Match length	44
% identity	84
NCBI Description	(Y16228) TOM7 protein [Solanum tuberosum]
Seq. No.	227219
Seq. ID	LIB3189-023-P1-K1-G11
Method	BLASTX
NCBI GI	g2330739
BLAST score	276
E value	2.0e-24
Match length	78
% identity	63
NCBI Description	(Z98598) putative transcriptional regulator [Schizosaccharomyces pombe]
Seq. No.	227220
Seq. ID	LIB3189-023-P1-K1-G12
Method	BLASTX
NCBI GI	g547683
BLAST score	388
E value	6.0e-38
Match length	78
% identity	96
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]
Seq. No.	227221
Seq. ID	LIB3189-023-P1-K1-G2
Method	BLASTX
NCBI GI	g1729874
BLAST score	267
E value	1.0e-23
Match length	77
% identity	69
NCBI Description	T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA) (CCT-GAMMA) >gi_1078806_pir__A55423 TpCCT-gamma protein -

Tetrahymena pyriformis (SGC5) >gi_2654380_emb_CAA84368_
(Z34885) TCP1gamma protein [Tetrahymena pyriformis]

Seq. No.	227222
Seq. ID	LIB3189-023-P1-K1-G4
Method	BLASTX
NCBI GI	g3687251
BLAST score	454
E value	2.0e-45
Match length	110
% identity	78
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	227223
Seq. ID	LIB3189-023-P1-K1-G7
Method	BLASTX
NCBI GI	g2245128
BLAST score	436
E value	4.0e-43
Match length	131
% identity	63
NCBI Description	(Z97344) peroxidase [Arabidopsis thaliana]

Seq. No.	227224
Seq. ID	LIB3189-023-P1-K1-H3
Method	BLASTX
NCBI GI	g129960
BLAST score	237
E value	8.0e-20
Match length	81
% identity	51
NCBI Description	4-NITROPHENYLPHOSPHATASE (PNPPASE)

Seq. No.	227225
Seq. ID	LIB3189-023-P1-K1-H5
Method	BLASTX
NCBI GI	g2213595
BLAST score	375
E value	5.0e-36
Match length	132
% identity	55
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	227226
Seq. ID	LIB3189-024-P1-K1-A10
Method	BLASTX
NCBI GI	g303750
BLAST score	218
E value	6.0e-18
Match length	42
% identity	100
NCBI Description	(D12548) GTP-binding protein [Pisum sativum] >gi_738940_prf__2001457H GTP-binding protein [Pisum sativum]

Seq. No.	227227
Seq. ID	LIB3189-024-P1-K1-A12

Method	BLASTX
NCBI GI	g4580389
BLAST score	469
E value	5.0e-47
Match length	106
% identity	81
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	227228
Seq. ID	LIB3189-024-P1-K1-B1
Method	BLASTX
NCBI GI	g1531674
BLAST score	700
E value	3.0e-74
Match length	136
% identity	97
NCBI Description	(U68462) actin [Striga asiatica]

Seq. No.	227229
Seq. ID	LIB3189-024-P1-K1-B5
Method	BLASTX
NCBI GI	g2827559
BLAST score	169
E value	7.0e-12
Match length	109
% identity	39
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	227230
Seq. ID	LIB3189-024-P1-K1-D11
Method	BLASTX
NCBI GI	g1402878
BLAST score	196
E value	3.0e-15
Match length	99
% identity	44
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	227231
Seq. ID	LIB3189-024-P1-K1-D12
Method	BLASTX
NCBI GI	g2288997
BLAST score	190
E value	2.0e-14
Match length	54
% identity	63
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227232
Seq. ID	LIB3189-024-P1-K1-D3
Method	BLASTX
NCBI GI	g3935165
BLAST score	142
E value	9.0e-09
Match length	57

% identity	67
NCBI Description	(AC004557) F17L21.8 [Arabidopsis thaliana]
Seq. No.	227233
Seq. ID	LIB3189-024-P1-K1-E1
Method	BLASTX
NCBI GI	g2497753
BLAST score	258
E value	2.0e-22
Match length	87
% identity	53
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]
Seq. No.	227234
Seq. ID	LIB3189-024-P1-K1-E3
Method	BLASTX
NCBI GI	g3377764
BLAST score	338
E value	1.0e-31
Match length	68
% identity	94
NCBI Description	(AF079851) nodule-enhanced sucrose synthase [Pisum sativum]
Seq. No.	227235
Seq. ID	LIB3189-024-P1-K1-E9
Method	BLASTX
NCBI GI	g2950472
BLAST score	191
E value	1.0e-14
Match length	81
% identity	47
NCBI Description	(AL022070) putative autophagocytosis protein [Schizosaccharomyces pombe]
Seq. No.	227236
Seq. ID	LIB3189-024-P1-K1-F1
Method	BLASTX
NCBI GI	g2642215
BLAST score	308
E value	4.0e-28
Match length	77
% identity	77
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]
Seq. No.	227237
Seq. ID	LIB3189-024-P1-K1-F2
Method	BLASTX
NCBI GI	g3158376
BLAST score	212
E value	7.0e-17
Match length	72
% identity	62
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]
Seq. No.	227238

Seq. ID	LIB3189-024-P1-K1-F6
Method	BLASTX
NCBI GI	g2829902
BLAST score	616
E value	2.0e-64
Match length	138
% identity	83
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	227239
Seq. ID	LIB3189-024-P1-K1-G1
Method	BLASTX
NCBI GI	g4455364
BLAST score	493
E value	8.0e-50
Match length	147
% identity	59
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	227240
Seq. ID	LIB3189-024-P1-K1-G7
Method	BLASTX
NCBI GI	g4056469
BLAST score	524
E value	2.0e-53
Match length	104
% identity	99
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	227241
Seq. ID	LIB3189-024-P1-K1-G9
Method	BLASTX
NCBI GI	g1172558
BLAST score	174
E value	1.0e-12
Match length	72
% identity	47
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_480122_pir__S36454 porin por1 - garden pea >gi_396819_emb_CAA80988_ (Z25540) Porin [Pisum sativum]

Seq. No.	227242
Seq. ID	LIB3189-024-P1-K1-H3
Method	BLASTX
NCBI GI	g3080420
BLAST score	476
E value	8.0e-50
Match length	120
% identity	83
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No.	227243
Seq. ID	LIB3189-024-P1-K1-H5
Method	BLASTX
NCBI GI	g3885334
BLAST score	145
E value	4.0e-09
Match length	41
% identity	66
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	227244
Seq. ID	LIB3189-024-P1-K1-H6
Method	BLASTX
NCBI GI	g4559358
BLAST score	383
E value	5.0e-37
Match length	100
% identity	72
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	227245
Seq. ID	LIB3189-024-P1-K1-H9
Method	BLASTX
NCBI GI	g3334113
BLAST score	401
E value	3.0e-39
Match length	78
% identity	97
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	227246
Seq. ID	LIB3189-025-P1-K1-A1
Method	BLASTX
NCBI GI	g3668089
BLAST score	171
E value	4.0e-12
Match length	86
% identity	41
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	227247
Seq. ID	LIB3189-025-P1-K1-A9
Method	BLASTX
NCBI GI	g1169009
BLAST score	238
E value	4.0e-20
Match length	107
% identity	48
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir__S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree

>gi_437777_emb_CAA52814_ (X74814) O-Methyltransferase [Eucalyptus gunnii]

Seq. No.	227248
Seq. ID	LIB3189-025-P1-K1-B1
Method	BLASTX
NCBI GI	g3377805
BLAST score	168
E value	3.0e-12
Match length	47
% identity	64
NCBI Description	(AF075597) contains similarity to several apoptosis or programmed cell death proteins such as rat apoptosis protein RP-8 (GB:M80601) [Arabidopsis thaliana] >gi_3912928_gb_AAC78712.1_ (AF001308) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	227249
Seq. ID	LIB3189-025-P1-K1-B10
Method	BLASTX
NCBI GI	g4510373
BLAST score	234
E value	2.0e-30
Match length	126
% identity	60
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	227250
Seq. ID	LIB3189-025-P1-K1-B2
Method	BLASTX
NCBI GI	g1620898
BLAST score	560
E value	1.0e-57
Match length	138
% identity	80
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]

Seq. No.	227251
Seq. ID	LIB3189-025-P1-K1-B3
Method	BLASTX
NCBI GI	g2160169
BLAST score	194
E value	8.0e-15
Match length	75
% identity	55
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	227252
Seq. ID	LIB3189-025-P1-K1-B4
Method	BLASTX
NCBI GI	g2623310
BLAST score	349
E value	4.0e-33
Match length	100
% identity	67

NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3402721 (AC004261) unknown protein [Arabidopsis thaliana]
Seq. No.	227253
Seq. ID	LIB3189-025-P1-K1-B5
Method	BLASTX
NCBI GI	g4510373
BLAST score	220
E value	3.0e-28
Match length	82
% identity	80
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]
Seq. No.	227254
Seq. ID	LIB3189-025-P1-K1-B8
Method	BLASTX
NCBI GI	g2088649
BLAST score	304
E value	1.0e-27
Match length	90
% identity	66
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]
Seq. No.	227255
Seq. ID	LIB3189-025-P1-K1-B9
Method	BLASTX
NCBI GI	g133409
BLAST score	595
E value	7.0e-62
Match length	129
% identity	88
NCBI Description	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi_66962_pir__RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast >gi_11860_emb_CAA77376_ (Z00044) RNA polymerase alpha subunit [Nicotiana tabacum] >gi_225228_prf__1211235BK RNA polymerase alpha [Nicotiana tabacum]
Seq. No.	227256
Seq. ID	LIB3189-025-P1-K1-C5
Method	BLASTX
NCBI GI	g167367
BLAST score	259
E value	5.0e-23
Match length	61
% identity	80
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	227257
Seq. ID	LIB3189-025-P1-K1-D3
Method	BLASTX
NCBI GI	g2605621
BLAST score	382
E value	2.0e-37
Match length	80

% identity	88
NCBI Description	(D88619) OSMYB3 [Oryza sativa]

Seq. No.	227258
Seq. ID	LIB3189-025-P1-K1-E8
Method	BLASTX
NCBI GI	g4538897
BLAST score	522
E value	3.0e-53
Match length	151
% identity	64
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	227259
Seq. ID	LIB3189-025-P1-K1-F2
Method	BLASTX
NCBI GI	g1350944
BLAST score	301
E value	7.0e-28
Match length	63
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	227260
Seq. ID	LIB3189-025-P1-K1-F4
Method	BLASTX
NCBI GI	g2961300
BLAST score	387
E value	1.0e-37
Match length	78
% identity	96
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	227261
Seq. ID	LIB3189-025-P1-K1-G8
Method	BLASTX
NCBI GI	g3851001
BLAST score	395
E value	2.0e-38
Match length	96
% identity	81
NCBI Description	(AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]

Seq. No.	227262
Seq. ID	LIB3189-025-P1-K1-H12
Method	BLASTX
NCBI GI	g2130073
BLAST score	387
E value	1.0e-37
Match length	86
% identity	90
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	227263
Seq. ID	LIB3189-026-P1-K1-A11
Method	BLASTX
NCBI GI	g3415117
BLAST score	251
E value	2.0e-21
Match length	71
% identity	66
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	227264
Seq. ID	LIB3189-026-P1-K1-A7
Method	BLASTX
NCBI GI	g3024126
BLAST score	572
E value	4.0e-59
Match length	118
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	227265
Seq. ID	LIB3189-026-P1-K1-B12
Method	BLASTX
NCBI GI	g140207
BLAST score	147
E value	6.0e-10
Match length	38
% identity	63
NCBI Description	PROBABLE 40S RIBOSOMAL PROTEIN S9 >gi_102109_pir__S12674 ribosomal protein S9.e - Trypanosoma brucei >gi_10399_emb_CAA36818_ (X52586) ald orfU protein (AA 1 - 190) [Trypanosoma brucei]

Seq. No.	227266
Seq. ID	LIB3189-026-P1-K1-B4
Method	BLASTX
NCBI GI	g3603401
BLAST score	230
E value	1.0e-19
Match length	60
% identity	75
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	227267
Seq. ID	LIB3189-026-P1-K1-B5
Method	BLASTX
NCBI GI	g2244867
BLAST score	200
E value	9.0e-16
Match length	101
% identity	43
NCBI Description	(Z97337) hydroxynitrile lyase [Arabidopsis thaliana]

Seq. No. 227268

Seq. ID	LIB3189-026-P1-K1-B7
Method	BLASTX
NCBI GI	g3915847
BLAST score	391
E value	5.0e-38
Match length	85
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	227269
Seq. ID	LIB3189-026-P1-K1-C4
Method	BLASTX
NCBI GI	g3785978
BLAST score	234
E value	1.0e-19
Match length	91
% identity	56
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	227270
Seq. ID	LIB3189-026-P1-K1-C9
Method	BLASTX
NCBI GI	g1171965
BLAST score	227
E value	3.0e-19
Match length	52
% identity	87
NCBI Description	PHOSPHATIDYLINOSITOL 3-KINASE, ROOT ISOFORM (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) (SPI3K-5) >gi_736339 (L27265) phosphatidylinositol 3-kinase [Glycine max]

Seq. No.	227271
Seq. ID	LIB3189-026-P1-K1-F11
Method	BLASTX
NCBI GI	g1362086
BLAST score	195
E value	1.0e-15
Match length	46
% identity	87
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	227272
Seq. ID	LIB3189-026-P1-K1-F4
Method	BLASTX
NCBI GI	g3650032
BLAST score	141
E value	3.0e-09
Match length	38
% identity	61
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No.	227273
Seq. ID	LIB3189-026-P1-K1-G1
Method	BLASTX
NCBI GI	g267122
BLAST score	172
E value	8.0e-13
Match length	50
% identity	66
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) >gi_478400_pir__JQ2242 thioredoxin h - Arabidopsis thaliana >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi_1388080 (U35827) thioredoxin h [Arabidopsis thaliana]

Seq. No.	227274
Seq. ID	LIB3189-026-P1-K1-G12
Method	BLASTX
NCBI GI	g942594
BLAST score	196
E value	1.0e-15
Match length	49
% identity	78
NCBI Description	(U30456) heat shock cognate protein [Urechis caupo]

Seq. No.	227275
Seq. ID	LIB3189-026-P1-K1-G5
Method	BLASTX
NCBI GI	g1076696
BLAST score	174
E value	5.0e-13
Match length	42
% identity	74
NCBI Description	cyprosin - cardoon >gi_556819_emb_CAA57510_ (X81984) cyprosin [Cynara cardunculus]

Seq. No.	227276
Seq. ID	LIB3189-026-P1-K1-G6
Method	BLASTX
NCBI GI	g3024017
BLAST score	377
E value	3.0e-38
Match length	95
% identity	81
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	227277
Seq. ID	LIB3189-026-P1-K1-H12
Method	BLASTX
NCBI GI	g267069
BLAST score	238
E value	2.0e-20
Match length	49
% identity	88

NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227278
Seq. ID	LIB3189-026-P1-K1-H8
Method	BLASTX
NCBI GI	g3451072
BLAST score	230
E value	3.0e-19
Match length	69
% identity	61
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	227279
Seq. ID	LIB3189-027-P1-K1-A6
Method	BLASTX
NCBI GI	g2388574
BLAST score	151
E value	2.0e-10
Match length	46
% identity	65
NCBI Description	(AC000098) Strong similarity to Phalaenopsis homeobox protein (gb_U34743). [Arabidopsis thaliana]

Seq. No.	227280
Seq. ID	LIB3189-027-P1-K1-B3
Method	BLASTX
NCBI GI	g2062167
BLAST score	354
E value	3.0e-35
Match length	107
% identity	73
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	227281
Seq. ID	LIB3189-027-P1-K1-B6
Method	BLASTX
NCBI GI	g3420008
BLAST score	193
E value	7.0e-15
Match length	77
% identity	47
NCBI Description	(AF000307) steroid sulfotransferase 3 [Brassica napus]

Seq. No.	227282
Seq. ID	LIB3189-027-P1-K1-C1
Method	BLASTX
NCBI GI	g1370198
BLAST score	239
E value	1.0e-20
Match length	57
% identity	86
NCBI Description	(Z73948) RAB8E [Lotus japonicus]

Seq. No.	227283
Seq. ID	LIB3189-027-P1-K1-D7
Method	BLASTX
NCBI GI	g2499610
BLAST score	571
E value	5.0e-59
Match length	148
% identity	78
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6) (ATMPK6) >gi_629547_pir__S40472 mitogen-activated protein kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457404_dbj_BAA04869_ (D21842) MAP kinase [Arabidopsis thaliana] >gi_2281091 (AC002333) MAP Kinase 6 [Arabidopsis thaliana]

Seq. No.	227284
Seq. ID	LIB3189-027-P1-K1-E11
Method	BLASTX
NCBI GI	g167367
BLAST score	290
E value	3.0e-26
Match length	58
% identity	95
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	227285
Seq. ID	LIB3189-027-P1-K1-F12
Method	BLASTX
NCBI GI	g1707955
BLAST score	557
E value	2.0e-57
Match length	111
% identity	95
NCBI Description	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 (GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_ (X94320) glutamine synthetase [Vitis vinifera]

Seq. No.	227286
Seq. ID	LIB3189-027-P1-K1-F7
Method	BLASTX
NCBI GI	g2961377
BLAST score	185
E value	7.0e-14
Match length	122
% identity	3
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	227287
Seq. ID	LIB3189-027-P1-K1-F8
Method	BLASTX
NCBI GI	g3337361
BLAST score	213
E value	5.0e-17
Match length	64
% identity	59
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	227288
Seq. ID	LIB3189-027-P1-K1-G5
Method	BLASTX
NCBI GI	g2340166
BLAST score	212
E value	6.0e-17
Match length	92
% identity	52
NCBI Description	(AF008124) glutathione S-conjugate transporting ATPase [Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug resistance-associated protein homolog [Arabidopsis thaliana]

Seq. No.	227289
Seq. ID	LIB3189-027-P1-K1-G7
Method	BLASTX
NCBI GI	g4098129
BLAST score	446
E value	2.0e-44
Match length	83
% identity	100
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	227290
Seq. ID	LIB3189-027-P1-K1-H2
Method	BLASTX
NCBI GI	g1694621
BLAST score	187
E value	4.0e-14
Match length	76
% identity	53
NCBI Description	(D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No.	227291
Seq. ID	LIB3189-027-P1-K1-H3
Method	BLASTX
NCBI GI	g2961300
BLAST score	483
E value	8.0e-49
Match length	117
% identity	80
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	227292
Seq. ID	LIB3189-027-P1-K1-H4
Method	BLASTX
NCBI GI	g2661840
BLAST score	366
E value	5.0e-35
Match length	98
% identity	68
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	227293
Seq. ID	LIB3189-027-P1-K1-H5
Method	BLASTX

NCBI GI	g3914394
BLAST score	292
E value	2.0e-36
Match length	97
% identity	74
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	227294
Seq. ID	LIB3189-027-P1-K1-H6
Method	BLASTX
NCBI GI	g3986695
BLAST score	537
E value	4.0e-55
Match length	121
% identity	90
NCBI Description	(AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No.	227295
Seq. ID	LIB3189-027-P1-K1-H8
Method	BLASTX
NCBI GI	g1694621
BLAST score	387
E value	2.0e-37
Match length	115
% identity	70
NCBI Description	(D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No.	227296
Seq. ID	LIB3189-028-P1-K1-A10
Method	BLASTX
NCBI GI	g1293835
BLAST score	225
E value	2.0e-18
Match length	135
% identity	33
NCBI Description	(U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No.	227297
Seq. ID	LIB3189-028-P1-K1-A12
Method	BLASTX
NCBI GI	g1917019
BLAST score	559
E value	1.0e-57
Match length	118
% identity	89
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.	227298
Seq. ID	LIB3189-028-P1-K1-A7
Method	BLASTX
NCBI GI	g3785989
BLAST score	228
E value	3.0e-19

Match length	68
% identity	68
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	227299
Seq. ID	LIB3189-028-P1-K1-B12
Method	BLASTX
NCBI GI	g167367
BLAST score	534
E value	1.0e-54
Match length	126
% identity	84
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	227300
Seq. ID	LIB3189-028-P1-K1-C12
Method	BLASTX
NCBI GI	g2829204
BLAST score	189
E value	1.0e-14
Match length	35
% identity	100
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	227301
Seq. ID	LIB3189-028-P1-K1-C7
Method	BLASTX
NCBI GI	g71498
BLAST score	261
E value	1.0e-22
Match length	116
% identity	50
NCBI Description	heat shock protein 17.7 - garden pea

Seq. No.	227302
Seq. ID	LIB3189-028-P1-K1-D10
Method	BLASTX
NCBI GI	g1364059
BLAST score	231
E value	3.0e-19
Match length	109
% identity	44
NCBI Description	dioscorin class A precursor - Dioscorea cayenensis >gi_433463_emb_CAA53781_ (X76187) storage protein [Dioscorea cayenensis]

Seq. No.	227303
Seq. ID	LIB3189-028-P1-K1-D6
Method	BLASTX
NCBI GI	g4006848
BLAST score	153
E value	5.0e-10
Match length	37
% identity	78
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	227304
Seq. ID	LIB3189-028-P1-K1-D7
Method	BLASTX
NCBI GI	g3420239
BLAST score	153
E value	2.0e-10
Match length	31
% identity	97
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	227305
Seq. ID	LIB3189-028-P1-K1-D9
Method	BLASTX
NCBI GI	g4508073
BLAST score	309
E value	2.0e-28
Match length	95
% identity	62
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	227306
Seq. ID	LIB3189-028-P1-K1-F11
Method	BLASTX
NCBI GI	g3288113
BLAST score	386
E value	2.0e-37
Match length	106
% identity	74
NCBI Description	(Z97067) elongation factor 1-beta [Beta vulgaris]

Seq. No.	227307
Seq. ID	LIB3189-028-P1-K1-F12
Method	BLASTX
NCBI GI	g1076708
BLAST score	643
E value	2.0e-67
Match length	129
% identity	28
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]

Seq. No.	227308
Seq. ID	LIB3189-028-P1-K1-F6
Method	BLASTX
NCBI GI	g2129499
BLAST score	655
E value	7.0e-69
Match length	133
% identity	92

NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	227309
Seq. ID	LIB3189-028-P1-K1-F7
Method	BLASTX
NCBI GI	g167367
BLAST score	666
E value	3.0e-70
Match length	125
% identity	98
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	227310
Seq. ID	LIB3189-028-P1-K1-F8
Method	BLASTX
NCBI GI	g1762945
BLAST score	347
E value	8.0e-33
Match length	103
% identity	61
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]
Seq. No.	227311
Seq. ID	LIB3189-028-P1-K1-F9
Method	BLASTX
NCBI GI	g3023751
BLAST score	499
E value	1.0e-50
Match length	136
% identity	71
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]
Seq. No.	227312
Seq. ID	LIB3189-028-P1-K1-G2
Method	BLASTX
NCBI GI	g4193388
BLAST score	280
E value	4.0e-25
Match length	80
% identity	69
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	227313
Seq. ID	LIB3189-028-P1-K1-G4
Method	BLASTX
NCBI GI	g1304128
BLAST score	304
E value	6.0e-28
Match length	77
% identity	10

NCBI Description	(D63791) polyubiquitin [Homo sapiens]
Seq. No.	227314
Seq. ID	LIB3189-028-P1-K1-G5
Method	BLASTX
NCBI GI	g2262158
BLAST score	333
E value	4.0e-31
Match length	126
% identity	58
NCBI Description	(AC002329) putative mitochondrial phosphate translocator protein [Arabidopsis thaliana]
Seq. No.	227315
Seq. ID	LIB3189-028-P1-K1-G7
Method	BLASTX
NCBI GI	g992706
BLAST score	528
E value	3.0e-54
Match length	113
% identity	91
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]
Seq. No.	227316
Seq. ID	LIB3189-028-P1-K1-G9
Method	BLASTX
NCBI GI	g730583
BLAST score	241
E value	2.0e-20
Match length	62
% identity	77
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]
Seq. No.	227317
Seq. ID	LIB3189-028-P1-K1-H1
Method	BLASTX
NCBI GI	g1402878
BLAST score	241
E value	2.0e-20
Match length	86
% identity	56
NCBI Description	(X98130) unknown [Arabidopsis thaliana]
Seq. No.	227318
Seq. ID	LIB3189-028-P1-K1-H2
Method	BLASTX
NCBI GI	g4325338
BLAST score	499
E value	1.0e-50
Match length	118
% identity	76
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]
Seq. No.	227319
Seq. ID	LIB3189-028-P1-K1-H3

Method	BLASTX
NCBI GI	g3935145
BLAST score	231
E value	3.0e-19
Match length	95
% identity	50
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	227320
Seq. ID	LIB3189-028-P1-K1-H4
Method	BLASTX
NCBI GI	g1332579
BLAST score	189
E value	2.0e-14
Match length	83
% identity	6
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	227321
Seq. ID	LIB3189-028-P1-K1-H7
Method	BLASTX
NCBI GI	g2129735
BLAST score	349
E value	4.0e-33
Match length	113
% identity	57
NCBI Description	serine/threonine-specific kinase (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_1405837_emb_CAA62824_ (X91630) receptor-like kinase [Arabidopsis thaliana] >gi_2150023 (AF001168) receptor-like kinase LECRK1 [Arabidopsis thaliana]

Seq. No.	227322
Seq. ID	LIB3189-028-P1-K1-H8
Method	BLASTX
NCBI GI	g2980767
BLAST score	220
E value	5.0e-24
Match length	111
% identity	62
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	227323
Seq. ID	LIB3189-030-P1-K1-A1
Method	BLASTX
NCBI GI	g2369766
BLAST score	378
E value	1.0e-36
Match length	106
% identity	70
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	227324
Seq. ID	LIB3189-030-P1-K1-A4
Method	BLASTX
NCBI GI	g3869088
BLAST score	582

E value	2.0e-60
Match length	117
% identity	96
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	227325
Seq. ID	LIB3189-030-P1-K1-B12
Method	BLASTX
NCBI GI	g730645
BLAST score	171
E value	1.0e-12
Match length	38
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	227326
Seq. ID	LIB3189-030-P1-K1-B2
Method	BLASTX
NCBI GI	g4538913
BLAST score	244
E value	8.0e-21
Match length	62
% identity	79
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	227327
Seq. ID	LIB3189-030-P1-K1-B3
Method	BLASTX
NCBI GI	g3204125
BLAST score	345
E value	2.0e-32
Match length	83
% identity	81
NCBI Description	(AJ006766) putative Pi starvation-induced protein [Cicer arietinum]

Seq. No.	227328
Seq. ID	LIB3189-030-P1-K1-B4
Method	BLASTX
NCBI GI	g1843527
BLAST score	293
E value	8.0e-27
Match length	74
% identity	80
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	227329
Seq. ID	LIB3189-030-P1-K1-B8
Method	BLASTX
NCBI GI	g464981

BLAST score	249
E value	2.0e-21
Match length	48
% identity	96
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	227330
Seq. ID	LIB3189-030-P1-K1-C11
Method	BLASTX
NCBI GI	g464621
BLAST score	215
E value	1.0e-17
Match length	66
% identity	59
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	227331
Seq. ID	LIB3189-030-P1-K1-C12
Method	BLASTX
NCBI GI	g3882081
BLAST score	491
E value	9.0e-50
Match length	101
% identity	36
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	227332
Seq. ID	LIB3189-030-P1-K1-C3
Method	BLASTX
NCBI GI	g2661840
BLAST score	373
E value	9.0e-36
Match length	99
% identity	72
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	227333
Seq. ID	LIB3189-030-P1-K1-C4
Method	BLASTX
NCBI GI	g3421140
BLAST score	338
E value	8.0e-32
Match length	118
% identity	59
NCBI Description	(AF045668) arginine decarboxylase [Polanisia dodecandra]

Seq. No.	227334
Seq. ID	LIB3189-030-P1-K1-D1
Method	BLASTX
NCBI GI	g4008159
BLAST score	517
E value	1.0e-52

Match length	139
% identity	94
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	227335
Seq. ID	LIB3189-030-P1-K1-D11
Method	BLASTX
NCBI GI	g124226
BLAST score	332
E value	4.0e-31
Match length	70
% identity	93
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	227336
Seq. ID	LIB3189-030-P1-K1-D12
Method	BLASTX
NCBI GI	g4406372
BLAST score	445
E value	3.0e-44
Match length	139
% identity	65
NCBI Description	(AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No.	227337
Seq. ID	LIB3189-030-P1-K1-D2
Method	BLASTX
NCBI GI	g4455150
BLAST score	296
E value	7.0e-27
Match length	126
% identity	48
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	227338
Seq. ID	LIB3189-030-P1-K1-D9
Method	BLASTX
NCBI GI	g115492
BLAST score	560
E value	9.0e-58
Match length	112
% identity	52
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	227339
Seq. ID	LIB3189-030-P1-K1-E12
Method	BLASTX
NCBI GI	g3334115
BLAST score	163
E value	1.0e-11
Match length	48

% identity	65
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	227340
Seq. ID	LIB3189-030-P1-K1-E2
Method	BLASTX
NCBI GI	g1174592
BLAST score	659
E value	3.0e-69
Match length	123
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	227341
Seq. ID	LIB3189-030-P1-K1-E4
Method	BLASTX
NCBI GI	g2462746
BLAST score	279
E value	4.0e-25
Match length	74
% identity	72
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	227342
Seq. ID	LIB3189-030-P1-K1-E6
Method	BLASTX
NCBI GI	g2829204
BLAST score	189
E value	1.0e-14
Match length	35
% identity	100
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	227343
Seq. ID	LIB3189-030-P1-K1-E8
Method	BLASTX
NCBI GI	g3023751
BLAST score	470
E value	2.0e-47
Match length	110
% identity	31
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	227344
Seq. ID	LIB3189-030-P1-K1-F1
Method	BLASTX

NCBI GI	g3355617
BLAST score	216
E value	2.0e-17
Match length	56
% identity	75
NCBI Description	(AJ000229) unnamed protein product [Hordeum vulgare]

Seq. No.	227345
Seq. ID	LIB3189-030-P1-K1-F10
Method	BLASTX
NCBI GI	g1351408
BLAST score	403
E value	2.0e-39
Match length	98
% identity	76
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	227346
Seq. ID	LIB3189-030-P1-K1-F2
Method	BLASTX
NCBI GI	g1703574
BLAST score	339
E value	8.0e-32
Match length	142
% identity	46
NCBI Description	(U80437) C43E11.9 [Caenorhabditis elegans]

Seq. No.	227347
Seq. ID	LIB3189-030-P1-K1-F3
Method	BLASTX
NCBI GI	g2924520
BLAST score	544
E value	8.0e-56
Match length	144
% identity	74
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	227348
Seq. ID	LIB3189-030-P1-K1-F4
Method	BLASTX
NCBI GI	g267082
BLAST score	523
E value	2.0e-53
Match length	100
% identity	99
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	227349
Seq. ID	LIB3189-030-P1-K1-F7
Method	BLASTX

NCBI GI	g3738338
BLAST score	188
E value	2.0e-14
Match length	79
% identity	57
NCBI Description	(AC005170) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	227350
Seq. ID	LIB3189-030-P1-K1-G11
Method	BLASTX
NCBI GI	g3184082
BLAST score	290
E value	5.0e-26
Match length	148
% identity	42
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	227351
Seq. ID	LIB3189-030-P1-K1-G12
Method	BLASTX
NCBI GI	g2564066
BLAST score	222
E value	3.0e-18
Match length	80
% identity	55
NCBI Description	(D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Seq. No.	227352
Seq. ID	LIB3189-030-P1-K1-G3
Method	BLASTX
NCBI GI	g1076738
BLAST score	531
E value	3.0e-54
Match length	103
% identity	94
NCBI Description	beta-tubulin R2242 - rice

Seq. No.	227353
Seq. ID	LIB3189-030-P1-K1-G4
Method	BLASTX
NCBI GI	g3549648
BLAST score	386
E value	2.0e-37
Match length	120
% identity	62
NCBI Description	(AJ010728) alpha amylase [Avena fatua]

Seq. No.	227354
Seq. ID	LIB3189-030-P1-K1-H1
Method	BLASTX
NCBI GI	g3913633
BLAST score	157
E value	3.0e-18
Match length	87
% identity	61

NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown protein [Arabidopsis thaliana]
Seq. No.	227355
Seq. ID	LIB3189-030-P1-K1-H11
Method	BLASTX
NCBI GI	g2129499
BLAST score	353
E value	1.0e-41
Match length	129
% identity	71
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	227356
Seq. ID	LIB3189-030-P1-K1-H12
Method	BLASTX
NCBI GI	g1935912
BLAST score	161
E value	6.0e-11
Match length	93
% identity	39
NCBI Description	(U77346) LLS1 [Zea mays]
Seq. No.	227357
Seq. ID	LIB3189-030-P1-K1-H3
Method	BLASTX
NCBI GI	g464981
BLAST score	480
E value	3.0e-48
Match length	101
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.	227358
Seq. ID	LIB3189-030-P1-K1-H5
Method	BLASTX
NCBI GI	g2529229
BLAST score	159
E value	5.0e-11
Match length	51
% identity	65
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
Seq. No.	227359
Seq. ID	LIB3189-030-P1-K1-H6
Method	BLASTX
NCBI GI	g2129499
BLAST score	707
E value	6.0e-75
Match length	142
% identity	93
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227360
Seq. ID	LIB3189-031-P1-K1-A10
Method	BLASTX
NCBI GI	g1172873
BLAST score	444
E value	4.0e-44
Match length	147
% identity	56
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	227361
Seq. ID	LIB3189-031-P1-K1-A11
Method	BLASTX
NCBI GI	g1076316
BLAST score	158
E value	1.0e-10
Match length	62
% identity	45
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	227362
Seq. ID	LIB3189-031-P1-K1-A2
Method	BLASTX
NCBI GI	g267069
BLAST score	361
E value	1.0e-34
Match length	71
% identity	94
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227363
Seq. ID	LIB3189-031-P1-K1-A4
Method	BLASTX
NCBI GI	g3128228
BLAST score	144
E value	1.0e-09
Match length	40
% identity	72
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	227364
Seq. ID	LIB3189-031-P1-K1-A6
Method	BLASTX
NCBI GI	g1619297
BLAST score	451
E value	4.0e-45
Match length	87

% identity	95
NCBI Description	(Y08490) alpha-tubulin 2 [Hordeum vulgare]

Seq. No.	227365
Seq. ID	LIB3189-031-P1-K1-A8
Method	BLASTX
NCBI GI	g267069
BLAST score	296
E value	3.0e-27
Match length	56
% identity	95
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227366
Seq. ID	LIB3189-031-P1-K1-A9
Method	BLASTX
NCBI GI	g4567274
BLAST score	530
E value	2.0e-54
Match length	110
% identity	85
NCBI Description	(AC006841) putative cysteine proteinase precursor [Arabidopsis thaliana]

Seq. No.	227367
Seq. ID	LIB3189-031-P1-K1-B11
Method	BLASTX
NCBI GI	g3047085
BLAST score	382
E value	7.0e-37
Match length	124
% identity	61
NCBI Description	(AF058914) No definition line found [Arabidopsis thaliana]

Seq. No.	227368
Seq. ID	LIB3189-031-P1-K1-B3
Method	BLASTX
NCBI GI	g2369766
BLAST score	294
E value	3.0e-44
Match length	139
% identity	68
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	227369
Seq. ID	LIB3189-031-P1-K1-C10
Method	BLASTX
NCBI GI	g3135257
BLAST score	146
E value	4.0e-09
Match length	84
% identity	55
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	227370
Seq. ID	LIB3189-031-P1-K1-C12
Method	BLASTX
NCBI GI	g267069
BLAST score	648
E value	5.0e-68
Match length	120
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227371
Seq. ID	LIB3189-031-P1-K1-C3
Method	BLASTX
NCBI GI	g4567274
BLAST score	589
E value	3.0e-61
Match length	119
% identity	87
NCBI Description	(AC006841) putative cysteine proteinase precursor [Arabidopsis thaliana]

Seq. No.	227372
Seq. ID	LIB3189-031-P1-K1-C6
Method	BLASTX
NCBI GI	g267075
BLAST score	677
E value	2.0e-71
Match length	132
% identity	93
NCBI Description	TUBULIN BETA-2 CHAIN >gi_388254_emb_CAA38614_ (X54845) beta-tubulin 2 [Pisum sativum]

Seq. No.	227373
Seq. ID	LIB3189-031-P1-K1-C9
Method	BLASTX
NCBI GI	g3158376
BLAST score	259
E value	2.0e-29
Match length	100
% identity	68
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	227374
Seq. ID	LIB3189-031-P1-K1-D11
Method	BLASTX
NCBI GI	g112717
BLAST score	265
E value	4.0e-23
Match length	115
% identity	43
NCBI Description	21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi_82050_pir__S10911 hypothetical protein precursor - carrot >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA -22 to 171) [Daucus carota]

Seq. No.	227375
Seq. ID	LIB3189-031-P1-K1-D3
Method	BLASTX
NCBI GI	g1732511
BLAST score	477
E value	6.0e-48
Match length	103
% identity	85
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	227376
Seq. ID	LIB3189-031-P1-K1-D4
Method	BLASTX
NCBI GI	g2982322
BLAST score	212
E value	1.0e-17
Match length	46
% identity	87
NCBI Description	(AF051246) probable proteasome subunit [Picea mariana]

Seq. No.	227377
Seq. ID	LIB3189-031-P1-K1-D7
Method	BLASTX
NCBI GI	g3790102
BLAST score	189
E value	1.0e-14
Match length	43
% identity	81
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	227378
Seq. ID	LIB3189-031-P1-K1-E9
Method	BLASTX
NCBI GI	g4049349
BLAST score	206
E value	8.0e-17
Match length	97
% identity	53
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	227379
Seq. ID	LIB3189-031-P1-K1-F1
Method	BLASTX
NCBI GI	g129248
BLAST score	184
E value	1.0e-13
Match length	100
% identity	23
NCBI Description	ORGAN SPECIFIC PROTEIN S2 >gi_72318_pir__KNPMS2 protein S2 - garden pea >gi_295831_emb_CAA35944_ (X51595) S2 protein [Pisum sativum]

Seq. No.	227380

Seq. ID	LIB3189-031-P1-K1-F10
Method	BLASTX
NCBI GI	g2129499
BLAST score	641
E value	3.0e-67
Match length	132
% identity	91
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227381
Seq. ID	LIB3189-031-P1-K1-F12
Method	BLASTX
NCBI GI	g464849
BLAST score	402
E value	2.0e-39
Match length	98
% identity	83
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	227382
Seq. ID	LIB3189-031-P1-K1-F4
Method	BLASTX
NCBI GI	g1351856
BLAST score	366
E value	3.0e-35
Match length	94
% identity	79
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	227383
Seq. ID	LIB3189-031-P1-K1-F6
Method	BLASTX
NCBI GI	g3348122
BLAST score	295
E value	1.0e-28
Match length	67
% identity	81
NCBI Description	(AF078670) tubulin alpha chain [Artemia franciscana]

Seq. No.	227384
Seq. ID	LIB3189-031-P1-K1-F8
Method	BLASTX
NCBI GI	g2129770
BLAST score	191
E value	2.0e-14
Match length	57
% identity	58
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No.	227385
Seq. ID	LIB3189-031-P1-K1-G1
Method	BLASTX
NCBI GI	g267069
BLAST score	268
E value	5.0e-24
Match length	52
% identity	92
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227386
Seq. ID	LIB3189-031-P1-K1-G10
Method	BLASTX
NCBI GI	g121344
BLAST score	219
E value	1.0e-22
Match length	79
% identity	70
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2) >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - garden pea >gi_169059 (M20664) glutamine synthetase (chloroplast GS2) (EC 6.3.1.2) [Pisum sativum]

Seq. No.	227387
Seq. ID	LIB3189-031-P1-K1-G6
Method	BLASTX
NCBI GI	g2632252
BLAST score	273
E value	3.0e-24
Match length	74
% identity	73
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	227388
Seq. ID	LIB3189-031-P1-K1-G7
Method	BLASTX
NCBI GI	g120674
BLAST score	158
E value	6.0e-15
Match length	74
% identity	72
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66015_pir__DENDG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - common buttercup >gi_21066_emb_CAA42903_ (X60345) glyceraldehyde 3-phosphate dehydrogenase [Ranunculus acris]

Seq. No.	227389
Seq. ID	LIB3189-031-P1-K1-H12
Method	BLASTX
NCBI GI	g3114901

BLAST score	140
E value	4.0e-09
Match length	32
% identity	81
NCBI Description	(AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] >gi_3114905_emb_CAA06709_ (AJ005806) pceberh [Populus balsamifera subsp. trichocarpa]

Seq. No.	227390
Seq. ID	LIB3189-031-P1-K1-H4
Method	BLASTX
NCBI GI	g232024
BLAST score	718
E value	2.0e-76
Match length	134
% identity	100
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	227391
Seq. ID	LIB3189-031-P1-K1-H8
Method	BLASTX
NCBI GI	g2842490
BLAST score	174
E value	2.0e-12
Match length	68
% identity	46
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	227392
Seq. ID	LIB3189-032-P1-K1-A11
Method	BLASTX
NCBI GI	g120669
BLAST score	520
E value	4.0e-53
Match length	103
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	227393
Seq. ID	LIB3189-032-P1-K1-A12
Method	BLASTX
NCBI GI	g2129499
BLAST score	590
E value	3.0e-61
Match length	132
% identity	83
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227394
Seq. ID	LIB3189-032-P1-K1-A3
Method	BLASTX
NCBI GI	g2078350
BLAST score	160
E value	2.0e-11
Match length	44
% identity	82
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	227395
Seq. ID	LIB3189-032-P1-K1-A6
Method	BLASTX
NCBI GI	g2465015
BLAST score	165
E value	2.0e-11
Match length	128
% identity	35
NCBI Description	(AJ001449) ripening-induced protein [Fragaria vesca]

Seq. No.	227396
Seq. ID	LIB3189-032-P1-K1-B1
Method	BLASTX
NCBI GI	g3176098
BLAST score	463
E value	2.0e-46
Match length	129
% identity	26
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	227397
Seq. ID	LIB3189-032-P1-K1-B2
Method	BLASTX
NCBI GI	g3334405
BLAST score	605
E value	5.0e-63
Match length	128
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	227398
Seq. ID	LIB3189-032-P1-K1-B3
Method	BLASTX
NCBI GI	g2497743
BLAST score	177
E value	5.0e-13
Match length	57
% identity	61
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	227399
Seq. ID	LIB3189-032-P1-K1-B7

Method	BLASTX
NCBI GI	g2129499
BLAST score	611
E value	9.0e-64
Match length	130
% identity	88
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227400
Seq. ID	LIB3189-032-P1-K1-C10
Method	BLASTX
NCBI GI	g4539335
BLAST score	179
E value	2.0e-13
Match length	97
% identity	35
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	227401
Seq. ID	LIB3189-032-P1-K1-C3
Method	BLASTX
NCBI GI	g3643603
BLAST score	367
E value	4.0e-35
Match length	83
% identity	86
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	227402
Seq. ID	LIB3189-032-P1-K1-D1
Method	BLASTX
NCBI GI	g1707017
BLAST score	137
E value	1.0e-08
Match length	33
% identity	79
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	227403
Seq. ID	LIB3189-032-P1-K1-D11
Method	BLASTX
NCBI GI	g3717946
BLAST score	279
E value	8.0e-25
Match length	92
% identity	63
NCBI Description	(AJ005901) vag1 [Arabidopsis thaliana]

Seq. No.	227404
Seq. ID	LIB3189-032-P1-K1-D12
Method	BLASTX
NCBI GI	g3450893
BLAST score	516
E value	1.0e-52
Match length	124
% identity	81

NCBI Description	(AF084005) ras-like small monomeric GTP-binding protein [Avena fatua]
Seq. No.	227405
Seq. ID	LIB3189-032-P1-K1-D3
Method	BLASTX
NCBI GI	g3334115
BLAST score	406
E value	1.0e-39
Match length	100
% identity	82
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]
Seq. No.	227406
Seq. ID	LIB3189-032-P1-K1-E6
Method	BLASTX
NCBI GI	g2129499
BLAST score	413
E value	7.0e-41
Match length	80
% identity	99
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	227407
Seq. ID	LIB3189-032-P1-K1-F3
Method	BLASTX
NCBI GI	g2981439
BLAST score	267
E value	3.0e-30
Match length	146
% identity	55
NCBI Description	(AF051853) t-SNARE SED5 [Arabidopsis thaliana]
Seq. No.	227408
Seq. ID	LIB3189-032-P1-K1-F5
Method	BLASTX
NCBI GI	g464846
BLAST score	522
E value	3.0e-53
Match length	103
% identity	93
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]
Seq. No.	227409
Seq. ID	LIB3189-032-P1-K1-F6
Method	BLASTX
NCBI GI	g464846
BLAST score	220
E value	3.0e-18
Match length	48
% identity	83

NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]
Seq. No.	227410
Seq. ID	LIB3189-032-P1-K1-F8
Method	BLASTX
NCBI GI	g3763925
BLAST score	266
E value	2.0e-23
Match length	59
% identity	83
NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]
Seq. No.	227411
Seq. ID	LIB3189-032-P1-K1-G10
Method	BLASTX
NCBI GI	g3122060
BLAST score	286
E value	5.0e-26
Match length	60
% identity	93
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2598657_emb_CAA10847_ (AJ222579) elongation factor 1-alpha (EF1-a) [Vicia faba]
Seq. No.	227412
Seq. ID	LIB3189-032-P1-K1-G2
Method	BLASTX
NCBI GI	g1708314
BLAST score	231
E value	2.0e-27
Match length	66
% identity	98
NCBI Description	HEAT SHOCK PROTEIN 83 >gi_169296 (M99431) heat shock protein 83 [Pharbitis nil] >gi_445625_prf__1909372A heat shock protein 83 [Ipomoea nil]
Seq. No.	227413
Seq. ID	LIB3189-032-P1-K1-G3
Method	BLASTX
NCBI GI	g1172874
BLAST score	254
E value	7.0e-22
Match length	59
% identity	73
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]
Seq. No.	227414
Seq. ID	LIB3189-032-P1-K1-H1
Method	BLASTX
NCBI GI	g3219772
BLAST score	428

E value	4.0e-47
Match length	104
% identity	93
NCBI Description	ACTIN 51 >gi_1498366 (U60481) actin [Lycopersicon esculentum]

Seq. No.	227415
Seq. ID	LIB3189-032-P1-K1-H10
Method	BLASTX
NCBI GI	g4406780
BLAST score	355
E value	8.0e-34
Match length	68
% identity	94
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	227416
Seq. ID	LIB3189-032-P1-K1-H12
Method	BLASTX
NCBI GI	g2160177
BLAST score	219
E value	6.0e-18
Match length	111
% identity	41
NCBI Description	(AC000132) EST gb_R64758 comes from this gene. [Arabidopsis thaliana]

Seq. No.	227417
Seq. ID	LIB3189-032-P1-K1-H2
Method	BLASTX
NCBI GI	g2326372
BLAST score	563
E value	4.0e-58
Match length	146
% identity	73
NCBI Description	(Y14404) putative arabinose kinase [Arabidopsis thaliana]

Seq. No.	227418
Seq. ID	LIB3189-033-P1-K1-A11
Method	BLASTX
NCBI GI	g4567251
BLAST score	231
E value	3.0e-19
Match length	50
% identity	76
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	227419
Seq. ID	LIB3189-033-P1-K1-A4
Method	BLASTX
NCBI GI	g3063695
BLAST score	278
E value	8.0e-25
Match length	78
% identity	67
NCBI Description	(AL022537) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227420
Seq. ID	LIB3189-033-P1-K1-A6
Method	BLASTX
NCBI GI	g2244750
BLAST score	542
E value	8.0e-56
Match length	111
% identity	95
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	227421
Seq. ID	LIB3189-033-P1-K1-A8
Method	BLASTX
NCBI GI	g3128177
BLAST score	437
E value	2.0e-43
Match length	107
% identity	80
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	227422
Seq. ID	LIB3189-033-P1-K1-B11
Method	BLASTX
NCBI GI	g2760830
BLAST score	208
E value	1.0e-16
Match length	93
% identity	37
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	227423
Seq. ID	LIB3189-033-P1-K1-B5
Method	BLASTX
NCBI GI	g477819
BLAST score	524
E value	2.0e-53
Match length	143
% identity	71
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	227424
Seq. ID	LIB3189-033-P1-K1-B9
Method	BLASTX
NCBI GI	g1332579
BLAST score	373
E value	5.0e-36
Match length	90
% identity	9
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	227425
Seq. ID	LIB3189-033-P1-K1-C1
Method	BLASTX
NCBI GI	g1545805
BLAST score	164
E value	8.0e-12
Match length	73
% identity	52
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	227426
Seq. ID	LIB3189-033-P1-K1-C10
Method	BLASTX
NCBI GI	g114182
BLAST score	361
E value	8.0e-35
Match length	80
% identity	86
NCBI Description	CHORISMATE SYNTHASE PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE) >gi_99502_pir__A41197 chorismate synthase (EC 4.6.1.4) - pink corydalis >gi_18256_emb_CAA43034_ (X60544) chorismate synthase [Corydalis sempervirens]

Seq. No.	227427
Seq. ID	LIB3189-033-P1-K1-C11
Method	BLASTX
NCBI GI	g4006834
BLAST score	482
E value	1.0e-48
Match length	104
% identity	88
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	227428
Seq. ID	LIB3189-033-P1-K1-C12
Method	BLASTX
NCBI GI	g3402722
BLAST score	489
E value	1.0e-49
Match length	115
% identity	81
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	227429
Seq. ID	LIB3189-033-P1-K1-C2
Method	BLASTX
NCBI GI	g115492
BLAST score	308
E value	2.0e-49
Match length	113
% identity	47
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	227430
Seq. ID	LIB3189-033-P1-K1-C3
Method	BLASTX
NCBI GI	g1743354
BLAST score	208
E value	7.0e-17
Match length	54
% identity	70
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	227431
Seq. ID	LIB3189-033-P1-K1-C5
Method	BLASTX
NCBI GI	g3860333
BLAST score	298
E value	4.0e-27
Match length	79
% identity	67
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No.	227432
Seq. ID	LIB3189-033-P1-K1-C7
Method	BLASTX
NCBI GI	g2231702
BLAST score	547
E value	3.0e-56
Match length	118
% identity	86
NCBI Description	(U92086) clathrin assembly protein AP19 homolog [Arabidopsis thaliana] >gi_3080409_emb_CAA18728_ (AL022604) clathrin assembly protein AP19 homolog [Arabidopsis thaliana]

Seq. No.	227433
Seq. ID	LIB3189-033-P1-K1-C9
Method	BLASTX
NCBI GI	g3128176
BLAST score	167
E value	8.0e-12
Match length	113
% identity	36
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	227434
Seq. ID	LIB3189-033-P1-K1-D1
Method	BLASTX
NCBI GI	g3776005
BLAST score	155
E value	1.0e-10
Match length	74
% identity	49
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	227435
Seq. ID	LIB3189-033-P1-K1-D10
Method	BLASTX
NCBI GI	g1619602

BLAST score	414
E value	9.0e-41
Match length	112
% identity	39
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	227436
Seq. ID	LIB3189-033-P1-K1-D12
Method	BLASTX
NCBI GI	g2511594
BLAST score	280
E value	5.0e-25
Match length	59
% identity	90
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	227437
Seq. ID	LIB3189-033-P1-K1-D9
Method	BLASTX
NCBI GI	g3122673
BLAST score	479
E value	3.0e-48
Match length	121
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	227438
Seq. ID	LIB3189-033-P1-K1-E2
Method	BLASTX
NCBI GI	g2791834
BLAST score	149
E value	4.0e-15
Match length	72
% identity	68
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	227439
Seq. ID	LIB3189-033-P1-K1-E4
Method	BLASTX
NCBI GI	g2832696
BLAST score	155
E value	2.0e-10
Match length	74
% identity	42
NCBI Description	(AL021713) putative protein [Arabidopsis thaliana]

Seq. No.	227440
Seq. ID	LIB3189-033-P1-K1-E6
Method	BLASTX
NCBI GI	g2245020
BLAST score	502

E value	5.0e-51
Match length	137
% identity	69
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	227441
Seq. ID	LIB3189-033-P1-K1-F1
Method	BLASTX
NCBI GI	g1699370
BLAST score	244
E value	7.0e-21
Match length	112
% identity	45
NCBI Description	(S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9} [mice, liver, Peptide, 493 aa] [Mus sp.]

Seq. No.	227442
Seq. ID	LIB3189-033-P1-K1-F10
Method	BLASTX
NCBI GI	g2828296
BLAST score	364
E value	7.0e-35
Match length	75
% identity	92
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	227443
Seq. ID	LIB3189-033-P1-K1-F12
Method	BLASTX
NCBI GI	g2894378
BLAST score	585
E value	1.0e-60
Match length	144
% identity	71
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	227444
Seq. ID	LIB3189-033-P1-K1-F2
Method	BLASTX
NCBI GI	g3947719
BLAST score	249
E value	3.0e-21
Match length	53
% identity	92
NCBI Description	(AJ012653) ribosomal protein S28 [Prunus persica] >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28 [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655) ribosomal protein S28 [Prunus persica]

Seq. No.	227445
Seq. ID	LIB3189-033-P1-K1-F5
Method	BLASTX
NCBI GI	g1419088
BLAST score	651
E value	2.0e-68
Match length	147
% identity	82

NCBI Description	(Z71395) calreticulin [Nicotiana plumbaginifolia]
Seq. No.	227446
Seq. ID	LIB3189-033-P1-K1-F6
Method	BLASTX
NCBI GI	g1899188
BLAST score	448
E value	1.0e-44
Match length	138
% identity	24
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.	227447
Seq. ID	LIB3189-033-P1-K1-F7
Method	BLASTX
NCBI GI	g133939
BLAST score	455
E value	2.0e-45
Match length	101
% identity	85
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70865_pir__R3NT3 ribosomal protein S3 - common tobacco chloroplast >gi_11865_emb_CAA77381_ (Z00044) ribosomal protein S3 [Nicotiana tabacum] >gi_225235_prf__1211235BT ribosomal protein S3 [Nicotiana tabacum]
Seq. No.	227448
Seq. ID	LIB3189-033-P1-K1-G11
Method	BLASTX
NCBI GI	g136636
BLAST score	252
E value	1.0e-21
Match length	71
% identity	70
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
Seq. No.	227449
Seq. ID	LIB3189-033-P1-K1-G12
Method	BLASTX
NCBI GI	g4467151
BLAST score	342
E value	3.0e-32
Match length	130
% identity	52
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]
Seq. No.	227450
Seq. ID	LIB3189-033-P1-K1-G4
Method	BLASTX

NCBI GI	g4158232
BLAST score	284
E value	9.0e-26
Match length	65
% identity	88
NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No.	227451
Seq. ID	LIB3189-033-P1-K1-G6
Method	BLASTX
NCBI GI	g267069
BLAST score	641
E value	3.0e-67
Match length	120
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227452
Seq. ID	LIB3189-033-P1-K1-G7
Method	BLASTX
NCBI GI	g2369714
BLAST score	583
E value	2.0e-60
Match length	128
% identity	84
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	227453
Seq. ID	LIB3189-033-P1-K1-G9
Method	BLASTX
NCBI GI	g3097321
BLAST score	189
E value	3.0e-14
Match length	88
% identity	43
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	227454
Seq. ID	LIB3189-033-P1-K1-H1
Method	BLASTX
NCBI GI	g1771780
BLAST score	404
E value	1.0e-39
Match length	112
% identity	72
NCBI Description	(Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No.	227455
Seq. ID	LIB3189-033-P1-K1-H11
Method	BLASTX
NCBI GI	g3096947
BLAST score	199
E value	1.0e-16

Match length	92
% identity	52
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	227456
Seq. ID	LIB3189-033-P1-K1-H12
Method	BLASTX
NCBI GI	g2754746
BLAST score	385
E value	2.0e-37
Match length	97
% identity	70
NCBI Description	(U85448) sucrose-phosphate synthase [Actinidia deliciosa]

Seq. No.	227457
Seq. ID	LIB3189-033-P1-K1-H2
Method	BLASTX
NCBI GI	g3184281
BLAST score	252
E value	1.0e-21
Match length	70
% identity	67
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	227458
Seq. ID	LIB3189-033-P1-K1-H3
Method	BLASTX
NCBI GI	g2738982
BLAST score	180
E value	3.0e-13
Match length	57
% identity	58
NCBI Description	(AF022157) CYP71A10 [Glycine max]

Seq. No.	227459
Seq. ID	LIB3189-033-P1-K1-H4
Method	BLASTX
NCBI GI	g1843527
BLAST score	477
E value	5.0e-48
Match length	129
% identity	78
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	227460
Seq. ID	LIB3189-033-P1-K1-H6
Method	BLASTX
NCBI GI	g2811278
BLAST score	445
E value	2.0e-44
Match length	123
% identity	71
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227461
Seq. ID	LIB3189-033-P1-K1-H8

Method	BLASTX
NCBI GI	g2586127
BLAST score	329
E value	8.0e-31
Match length	106
% identity	61
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	227462
Seq. ID	LIB3189-033-P1-K1-H9
Method	BLASTX
NCBI GI	g461736
BLAST score	541
E value	1.0e-55
Match length	125
% identity	86
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_478786_pir__S29316 chaperonin 60 - cucurbit >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita sp.]

Seq. No.	227463
Seq. ID	LIB3189-034-P1-K1-A1
Method	BLASTX
NCBI GI	g2271477
BLAST score	375
E value	5.0e-36
Match length	100
% identity	75
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	227464
Seq. ID	LIB3189-034-P1-K1-A11
Method	BLASTX
NCBI GI	g1723176
BLAST score	193
E value	1.0e-14
Match length	113
% identity	42
NCBI Description	HYPOTHETICAL 22.4 KD PROTEIN SLL0615 >gi_1001617_dbj_BAA10348_ (D64002) transmembrane protein FT27 [Synechocystis sp.] >gi_1256592 (U38892) similar to Mus musculus transmembrane protein (clone pFT27); Method: conceptual translation supplied by author; ORF206 [Synechocystis sp.]

Seq. No.	227465
Seq. ID	LIB3189-034-P1-K1-A12
Method	BLASTX
NCBI GI	g112717
BLAST score	251
E value	2.0e-21
Match length	94
% identity	49
NCBI Description	21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi_82050_pir__S10911 hypothetical protein precursor - carrot >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA

-22 to 171) [Daucus carota]

Seq. No.	227466
Seq. ID	LIB3189-034-P1-K1-A2
Method	BLASTX
NCBI GI	g1914683
BLAST score	292
E value	2.0e-26
Match length	78
% identity	73
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	227467
Seq. ID	LIB3189-034-P1-K1-A3
Method	BLASTX
NCBI GI	g1657948
BLAST score	434
E value	5.0e-43
Match length	119
% identity	73
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	227468
Seq. ID	LIB3189-034-P1-K1-A4
Method	BLASTX
NCBI GI	g132866
BLAST score	477
E value	6.0e-48
Match length	94
% identity	94
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_71086_pir__R5NT2 ribosomal protein L2 - common tobacco chloroplast >gi_435269_emb_CAA77384_ (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi_1223691_emb_CAA77409_ (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi_225238_prf__1211235BW ribosomal protein L2 [Nicotiana tabacum]

Seq. No.	227469
Seq. ID	LIB3189-034-P1-K1-B1
Method	BLASTX
NCBI GI	g2982297
BLAST score	480
E value	2.0e-48
Match length	107
% identity	87
NCBI Description	(AF051233) KIAA0107-like protein [Picea mariana]

Seq. No.	227470
Seq. ID	LIB3189-034-P1-K1-B11
Method	BLASTX
NCBI GI	g71634
BLAST score	689
E value	8.0e-73
Match length	136
% identity	97
NCBI Description	actin 1 - rice

Seq. No.	227471
Seq. ID	LIB3189-034-P1-K1-B2
Method	BLASTX
NCBI GI	g2129739
BLAST score	376
E value	2.0e-36
Match length	82
% identity	91
NCBI Description	shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No.	227472
Seq. ID	LIB3189-034-P1-K1-B5
Method	BLASTX
NCBI GI	g125051
BLAST score	431
E value	1.0e-42
Match length	110
% identity	76
NCBI Description	ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD) >gi_88038_pir__A37033 isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human >gi_306897 (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens] >gi_4504799_ref_NP_002216.1_pIVD_ isovaleryl Coenzyme A dehydrogenase

Seq. No.	227473
Seq. ID	LIB3189-034-P1-K1-B7
Method	BLASTX
NCBI GI	g2811278
BLAST score	555
E value	4.0e-57
Match length	141
% identity	74
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227474
Seq. ID	LIB3189-034-P1-K1-C1
Method	BLASTX
NCBI GI	g3876865
BLAST score	161
E value	7.0e-11
Match length	73
% identity	40
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227475
Seq. ID	LIB3189-034-P1-K1-C2
Method	BLASTX
NCBI GI	g3913633
BLAST score	176

E value	6.0e-13
Match length	43
% identity	84
NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	227476
Seq. ID	LIB3189-034-P1-K1-D1
Method	BLASTX
NCBI GI	g832876
BLAST score	629
E value	8.0e-66
Match length	140
% identity	88
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	227477
Seq. ID	LIB3189-034-P1-K1-D10
Method	BLASTX
NCBI GI	g2431769
BLAST score	270
E value	1.0e-23
Match length	112
% identity	54
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	227478
Seq. ID	LIB3189-034-P1-K1-D12
Method	BLASTX
NCBI GI	g2244786
BLAST score	202
E value	4.0e-28
Match length	104
% identity	47
NCBI Description	(Z97335) ribonucleoprotein homolog [Arabidopsis thaliana]

Seq. No.	227479
Seq. ID	LIB3189-034-P1-K1-D5
Method	BLASTX
NCBI GI	g2129499
BLAST score	783
E value	8.0e-84
Match length	156
% identity	94
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227480
Seq. ID	LIB3189-034-P1-K1-D6
Method	BLASTX
NCBI GI	g4115934
BLAST score	604
E value	8.0e-63
Match length	133
% identity	81

NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]
Seq. No.	227481
Seq. ID	LIB3189-034-P1-K1-D7
Method	BLASTX
NCBI GI	g2244736
BLAST score	706
E value	8.0e-75
Match length	134
% identity	96
NCBI Description	(D88415) expansin [Gossypium hirsutum]
Seq. No.	227482
Seq. ID	LIB3189-034-P1-K1-D8
Method	BLASTX
NCBI GI	g4510354
BLAST score	261
E value	1.0e-22
Match length	132
% identity	48
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.	227483
Seq. ID	LIB3189-034-P1-K1-E10
Method	BLASTX
NCBI GI	g3024657
BLAST score	380
E value	1.0e-36
Match length	112
% identity	68
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_2668740 (AF034944) translation initiation factor; GOS2 [Zea mays]
Seq. No.	227484
Seq. ID	LIB3189-034-P1-K1-E2
Method	BLASTX
NCBI GI	g2119014
BLAST score	163
E value	4.0e-11
Match length	32
% identity	100
NCBI Description	histone H3 - African clawed frog (fragment) >gi_214274 (M21286) histone H3 [Xenopus laevis]
Seq. No.	227485
Seq. ID	LIB3189-034-P1-K1-E4
Method	BLASTX
NCBI GI	g462195
BLAST score	195
E value	6.0e-15
Match length	107
% identity	47
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice

	>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]
Seq. No.	227486
Seq. ID	LIB3189-034-P1-K1-E8
Method	BLASTX
NCBI GI	g231660
BLAST score	412
E value	9.0e-49
Match length	147
% identity	71
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.	227487
Seq. ID	LIB3189-034-P1-K1-E9
Method	BLASTX
NCBI GI	g532530
BLAST score	475
E value	7.0e-48
Match length	109
% identity	75
NCBI Description	(U07953) 1-aminocyclopropane-1-carboxylate oxidase [Pelargonium hortorum] >gi_1093803_prf__2104412A aminocyclopropane carboxylate oxidase [Pelargonium hortorum]
Seq. No.	227488
Seq. ID	LIB3189-034-P1-K1-F1
Method	BLASTX
NCBI GI	g4063751
BLAST score	201
E value	1.0e-15
Match length	133
% identity	29
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]
Seq. No.	227489
Seq. ID	LIB3189-034-P1-K1-F11
Method	BLASTX
NCBI GI	g3983663
BLAST score	160
E value	5.0e-11
Match length	54
% identity	56
NCBI Description	(AB011270) importin-beta1 [Oryza sativa]
Seq. No.	227490
Seq. ID	LIB3189-034-P1-K1-F12
Method	BLASTX
NCBI GI	g1872521
BLAST score	507
E value	2.0e-51
Match length	132
% identity	71

NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]
Seq. No.	227491
Seq. ID	LIB3189-034-P1-K1-F2
Method	BLASTX
NCBI GI	g4539422
BLAST score	490
E value	2.0e-49
Match length	140
% identity	70
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]
Seq. No.	227492
Seq. ID	LIB3189-034-P1-K1-F4
Method	BLASTX
NCBI GI	g3421090
BLAST score	140
E value	1.0e-19
Match length	91
% identity	62
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]
Seq. No.	227493
Seq. ID	LIB3189-034-P1-K1-F8
Method	BLASTX
NCBI GI	g1170509
BLAST score	576
E value	9.0e-60
Match length	119
% identity	95
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_478306_pir__JN0839 translation initiation factor eIF-4A - wheat
Seq. No.	227494
Seq. ID	LIB3189-034-P1-K1-F9
Method	BLASTX
NCBI GI	g3152565
BLAST score	177
E value	9.0e-13
Match length	80
% identity	57
NCBI Description	(AC002986) EST gb_N65759 comes from this gene. [Arabidopsis thaliana]
Seq. No.	227495
Seq. ID	LIB3189-034-P1-K1-G1
Method	BLASTX
NCBI GI	g1107526
BLAST score	368
E value	3.0e-35
Match length	115
% identity	63
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	227496
Seq. ID	LIB3189-034-P1-K1-G10
Method	BLASTX
NCBI GI	g2791834
BLAST score	584
E value	1.0e-60
Match length	116
% identity	97
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	227497
Seq. ID	LIB3189-034-P1-K1-G12
Method	BLASTX
NCBI GI	g2979555
BLAST score	160
E value	8.0e-11
Match length	111
% identity	32
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	227498
Seq. ID	LIB3189-034-P1-K1-G3
Method	BLASTX
NCBI GI	g730583
BLAST score	245
E value	6.0e-21
Match length	62
% identity	79
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	227499
Seq. ID	LIB3189-034-P1-K1-G4
Method	BLASTX
NCBI GI	g1279588
BLAST score	437
E value	3.0e-43
Match length	129
% identity	65
NCBI Description	(Z71749) glutathione S-transferase [Nicotiana plumbaginifolia]

Seq. No.	227500
Seq. ID	LIB3189-034-P1-K1-G7
Method	BLASTX
NCBI GI	g2995384
BLAST score	122
E value	6.0e-15
Match length	57
% identity	52
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	227501
Seq. ID	LIB3189-034-P1-K1-G8
Method	BLASTX

NCBI GI	g1209756
BLAST score	396
E value	1.0e-38
Match length	101
% identity	85
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	227502
Seq. ID	LIB3189-034-P1-K1-H10
Method	BLASTX
NCBI GI	g2160151
BLAST score	195
E value	1.0e-15
Match length	64
% identity	58
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	227503
Seq. ID	LIB3189-034-P1-K1-H2
Method	BLASTX
NCBI GI	g294845
BLAST score	552
E value	1.0e-56
Match length	152
% identity	70
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	227504
Seq. ID	LIB3189-034-P1-K1-H3
Method	BLASTX
NCBI GI	g2062175
BLAST score	578
E value	7.0e-60
Match length	141
% identity	82
NCBI Description	(AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227505
Seq. ID	LIB3189-034-P1-K1-H4
Method	BLASTX
NCBI GI	g3036807
BLAST score	442
E value	8.0e-44
Match length	142
% identity	62
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	227506
Seq. ID	LIB3189-034-P1-K1-H6
Method	BLASTX
NCBI GI	g3493172
BLAST score	181
E value	6.0e-14
Match length	67
% identity	60

NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	227507
Seq. ID	LIB3189-034-P1-K1-H7
Method	BLASTX
NCBI GI	g266945
BLAST score	550
E value	2.0e-56
Match length	131
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi_100065_pir__S19978 ribosomal protein L9 - garden pea >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum] >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9 [Pisum sativum]

Seq. No.	227508
Seq. ID	LIB3189-034-P1-K1-H8
Method	BLASTX
NCBI GI	g1785488
BLAST score	215
E value	3.0e-17
Match length	120
% identity	37
NCBI Description	(D14590) flavonoid 3',5'-hydroxylase [Campanula medium]

Seq. No.	227509
Seq. ID	LIB3189-034-P1-K1-H9
Method	BLASTX
NCBI GI	g2497743
BLAST score	606
E value	5.0e-63
Match length	120
% identity	97
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	227510
Seq. ID	LIB3189-035-P1-K1-A1
Method	BLASTX
NCBI GI	g4056497
BLAST score	210
E value	7.0e-17
Match length	85
% identity	59
NCBI Description	(AC005896) putative histone H2B [Arabidopsis thaliana]

Seq. No.	227511
Seq. ID	LIB3189-035-P1-K1-A11
Method	BLASTX
NCBI GI	g4262154
BLAST score	496
E value	3.0e-50
Match length	135
% identity	76

NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]
Seq. No.	227512
Seq. ID	LIB3189-035-P1-K1-A4
Method	BLASTX
NCBI GI	g4027897
BLAST score	108
E value	2.0e-12
Match length	67
% identity	66
NCBI Description	(AF049353) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.	227513
Seq. ID	LIB3189-035-P1-K1-A5
Method	BLASTX
NCBI GI	g464775
BLAST score	247
E value	4.0e-21
Match length	115
% identity	55
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]
Seq. No.	227514
Seq. ID	LIB3189-035-P1-K1-B10
Method	BLASTX
NCBI GI	g4539307
BLAST score	155
E value	1.0e-10
Match length	69
% identity	49
NCBI Description	(AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]
Seq. No.	227515
Seq. ID	LIB3189-035-P1-K1-B2
Method	BLASTX
NCBI GI	g2781357
BLAST score	302
E value	8.0e-32
Match length	107
% identity	67
NCBI Description	(AC003113) F24O1.13 [Arabidopsis thaliana]
Seq. No.	227516
Seq. ID	LIB3189-035-P1-K1-C1
Method	BLASTX
NCBI GI	g2462925
BLAST score	644
E value	1.0e-67
Match length	140
% identity	89
NCBI Description	(AJ000053) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana]

Seq. No.	227517
Seq. ID	LIB3189-035-P1-K1-C3
Method	BLASTX
NCBI GI	g125887
BLAST score	198
E value	3.0e-15
Match length	100
% identity	46
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	227518
Seq. ID	LIB3189-035-P1-K1-C7
Method	BLASTX
NCBI GI	g3650032
BLAST score	235
E value	1.0e-19
Match length	66
% identity	58
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	227519
Seq. ID	LIB3189-035-P1-K1-D12
Method	BLASTX
NCBI GI	g3193301
BLAST score	276
E value	1.0e-25
Match length	100
% identity	60
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	227520
Seq. ID	LIB3189-035-P1-K1-D2
Method	BLASTX
NCBI GI	g4510378
BLAST score	214
E value	4.0e-17
Match length	77
% identity	51
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227521
Seq. ID	LIB3189-035-P1-K1-D3
Method	BLASTX
NCBI GI	g4567251
BLAST score	560
E value	1.0e-57
Match length	141
% identity	70
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	227522
Seq. ID	LIB3189-035-P1-K1-D4
Method	BLASTX
NCBI GI	g2281115
BLAST score	558
E value	2.0e-57
Match length	136
% identity	74
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	227523
Seq. ID	LIB3189-035-P1-K1-D5
Method	BLASTX
NCBI GI	g886401
BLAST score	204
E value	5.0e-16
Match length	72
% identity	54
NCBI Description	(L37526) MADS box protein [Oryza sativa]

Seq. No.	227524
Seq. ID	LIB3189-035-P1-K1-D6
Method	BLASTX
NCBI GI	g4467125
BLAST score	495
E value	2.0e-53
Match length	142
% identity	74
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	227525
Seq. ID	LIB3189-035-P1-K1-E1
Method	BLASTX
NCBI GI	g4559346
BLAST score	421
E value	2.0e-41
Match length	131
% identity	56
NCBI Description	(AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No.	227526
Seq. ID	LIB3189-035-P1-K1-E3
Method	BLASTX
NCBI GI	g3334138
BLAST score	382
E value	6.0e-37
Match length	88
% identity	77
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	227527
Seq. ID	LIB3189-035-P1-K1-E9
Method	BLASTX
NCBI GI	g1617274
BLAST score	301

E value	2.0e-27
Match length	111
% identity	60
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	227528
Seq. ID	LIB3189-035-P1-K1-F10
Method	BLASTX
NCBI GI	g2369714
BLAST score	512
E value	4.0e-52
Match length	118
% identity	86
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	227529
Seq. ID	LIB3189-035-P1-K1-F4
Method	BLASTX
NCBI GI	g1449179
BLAST score	202
E value	6.0e-16
Match length	62
% identity	58
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	227530
Seq. ID	LIB3189-035-P1-K1-F5
Method	BLASTX
NCBI GI	g4454014
BLAST score	186
E value	6.0e-14
Match length	122
% identity	34
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	227531
Seq. ID	LIB3189-035-P1-K1-G2
Method	BLASTX
NCBI GI	g2702281
BLAST score	302
E value	6.0e-33
Match length	101
% identity	44
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	227532
Seq. ID	LIB3189-035-P1-K1-G3
Method	BLASTX
NCBI GI	g2702281
BLAST score	157
E value	7.0e-11
Match length	55
% identity	64
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	227533
Seq. ID	LIB3189-035-P1-K1-G5
Method	BLASTX
NCBI GI	g2497753
BLAST score	232
E value	2.0e-19
Match length	117
% identity	44
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	227534
Seq. ID	LIB3189-035-P1-K1-G9
Method	BLASTX
NCBI GI	g541951
BLAST score	308
E value	3.0e-28
Match length	107
% identity	57
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	227535
Seq. ID	LIB3189-035-P1-K1-H1
Method	BLASTX
NCBI GI	g1350720
BLAST score	455
E value	2.0e-45
Match length	111
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	227536
Seq. ID	LIB3189-036-P1-K1-A1
Method	BLASTX
NCBI GI	g2497743
BLAST score	600
E value	2.0e-62
Match length	120
% identity	97
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	227537
Seq. ID	LIB3189-036-P1-K1-A12
Method	BLASTX
NCBI GI	g3927838
BLAST score	224
E value	2.0e-18
Match length	68
% identity	68
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	227538
Seq. ID	LIB3189-036-P1-K1-A2
Method	BLASTX
NCBI GI	g3328240
BLAST score	313
E value	9.0e-29
Match length	92
% identity	62
NCBI Description	(AF064775) early nodule-specific protein [Medicago truncatula]

Seq. No.	227539
Seq. ID	LIB3189-036-P1-K1-A6
Method	BLASTX
NCBI GI	g2738949
BLAST score	537
E value	4.0e-55
Match length	112
% identity	89
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	227540
Seq. ID	LIB3189-036-P1-K1-B6
Method	BLASTX
NCBI GI	g1843527
BLAST score	671
E value	9.0e-71
Match length	138
% identity	54
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	227541
Seq. ID	LIB3189-036-P1-K1-B7
Method	BLASTX
NCBI GI	g3420055
BLAST score	504
E value	4.0e-51
Match length	120
% identity	80
NCBI Description	(AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No.	227542
Seq. ID	LIB3189-036-P1-K1-B8
Method	BLASTX
NCBI GI	g3153902
BLAST score	426
E value	4.0e-42
Match length	107
% identity	79
NCBI Description	(AF066076) 14-3-3-like protein [Helianthus annuus]

Seq. No.	227543
Seq. ID	LIB3189-036-P1-K1-C1
Method	BLASTX
NCBI GI	g3004560
BLAST score	259

E value	2.0e-22
Match length	75
% identity	68
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]

Seq. No.	227544
Seq. ID	LIB3189-036-P1-K1-C2
Method	BLASTX
NCBI GI	g3152606
BLAST score	372
E value	1.0e-35
Match length	81
% identity	77
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	227545
Seq. ID	LIB3189-036-P1-K1-C3
Method	BLASTX
NCBI GI	g267069
BLAST score	630
E value	6.0e-66
Match length	117
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227546
Seq. ID	LIB3189-036-P1-K1-C5
Method	BLASTX
NCBI GI	g3915826
BLAST score	538
E value	4.0e-55
Match length	135
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	227547
Seq. ID	LIB3189-036-P1-K1-C7
Method	BLASTX
NCBI GI	g2829903
BLAST score	511
E value	6.0e-52
Match length	158
% identity	68
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	227548
Seq. ID	LIB3189-036-P1-K1-C8
Method	BLASTX
NCBI GI	g3688170
BLAST score	185
E value	9.0e-14
Match length	100

% identity	46
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	227549
Seq. ID	LIB3189-036-P1-K1-C9
Method	BLASTX
NCBI GI	g2570515
BLAST score	365
E value	7.0e-35
Match length	119
% identity	60
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	227550
Seq. ID	LIB3189-036-P1-K1-D3
Method	BLASTX
NCBI GI	g2149380
BLAST score	320
E value	9.0e-30
Match length	96
% identity	67
NCBI Description	(U85036) syntaxin homolog [Arabidopsis thaliana]

Seq. No.	227551
Seq. ID	LIB3189-036-P1-K1-D7
Method	BLASTX
NCBI GI	g2119934
BLAST score	545
E value	6.0e-56
Match length	115
% identity	90
NCBI Description	translation initiation factor eIF-4A.7 - common tobacco

Seq. No.	227552
Seq. ID	LIB3189-036-P1-K1-D8
Method	BLASTX
NCBI GI	g267069
BLAST score	676
E value	3.0e-71
Match length	126
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227553
Seq. ID	LIB3189-036-P1-K1-E4
Method	BLASTX
NCBI GI	g2507281
BLAST score	695
E value	1.0e-73
Match length	127
% identity	98
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	227554
Seq. ID	LIB3189-036-P1-K1-E6
Method	BLASTX
NCBI GI	g3688170
BLAST score	180
E value	3.0e-13
Match length	107
% identity	44
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	227555
Seq. ID	LIB3189-036-P1-K1-E8
Method	BLASTX
NCBI GI	g417103
BLAST score	676
E value	3.0e-71
Match length	136
% identity	99
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	227556
Seq. ID	LIB3189-036-P1-K1-E9
Method	BLASTX
NCBI GI	g4126473
BLAST score	698
E value	6.0e-74
Match length	134
% identity	100
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	227557
Seq. ID	LIB3189-036-P1-K1-F11
Method	BLASTX
NCBI GI	g2191130
BLAST score	210
E value	1.0e-16
Match length	144
% identity	40

NCBI Description	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]
Seq. No.	227558
Seq. ID	LIB3189-036-P1-K1-F12
Method	BLASTX
NCBI GI	g1785621
BLAST score	263
E value	6.0e-23
Match length	136
% identity	43
NCBI Description	(Z84202) AtPK2324 [Arabidopsis thaliana] >gi_2465927 (AF024650) receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi_4249408 (AC006072) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	227559
Seq. ID	LIB3189-036-P1-K1-F4
Method	BLASTX
NCBI GI	g3668089
BLAST score	212
E value	6.0e-17
Match length	78
% identity	47
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	227560
Seq. ID	LIB3189-036-P1-K1-F5
Method	BLASTX
NCBI GI	g2271477
BLAST score	305
E value	6.0e-28
Match length	62
% identity	94
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]
Seq. No.	227561
Seq. ID	LIB3189-036-P1-K1-F7
Method	BLASTX
NCBI GI	g2497743
BLAST score	555
E value	3.0e-57
Match length	113
% identity	96
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]
Seq. No.	227562
Seq. ID	LIB3189-036-P1-K1-G1
Method	BLASTX
NCBI GI	g1800281
BLAST score	556
E value	3.0e-57
Match length	117
% identity	21
NCBI Description	(U82086) polyubiquitin [Fragaria x ananassa]

Seq. No.	227563
Seq. ID	LIB3189-036-P1-K1-G12
Method	BLASTX
NCBI GI	g2894378
BLAST score	249
E value	3.0e-21
Match length	126
% identity	44
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	227564
Seq. ID	LIB3189-036-P1-K1-G2
Method	BLASTX
NCBI GI	g2088652
BLAST score	544
E value	7.0e-56
Match length	129
% identity	78
NCBI Description	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No.	227565
Seq. ID	LIB3189-036-P1-K1-G3
Method	BLASTX
NCBI GI	g4263779
BLAST score	265
E value	4.0e-23
Match length	85
% identity	62
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227566
Seq. ID	LIB3189-036-P1-K1-G5
Method	BLASTX
NCBI GI	g3603401
BLAST score	370
E value	1.0e-35
Match length	100
% identity	69
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	227567
Seq. ID	LIB3189-036-P1-K1-G6
Method	BLASTX
NCBI GI	g131773
BLAST score	548
E value	2.0e-56
Match length	137
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	227568

Seq. ID	LIB3189-036-P1-K1-H10
Method	BLASTX
NCBI GI	g2129499
BLAST score	437
E value	3.0e-43
Match length	139
% identity	64
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227569
Seq. ID	LIB3189-036-P1-K1-H3
Method	BLASTX
NCBI GI	g3023945
BLAST score	510
E value	7.0e-52
Match length	103
% identity	91
NCBI Description	HISTONE DEACETYLASE (HD) >gi_2318131 (AF014824) histone deacetylase [Arabidopsis thaliana]

Seq. No.	227570
Seq. ID	LIB3189-036-P1-K1-H4
Method	BLASTX
NCBI GI	g1174867
BLAST score	336
E value	1.0e-31
Match length	72
% identity	88
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf__2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No.	227571
Seq. ID	LIB3189-036-P1-K1-H8
Method	BLASTX
NCBI GI	g2801448
BLAST score	306
E value	3.0e-28
Match length	74
% identity	73
NCBI Description	(AF028341) ubiquitin-conjugating enzyme 18 [Arabidopsis thaliana]

Seq. No.	227572
Seq. ID	LIB3189-036-P1-K1-H9
Method	BLASTX
NCBI GI	g4512653
BLAST score	479
E value	3.0e-48
Match length	113
% identity	57
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	227573
Seq. ID	LIB3189-037-P1-K1-A10
Method	BLASTX
NCBI GI	g4138137
BLAST score	291
E value	8.0e-27
Match length	58
% identity	84
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	227574
Seq. ID	LIB3189-037-P1-K1-A3
Method	BLASTX
NCBI GI	g1053047
BLAST score	416
E value	4.0e-41
Match length	86
% identity	97
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	227575
Seq. ID	LIB3189-037-P1-K1-B10
Method	BLASTX
NCBI GI	g2129946
BLAST score	327
E value	4.0e-39
Match length	87
% identity	98
NCBI Description	ADP-ribosylation factor homolog GTP-binding protein NTGB1 - common tobacco (fragment) >gi_1184987 (U46927) NTGB1 [Nicotiana tabacum]

Seq. No.	227576
Seq. ID	LIB3189-037-P1-K1-B11
Method	BLASTX
NCBI GI	g4512699
BLAST score	278
E value	5.0e-25
Match length	91
% identity	68
NCBI Description	(AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No.	227577
Seq. ID	LIB3189-037-P1-K1-B12
Method	BLASTX
NCBI GI	g2262103
BLAST score	258
E value	2.0e-22
Match length	109
% identity	54
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	227578
Seq. ID	LIB3189-037-P1-K1-B8

Method	BLASTX
NCBI GI	g167367
BLAST score	470
E value	3.0e-47
Match length	113
% identity	81
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	227579
Seq. ID	LIB3189-037-P1-K1-C10
Method	BLASTX
NCBI GI	g2764941
BLAST score	230
E value	4.0e-19
Match length	85
% identity	41
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	227580
Seq. ID	LIB3189-037-P1-K1-C12
Method	BLASTX
NCBI GI	g2832717
BLAST score	314
E value	2.0e-29
Match length	70
% identity	83
NCBI Description	(AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No.	227581
Seq. ID	LIB3189-037-P1-K1-D10
Method	BLASTX
NCBI GI	g2677828
BLAST score	393
E value	3.0e-38
Match length	117
% identity	66
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	227582
Seq. ID	LIB3189-037-P1-K1-D5
Method	BLASTX
NCBI GI	g3395427
BLAST score	186
E value	4.0e-14
Match length	101
% identity	45
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	227583
Seq. ID	LIB3189-037-P1-K1-D6
Method	BLASTX
NCBI GI	g4098331
BLAST score	161
E value	1.0e-11
Match length	41

% identity	73
NCBI Description	(U76896) beta-tubulin 5 [Triticum aestivum]

Seq. No.	227584
Seq. ID	LIB3189-037-P1-K1-D7
Method	BLASTX
NCBI GI	g1703375
BLAST score	182
E value	8.0e-14
Match length	40
% identity	95
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	227585
Seq. ID	LIB3189-037-P1-K1-F1
Method	BLASTX
NCBI GI	g417154
BLAST score	208
E value	6.0e-17
Match length	43
% identity	93
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	227586
Seq. ID	LIB3189-037-P1-K1-G11
Method	BLASTX
NCBI GI	g2829204
BLAST score	322
E value	9.0e-30
Match length	85
% identity	82
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	227587
Seq. ID	LIB3189-037-P1-K1-G2
Method	BLASTX
NCBI GI	g4519507
BLAST score	264
E value	2.0e-28
Match length	91
% identity	77
NCBI Description	(D88434) protein abundantly expressed during apple fruit development [Malus domestica]

Seq. No.	227588
Seq. ID	LIB3189-037-P1-K1-G4
Method	BLASTX
NCBI GI	g466172
BLAST score	195
E value	3.0e-15
Match length	37
% identity	100

NCBI Description	GTP-BINDING PROTEIN YPTM2 >gi_283056_pir__B38202 ypt family - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]
Seq. No.	227589
Seq. ID	LIB3189-037-P1-K1-G6
Method	BLASTX
NCBI GI	g2829204
BLAST score	373
E value	4.0e-36
Match length	81
% identity	88
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]
Seq. No.	227590
Seq. ID	LIB3189-037-P1-K1-G8
Method	BLASTX
NCBI GI	g2511598
BLAST score	139
E value	9.0e-09
Match length	35
% identity	69
NCBI Description	(Y13696) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana]
Seq. No.	227591
Seq. ID	LIB3189-037-P1-K1-H8
Method	BLASTX
NCBI GI	g2435518
BLAST score	220
E value	8.0e-18
Match length	114
% identity	38
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]
Seq. No.	227592
Seq. ID	LIB3189-039-P1-K1-A11
Method	BLASTX
NCBI GI	g3023816
BLAST score	337
E value	9.0e-32
Match length	76
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]
Seq. No.	227593
Seq. ID	LIB3189-039-P1-K1-A3
Method	BLASTX
NCBI GI	g4102600
BLAST score	149
E value	2.0e-09
Match length	57
% identity	58
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	227594
Seq. ID	LIB3189-039-P1-K1-A5
Method	BLASTX
NCBI GI	g2493895
BLAST score	571
E value	6.0e-59
Match length	129
% identity	88
NCBI Description	CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_1071911_pir__S46438 cysteine synthase (EC 4.2.99.8) - watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine synthase [Citrullus lanatus]

Seq. No.	227595
Seq. ID	LIB3189-039-P1-K1-A7
Method	BLASTX
NCBI GI	g1848212
BLAST score	435
E value	3.0e-43
Match length	83
% identity	47
NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]

Seq. No.	227596
Seq. ID	LIB3189-039-P1-K1-A8
Method	BLASTX
NCBI GI	g2190494
BLAST score	256
E value	4.0e-22
Match length	52
% identity	98
NCBI Description	(Y13646) cyclin dependent kinase [Petunia x hybrida]

Seq. No.	227597
Seq. ID	LIB3189-039-P1-K1-A9
Method	BLASTX
NCBI GI	g4154281
BLAST score	425
E value	4.0e-42
Match length	109
% identity	70
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	227598
Seq. ID	LIB3189-039-P1-K1-B11
Method	BLASTX
NCBI GI	g3540195
BLAST score	667
E value	3.0e-70
Match length	143
% identity	46
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 227599

Seq. ID	LIB3189-039-P1-K1-B12
Method	BLASTX
NCBI GI	g2505940
BLAST score	554
E value	5.0e-57
Match length	130
% identity	82
NCBI Description	(Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No.	227600
Seq. ID	LIB3189-039-P1-K1-B2
Method	BLASTX
NCBI GI	g2462929
BLAST score	441
E value	6.0e-44
Match length	119
% identity	67
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	227601
Seq. ID	LIB3189-039-P1-K1-B3
Method	BLASTX
NCBI GI	g2462929
BLAST score	305
E value	4.0e-28
Match length	99
% identity	55
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	227602
Seq. ID	LIB3189-039-P1-K1-B4
Method	BLASTX
NCBI GI	g4567226
BLAST score	189
E value	4.0e-14
Match length	73
% identity	55
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	227603
Seq. ID	LIB3189-039-P1-K1-B5
Method	BLASTX
NCBI GI	g4567226
BLAST score	181
E value	3.0e-13
Match length	73
% identity	53
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	227604
Seq. ID	LIB3189-039-P1-K1-B6
Method	BLASTX
NCBI GI	g3024017
BLAST score	535
E value	1.0e-54
Match length	116
% identity	92

NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.	227605
Seq. ID	LIB3189-039-P1-K1-C11
Method	BLASTX
NCBI GI	g902584
BLAST score	682
E value	5.0e-72
Match length	147
% identity	14
NCBI Description	(U29159) polyubiquitin containing 7 ubiquitin monomers [Zea mays]
Seq. No.	227606
Seq. ID	LIB3189-039-P1-K1-C2
Method	BLASTX
NCBI GI	g4512666
BLAST score	216
E value	1.0e-17
Match length	90
% identity	51
NCBI Description	(AC006931) putative mei2 protein [Arabidopsis thaliana]
Seq. No.	227607
Seq. ID	LIB3189-039-P1-K1-C8
Method	BLASTX
NCBI GI	g2129499
BLAST score	386
E value	2.0e-37
Match length	115
% identity	66
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	227608
Seq. ID	LIB3189-039-P1-K1-D1
Method	BLASTX
NCBI GI	g4454014
BLAST score	299
E value	4.0e-27
Match length	145
% identity	46
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]
Seq. No.	227609
Seq. ID	LIB3189-039-P1-K1-D11
Method	BLASTX
NCBI GI	g3775993
BLAST score	371
E value	2.0e-35
Match length	127
% identity	59
NCBI Description	(AJ010460) RNA helicase [Arabidopsis thaliana]
Seq. No.	227610

Seq. ID	LIB3189-039-P1-K1-D2
Method	BLASTX
NCBI GI	g3879145
BLAST score	189
E value	2.0e-14
Match length	77
% identity	43
NCBI Description	(Z93386) predicted using Genefinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	227611
Seq. ID	LIB3189-039-P1-K1-D3
Method	BLASTX
NCBI GI	g559684
BLAST score	709
E value	4.0e-75
Match length	156
% identity	88
NCBI Description	(L36097) aquaporin [Mesembryanthemum crystallinum]

Seq. No.	227612
Seq. ID	LIB3189-039-P1-K1-D4
Method	BLASTX
NCBI GI	g1655545
BLAST score	328
E value	2.0e-30
Match length	142
% identity	46
NCBI Description	(X97190) endo-beta-1,4-glucanase [Capsicum annuum]

Seq. No.	227613
Seq. ID	LIB3189-039-P1-K1-D5
Method	BLASTX
NCBI GI	g2129559
BLAST score	238
E value	5.0e-20
Match length	120
% identity	46
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	227614
Seq. ID	LIB3189-039-P1-K1-E1
Method	BLASTX
NCBI GI	g1332579
BLAST score	689
E value	7.0e-73
Match length	138
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 227615

Seq. ID LIB3189-039-P1-K1-E10
Method BLASTX
NCBI GI g3757514
BLAST score 438
E value 1.0e-43
Match length 103
% identity 80
NCBI Description (AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No. 227616
Seq. ID LIB3189-039-P1-K1-E12
Method BLASTX
NCBI GI g1808656
BLAST score 199
E value 1.0e-15
Match length 84
% identity 54
NCBI Description (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No. 227617
Seq. ID LIB3189-039-P1-K1-E3
Method BLASTX
NCBI GI g3043428
BLAST score 664
E value 7.0e-70
Match length 144
% identity 90
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 227618
Seq. ID LIB3189-039-P1-K1-E4
Method BLASTX
NCBI GI g1168735
BLAST score 253
E value 1.0e-21
Match length 154
% identity 38
NCBI Description CYTOPLASMIC AXIAL FILAMENT PROTEIN >gi_1073970_pir__F64118 cytoplasmic axial filament protein (cafA) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1574815 (U32814) cytoplasmic axial filament protein (cafA) [Haemophilus influenzae Rd]

Seq. No. 227619
Seq. ID LIB3189-039-P1-K1-E5
Method BLASTX
NCBI GI g1168735
BLAST score 206
E value 4.0e-16
Match length 154
% identity 32
NCBI Description CYTOPLASMIC AXIAL FILAMENT PROTEIN >gi_1073970_pir__F64118 cytoplasmic axial filament protein (cafA) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1574815 (U32814) cytoplasmic axial filament protein (cafA) [Haemophilus influenzae Rd]

Seq. No.	227620
Seq. ID	LIB3189-039-P1-K1-E6
Method	BLASTX
NCBI GI	g1168735
BLAST score	233
E value	2.0e-19
Match length	147
% identity	37
NCBI Description	CYTOPLASMIC AXIAL FILAMENT PROTEIN >gi_1073970_pir__F64118 cytoplasmic axial filament protein (cafA) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1574815 (U32814) cytoplasmic axial filament protein (cafA) [Haemophilus influenzae Rd]

Seq. No.	227621
Seq. ID	LIB3189-039-P1-K1-F3
Method	BLASTX
NCBI GI	g3650032
BLAST score	233
E value	3.0e-19
Match length	49
% identity	71
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	227622
Seq. ID	LIB3189-039-P1-K1-F4
Method	BLASTX
NCBI GI	g1808656
BLAST score	634
E value	2.0e-66
Match length	152
% identity	78
NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No.	227623
Seq. ID	LIB3189-039-P1-K1-F6
Method	BLASTX
NCBI GI	g1808656
BLAST score	583
E value	2.0e-60
Match length	149
% identity	74
NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No.	227624
Seq. ID	LIB3189-039-P1-K1-F9
Method	BLASTX
NCBI GI	g3123515
BLAST score	186
E value	2.0e-14
Match length	41
% identity	90
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No. 227625

Seq. ID	LIB3189-039-P1-K1-G1
Method	BLASTX
NCBI GI	g3123515
BLAST score	550
E value	1.0e-56
Match length	115
% identity	90
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	227626
Seq. ID	LIB3189-039-P1-K1-G10
Method	BLASTX
NCBI GI	g2119278
BLAST score	703
E value	2.0e-74
Match length	133
% identity	96
NCBI Description	tubulin beta-1 chain - rice

Seq. No.	227627
Seq. ID	LIB3189-039-P1-K1-G12
Method	BLASTX
NCBI GI	g4539301
BLAST score	163
E value	2.0e-11
Match length	47
% identity	53
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	227628
Seq. ID	LIB3189-039-P1-K1-G2
Method	BLASTX
NCBI GI	g541800
BLAST score	708
E value	1.0e-81
Match length	159
% identity	92
NCBI Description	protein kinase (EC 2.7.1.37) cdc2-Pa - Norway spruce >gi_454980_emb_CAA54746_ (X77680) cdc2Pa [Picea abies]

Seq. No.	227629
Seq. ID	LIB3189-039-P1-K1-G3
Method	BLASTX
NCBI GI	g2190494
BLAST score	271
E value	4.0e-31
Match length	104
% identity	75
NCBI Description	(Y13646) cyclin dependent kinase [Petunia x hybrida]

Seq. No.	227630
Seq. ID	LIB3189-039-P1-K1-G9
Method	BLASTX
NCBI GI	g541951
BLAST score	148
E value	2.0e-09

Match length	63
% identity	51
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	227631
Seq. ID	LIB3189-039-P1-K1-H1
Method	BLASTX
NCBI GI	g1946371
BLAST score	209
E value	2.0e-16
Match length	67
% identity	60
NCBI Description	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No.	227632
Seq. ID	LIB3189-039-P1-K1-H11
Method	BLASTX
NCBI GI	g4544443
BLAST score	521
E value	4.0e-53
Match length	151
% identity	51
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	227633
Seq. ID	LIB3189-039-P1-K1-H2
Method	BLASTX
NCBI GI	g2829871
BLAST score	114
E value	1.0e-12
Match length	66
% identity	59
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	227634
Seq. ID	LIB3189-039-P1-K1-H3
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	8.0e-20
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	227635
Seq. ID	LIB3189-039-P1-K1-H5
Method	BLASTX
NCBI GI	g2829204
BLAST score	190
E value	1.0e-14
Match length	92
% identity	50
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

Seq. No.	227636
Seq. ID	LIB3189-039-P1-K1-H7
Method	BLASTX
NCBI GI	g285636
BLAST score	268
E value	2.0e-23
Match length	129
% identity	51
NCBI Description	(D14161) ORF [Hordeum vulgare]

Seq. No.	227637
Seq. ID	LIB3189-039-P1-K1-H8
Method	BLASTX
NCBI GI	g992706
BLAST score	572
E value	4.0e-59
Match length	122
% identity	84
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	227638
Seq. ID	LIB3189-039-P1-K1-H9
Method	BLASTX
NCBI GI	g4262250
BLAST score	495
E value	4.0e-50
Match length	144
% identity	73
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	227639
Seq. ID	LIB3189-040-P1-K1-A1
Method	BLASTX
NCBI GI	g1843527
BLAST score	248
E value	2.0e-21
Match length	55
% identity	91
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	227640
Seq. ID	LIB3189-040-P1-K1-A11
Method	BLASTX
NCBI GI	g1888357
BLAST score	238
E value	4.0e-20
Match length	120
% identity	45
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	227641
Seq. ID	LIB3189-040-P1-K1-A12
Method	BLASTX

NCBI GI	g4006829
BLAST score	375
E value	4.0e-36
Match length	123
% identity	59
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	227642
Seq. ID	LIB3189-040-P1-K1-A2
Method	BLASTX
NCBI GI	g2501850
BLAST score	203
E value	2.0e-16
Match length	39
% identity	100
NCBI Description	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No.	227643
Seq. ID	LIB3189-040-P1-K1-A6
Method	BLASTX
NCBI GI	g3980396
BLAST score	462
E value	3.0e-52
Match length	114
% identity	81
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	227644
Seq. ID	LIB3189-040-P1-K1-B1
Method	BLASTX
NCBI GI	g1173209
BLAST score	394
E value	1.0e-38
Match length	81
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No.	227645
Seq. ID	LIB3189-040-P1-K1-B10
Method	BLASTX
NCBI GI	g480450
BLAST score	442
E value	7.0e-44
Match length	122
% identity	75
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	227646
Seq. ID	LIB3189-040-P1-K1-B11
Method	BLASTX
NCBI GI	g586004

BLAST score 632
E value 4.0e-66
Match length 128
% identity 90
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139) superoxide dismutase [Ipomoea batatas]

Seq. No. 227647
Seq. ID LIB3189-040-P1-K1-B12
Method BLASTX
NCBI GI g2129473
BLAST score 237
E value 8.0e-20
Match length 92
% identity 50
NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 227648
Seq. ID LIB3189-040-P1-K1-B2
Method BLASTX
NCBI GI g1173209
BLAST score 150
E value 3.0e-10
Match length 51
% identity 67
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No. 227649
Seq. ID LIB3189-040-P1-K1-B8
Method BLASTX
NCBI GI g1172872
BLAST score 547
E value 3.0e-56
Match length 125
% identity 82
NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 227650
Seq. ID LIB3189-040-P1-K1-C10
Method BLASTX
NCBI GI g3334113
BLAST score 466
E value 1.0e-46
Match length 89
% identity 100

NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.	227651
Seq. ID	LIB3189-040-P1-K1-C11
Method	BLASTX
NCBI GI	g2970051
BLAST score	223
E value	2.0e-18
Match length	60
% identity	67
NCBI Description	(AB012110) ARG10 [Vigna radiata]
Seq. No.	227652
Seq. ID	LIB3189-040-P1-K1-C12
Method	BLASTX
NCBI GI	g3493172
BLAST score	411
E value	2.0e-40
Match length	91
% identity	89
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]
Seq. No.	227653
Seq. ID	LIB3189-040-P1-K1-C5
Method	BLASTX
NCBI GI	g3805845
BLAST score	240
E value	5.0e-20
Match length	86
% identity	56
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	227654
Seq. ID	LIB3189-040-P1-K1-C6
Method	BLASTX
NCBI GI	g3493172
BLAST score	275
E value	8.0e-25
Match length	64
% identity	84
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]
Seq. No.	227655
Seq. ID	LIB3189-040-P1-K1-C7
Method	BLASTX
NCBI GI	g1168257
BLAST score	579
E value	5.0e-60
Match length	137
% identity	82
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 1 (TRANSAMINASE A) >gi_693690 (U15033) aspartate aminotransferase [Arabidopsis thaliana]
Seq. No.	227656
Seq. ID	LIB3189-040-P1-K1-D10

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Method	BLASTX
NCBI GI	g3341681
BLAST score	657
E value	4.0e-69
Match length	140
% identity	91
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi_741994_prf__2008312A GTP-binding protein [Arabidopsis thaliana]

Seq. No.	227657
Seq. ID	LIB3189-040-P1-K1-D11
Method	BLASTX
NCBI GI	g1173104
BLAST score	584
E value	2.0e-60
Match length	125
% identity	76
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	227658
Seq. ID	LIB3189-040-P1-K1-D12
Method	BLASTX
NCBI GI	g2811278
BLAST score	727
E value	3.0e-77
Match length	149
% identity	89
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227659
Seq. ID	LIB3189-040-P1-K1-D9
Method	BLASTX
NCBI GI	g3461820
BLAST score	237
E value	9.0e-20
Match length	59
% identity	63
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	227660
Seq. ID	LIB3189-040-P1-K1-F10
Method	BLASTX
NCBI GI	g464707
BLAST score	692
E value	4.0e-73
Match length	152
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	227661
Seq. ID	LIB3189-040-P1-K1-F2
Method	BLASTX
NCBI GI	g113240
BLAST score	427
E value	2.0e-50
Match length	102
% identity	98
NCBI Description	ACTIN 2 >gi_71636_pir__ATRZ2 actin 2 - rice >gi_20329_emb_CAA33873_ (X15864) actin [Oryza sativa]

Seq. No.	227662
Seq. ID	LIB3189-040-P1-K1-F8
Method	BLASTX
NCBI GI	g3702368
BLAST score	644
E value	2.0e-67
Match length	159
% identity	74
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No.	227663
Seq. ID	LIB3189-040-P1-K1-G1
Method	BLASTX
NCBI GI	g3063698
BLAST score	148
E value	1.0e-09
Match length	44
% identity	66
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	227664
Seq. ID	LIB3189-040-P1-K1-G10
Method	BLASTX
NCBI GI	g1084358
BLAST score	498
E value	2.0e-50
Match length	143
% identity	69
NCBI Description	ATP synthase - soybean

Seq. No.	227665
Seq. ID	LIB3189-040-P1-K1-G12
Method	BLASTX
NCBI GI	g1350988
BLAST score	223
E value	7.0e-19

Match length	56
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S3B (S1B) >gi_2119058_pir__I51635 ribosomal protein S1 - African clawed frog >gi_587600_emb_CAA84291_ (Z34530) ribosomal protein S1 [Xenopus laevis] >gi_587602_emb_CAA84290_ (Z34529) ribosomal protein [Xenopus laevis]

Seq. No.	227666
Seq. ID	LIB3189-040-P1-K1-G3
Method	BLASTX
NCBI GI	g3757514
BLAST score	487
E value	3.0e-49
Match length	106
% identity	86
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	227667
Seq. ID	LIB3189-040-P1-K1-G4
Method	BLASTX
NCBI GI	g4204300
BLAST score	200
E value	2.0e-15
Match length	79
% identity	51
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	227668
Seq. ID	LIB3189-040-P1-K1-G6
Method	BLASTX
NCBI GI	g3643603
BLAST score	571
E value	4.0e-59
Match length	130
% identity	84
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	227669
Seq. ID	LIB3189-040-P1-K1-G9
Method	BLASTX
NCBI GI	g2129499
BLAST score	717
E value	4.0e-76
Match length	145
% identity	92
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227670
Seq. ID	LIB3189-040-P1-K1-H3
Method	BLASTX
NCBI GI	g3098571
BLAST score	174
E value	2.0e-12
Match length	151

% identity	36
NCBI Description	(AF049028) BURP domain containing protein [Brassica napus]

Seq. No.	227671
Seq. ID	LIB3189-040-P1-K1-H4
Method	BLASTX
NCBI GI	g4580395
BLAST score	224
E value	3.0e-18
Match length	121
% identity	45
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	227672
Seq. ID	LIB3189-040-P1-K1-H5
Method	BLASTX
NCBI GI	g2982268
BLAST score	547
E value	3.0e-56
Match length	115
% identity	93
NCBI Description	(AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No.	227673
Seq. ID	LIB3189-040-P1-K1-H7
Method	BLASTX
NCBI GI	g730645
BLAST score	226
E value	9.0e-19
Match length	72
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	227674
Seq. ID	LIB3189-040-P1-K1-H9
Method	BLASTX
NCBI GI	g1928981
BLAST score	242
E value	1.0e-20
Match length	72
% identity	74
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	227675
Seq. ID	LIB3189-041-P1-K1-A2
Method	BLASTX
NCBI GI	g4204300

BLAST score	187
E value	5.0e-14
Match length	72
% identity	53
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	227676
Seq. ID	LIB3189-041-P1-K1-A8
Method	BLASTX
NCBI GI	g1708152
BLAST score	143
E value	8.0e-09
Match length	97
% identity	44
NCBI Description	PROBABLE ATP-DEPENDENT RNA HELICASE DBP5 (HELICASE CA5/6) >gi_2133053_pir__S66920 probable RNA helicase CA5/6 - yeast (Saccharomyces cerevisiae) >gi_1353268 (U28135) Dbp5p [Saccharomyces cerevisiae] >gi_1420175_emb_CAA99237_ (Z74954) ORF YOR046c [Saccharomyces cerevisiae]

Seq. No.	227677
Seq. ID	LIB3189-041-P1-K1-B11
Method	BLASTX
NCBI GI	g4324967
BLAST score	541
E value	2.0e-55
Match length	103
% identity	100
NCBI Description	(AF114796) ADP-ribosylation factor [Glycine max]

Seq. No.	227678
Seq. ID	LIB3189-041-P1-K1-B6
Method	BLASTX
NCBI GI	g4210948
BLAST score	341
E value	3.0e-32
Match length	77
% identity	88
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	227679
Seq. ID	LIB3189-041-P1-K1-B7
Method	BLASTX
NCBI GI	g4210948
BLAST score	599
E value	3.0e-62
Match length	147
% identity	82
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	227680
Seq. ID	LIB3189-041-P1-K1-B9
Method	BLASTX
NCBI GI	g1173187
BLAST score	314
E value	7.0e-29
Match length	68

% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	227681
Seq. ID	LIB3189-041-P1-K1-C1
Method	BLASTX
NCBI GI	g2832717
BLAST score	304
E value	1.0e-27
Match length	93
% identity	63
NCBI Description	(AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No.	227682
Seq. ID	LIB3189-041-P1-K1-C11
Method	BLASTX
NCBI GI	g1332579
BLAST score	616
E value	3.0e-64
Match length	125
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	227683
Seq. ID	LIB3189-041-P1-K1-C12
Method	BLASTX
NCBI GI	g464621
BLAST score	376
E value	4.0e-36
Match length	97
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	227684
Seq. ID	LIB3189-041-P1-K1-C6
Method	BLASTX
NCBI GI	g70644
BLAST score	593
E value	1.0e-61
Match length	124
% identity	18
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	227685
Seq. ID	LIB3189-041-P1-K1-C7
Method	BLASTX
NCBI GI	g232202
BLAST score	446
E value	3.0e-44
Match length	136
% identity	63

NCBI Description	GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI) >gi_285295_pir__A41789 glutathione transferase (EC 2.5.1.18) - common tobacco >gi_218294_dbj_BAA01394_ (D10524) glutathione S-transferase [Nicotiana tabacum]
Seq. No.	227686
Seq. ID	LIB3189-041-P1-K1-D10
Method	BLASTX
NCBI GI	g2367392
BLAST score	180
E value	1.0e-13
Match length	82
% identity	40
NCBI Description	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]
Seq. No.	227687
Seq. ID	LIB3189-041-P1-K1-D12
Method	BLASTX
NCBI GI	g3080401
BLAST score	419
E value	3.0e-41
Match length	108
% identity	73
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein [Arabidopsis thaliana]
Seq. No.	227688
Seq. ID	LIB3189-041-P1-K1-D2
Method	BLASTX
NCBI GI	g3548818
BLAST score	179
E value	2.0e-13
Match length	41
% identity	83
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.	227689
Seq. ID	LIB3189-041-P1-K1-D6
Method	BLASTX
NCBI GI	g3914394
BLAST score	183
E value	1.0e-13
Match length	42
% identity	83
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]
Seq. No.	227690
Seq. ID	LIB3189-041-P1-K1-D7
Method	BLASTX
NCBI GI	g2959322
BLAST score	684

E value	3.0e-72
Match length	154
% identity	84
NCBI Description	(Y14616) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	227691
Seq. ID	LIB3189-041-P1-K1-D8
Method	BLASTX
NCBI GI	g136739
BLAST score	449
E value	1.0e-60
Match length	139
% identity	88
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	227692
Seq. ID	LIB3189-041-P1-K1-D9
Method	BLASTX
NCBI GI	g130720
BLAST score	269
E value	1.0e-23
Match length	123
% identity	42
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi_500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	227693
Seq. ID	LIB3189-041-P1-K1-E10
Method	BLASTX
NCBI GI	g4337175
BLAST score	485
E value	7.0e-49
Match length	138
% identity	68
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	227694
Seq. ID	LIB3189-041-P1-K1-E11
Method	BLASTX
NCBI GI	g1703375
BLAST score	509
E value	9.0e-52
Match length	99
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	227695
Seq. ID	LIB3189-041-P1-K1-E12
Method	BLASTX
NCBI GI	g2129630
BLAST score	415
E value	1.0e-40
Match length	106
% identity	67
NCBI Description	lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750_ (X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721) unknown [Arabidopsis thaliana]

Seq. No.	227696
Seq. ID	LIB3189-041-P1-K1-E4
Method	BLASTX
NCBI GI	g3702349
BLAST score	445
E value	3.0e-44
Match length	110
% identity	80
NCBI Description	(AC005397) putative protein kinase [Arabidopsis thaliana]

Seq. No.	227697
Seq. ID	LIB3189-041-P1-K1-E6
Method	BLASTX
NCBI GI	g126896
BLAST score	606
E value	4.0e-63
Match length	138
% identity	86
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - watermelon >gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27 to 320) [Citrullus lanatus]

Seq. No.	227698
Seq. ID	LIB3189-041-P1-K1-E7
Method	BLASTX
NCBI GI	g3264759
BLAST score	512
E value	4.0e-52
Match length	120
% identity	83
NCBI Description	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]

Seq. No.	227699
Seq. ID	LIB3189-041-P1-K1-F6
Method	BLASTX
NCBI GI	g1346675
BLAST score	529
E value	5.0e-54
Match length	107
% identity	92
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) >gi_499112 (U10283) nucleoside diphosphate kinase [Flaveria

bidentis]

Seq. No.	227700
Seq. ID	LIB3189-041-P1-K1-F7
Method	BLASTX
NCBI GI	g3123161
BLAST score	135
E value	1.0e-10
Match length	99
% identity	22
NCBI Description	HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F35G12.4 IN CHROMOSOME III >gi_3876723_emb_CAA86335_ (Z46242) similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL:D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

Seq. No.	227701
Seq. ID	LIB3189-041-P1-K1-F8
Method	BLASTX
NCBI GI	g1616659
BLAST score	678
E value	2.0e-71
Match length	150
% identity	85
NCBI Description	(U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No.	227702
Seq. ID	LIB3189-041-P1-K1-F9
Method	BLASTX
NCBI GI	g4204300
BLAST score	195
E value	6.0e-15
Match length	75
% identity	52
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	227703
Seq. ID	LIB3189-041-P1-K1-G10
Method	BLASTX
NCBI GI	g231586
BLAST score	760
E value	4.0e-81
Match length	155
% identity	97
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	227704
Seq. ID	LIB3189-041-P1-K1-G11
Method	BLASTX
NCBI GI	g1174592
BLAST score	709
E value	4.0e-75

Match length	134
% identity	98
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	227705
Seq. ID	LIB3189-041-P1-K1-G12
Method	BLASTX
NCBI GI	g2935416
BLAST score	662
E value	1.0e-69
Match length	157
% identity	81
NCBI Description	(AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No.	227706
Seq. ID	LIB3189-041-P1-K1-G3
Method	BLASTX
NCBI GI	g2384758
BLAST score	412
E value	2.0e-40
Match length	86
% identity	92
NCBI Description	(AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No.	227707
Seq. ID	LIB3189-041-P1-K1-G4
Method	BLASTX
NCBI GI	g4008159
BLAST score	631
E value	5.0e-66
Match length	154
% identity	79
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	227708
Seq. ID	LIB3189-041-P1-K1-G5
Method	BLASTX
NCBI GI	g1353516
BLAST score	314
E value	7.0e-29
Match length	109
% identity	60
NCBI Description	(U38651) sugar transporter [Medicago truncatula]

Seq. No.	227709
Seq. ID	LIB3189-041-P1-K1-G6
Method	BLASTX
NCBI GI	g1351974
BLAST score	548
E value	2.0e-56
Match length	112
% identity	96
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325 ADP-ribosylation factor - maize >gi_1076789_pir__S53486

	ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_ (X80042) ADP-ribosylation factor [Zea mays]
Seq. No.	227710
Seq. ID	LIB3189-041-P1-K1-G7
Method	BLASTX
NCBI GI	g2662343
BLAST score	583
E value	2.0e-60
Match length	113
% identity	98
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]
Seq. No.	227711
Seq. ID	LIB3189-041-P1-K1-G9
Method	BLASTX
NCBI GI	g3367534
BLAST score	505
E value	3.0e-59
Match length	125
% identity	81
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]
Seq. No.	227712
Seq. ID	LIB3189-041-P1-K1-H1
Method	BLASTX
NCBI GI	g2754860
BLAST score	199
E value	5.0e-16
Match length	46
% identity	83
NCBI Description	(AF039953) cytosolic ascorbate peroxidase [Fragaria x ananassa]
Seq. No.	227713
Seq. ID	LIB3189-041-P1-K1-H10
Method	BLASTX
NCBI GI	g3482967
BLAST score	279
E value	1.0e-24
Match length	70
% identity	77
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	227714
Seq. ID	LIB3189-041-P1-K1-H11
Method	BLASTX
NCBI GI	g2498885
BLAST score	219
E value	7.0e-18
Match length	121
% identity	41
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A

	>gi_1296664_emb_CAA65774_ (X97064) Sec23 protein [Homo sapiens]
Seq. No.	227715
Seq. ID	LIB3189-041-P1-K1-H12
Method	BLASTX
NCBI GI	g2231702
BLAST score	605
E value	5.0e-63
Match length	118
% identity	93
NCBI Description	(U92086) clathrin assembly protein AP19 homolog [Arabidopsis thaliana] >gi_3080409_emb_CAA18728_ (AL022604) clathrin assembly protein AP19 homolog [Arabidopsis thaliana]
Seq. No.	227716
Seq. ID	LIB3189-041-P1-K1-H2
Method	BLASTX
NCBI GI	g4056488
BLAST score	326
E value	3.0e-30
Match length	76
% identity	75
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.	227717
Seq. ID	LIB3189-041-P1-K1-H3
Method	BLASTX
NCBI GI	g1246403
BLAST score	286
E value	1.0e-25
Match length	88
% identity	66
NCBI Description	(X94698) TINY [Arabidopsis thaliana] >gi_3406035 (AC005405) TINY [Arabidopsis thaliana]
Seq. No.	227718
Seq. ID	LIB3189-041-P1-K1-H7
Method	BLASTX
NCBI GI	g3075398
BLAST score	238
E value	6.0e-20
Match length	89
% identity	51
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.	227719
Seq. ID	LIB3189-042-P1-K1-A11
Method	BLASTX
NCBI GI	g3702333
BLAST score	200
E value	2.0e-15
Match length	109
% identity	44
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227720
Seq. ID	LIB3189-042-P1-K1-A12
Method	BLASTX
NCBI GI	g3367534
BLAST score	677
E value	2.0e-71
Match length	155
% identity	81
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	227721
Seq. ID	LIB3189-042-P1-K1-A2
Method	BLASTX
NCBI GI	g3869088
BLAST score	528
E value	5.0e-54
Match length	105
% identity	97
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	227722
Seq. ID	LIB3189-042-P1-K1-A8
Method	BLASTX
NCBI GI	g2811278
BLAST score	565
E value	2.0e-58
Match length	119
% identity	87
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227723
Seq. ID	LIB3189-042-P1-K1-A9
Method	BLASTX
NCBI GI	g2244732
BLAST score	328
E value	6.0e-47
Match length	109
% identity	93
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	227724
Seq. ID	LIB3189-042-P1-K1-B11
Method	BLASTX
NCBI GI	g2497753
BLAST score	376
E value	4.0e-36
Match length	123
% identity	55
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	227725
Seq. ID	LIB3189-042-P1-K1-B12
Method	BLASTX

NCBI GI g1203832
BLAST score 670
E value 1.0e-70
Match length 149
% identity 86
NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No. 227726
Seq. ID LIB3189-042-P1-K1-B2
Method BLASTX
NCBI GI g2673912
BLAST score 427
E value 4.0e-42
Match length 125
% identity 65
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

Seq. No. 227727
Seq. ID LIB3189-042-P1-K1-B3
Method BLASTX
NCBI GI g2244931
BLAST score 169
E value 8.0e-12
Match length 130
% identity 35
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana] >gi_3426058_emb_CAA07572_ (AJ007585) IB1P8-4 protein [Arabidopsis thaliana]

Seq. No. 227728
Seq. ID LIB3189-042-P1-K1-B4
Method BLASTX
NCBI GI g3395426
BLAST score 225
E value 1.0e-18
Match length 90
% identity 49
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 227729
Seq. ID LIB3189-042-P1-K1-B6
Method BLASTX
NCBI GI g267069
BLAST score 377
E value 4.0e-65
Match length 124
% identity 99
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 227730
Seq. ID LIB3189-042-P1-K1-B8
Method BLASTX

NCBI GI	g2505879
BLAST score	246
E value	3.0e-21
Match length	55
% identity	85
NCBI Description	(Y12776) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227731
Seq. ID	LIB3189-042-P1-K1-C2
Method	BLASTX
NCBI GI	g4539404
BLAST score	194
E value	9.0e-15
Match length	101
% identity	45
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	227732
Seq. ID	LIB3189-042-P1-K1-C3
Method	BLASTX
NCBI GI	g3319921
BLAST score	275
E value	2.0e-24
Match length	99
% identity	60
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]

Seq. No.	227733
Seq. ID	LIB3189-042-P1-K1-C7
Method	BLASTX
NCBI GI	g2392772
BLAST score	162
E value	4.0e-11
Match length	86
% identity	48
NCBI Description	(AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	227734
Seq. ID	LIB3189-042-P1-K1-C8
Method	BLASTX
NCBI GI	g2129499
BLAST score	628
E value	1.0e-65
Match length	130
% identity	90
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	227735
Seq. ID	LIB3189-042-P1-K1-D11
Method	BLASTX
NCBI GI	g3269288

BLAST score	350
E value	4.0e-33
Match length	79
% identity	84
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	227736
Seq. ID	LIB3189-042-P1-K1-D2
Method	BLASTX
NCBI GI	g2117168
BLAST score	407
E value	9.0e-40
Match length	77
% identity	100
NCBI Description	(Z73961) RAC1 [Lotus japonicus]

Seq. No.	227737
Seq. ID	LIB3189-042-P1-K1-D4
Method	BLASTX
NCBI GI	g2735550
BLAST score	214
E value	4.0e-17
Match length	89
% identity	47
NCBI Description	(U96638) unc-50 related protein; URP [Rattus norvegicus]

Seq. No.	227738
Seq. ID	LIB3189-042-P1-K1-D5
Method	BLASTX
NCBI GI	g3482967
BLAST score	410
E value	4.0e-40
Match length	96
% identity	79
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	227739
Seq. ID	LIB3189-042-P1-K1-D6
Method	BLASTX
NCBI GI	g1246403
BLAST score	294
E value	1.0e-26
Match length	93
% identity	66
NCBI Description	(X94698) TINY [Arabidopsis thaliana] >gi_3406035_(AC005405) TINY [Arabidopsis thaliana]

Seq. No.	227740
Seq. ID	LIB3189-042-P1-K1-E4
Method	BLASTX
NCBI GI	g401213
BLAST score	225
E value	2.0e-18
Match length	87
% identity	61

NCBI Description	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi_166792 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi_445600_prf__1909347A phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	227741
Seq. ID	LIB3189-042-P1-K1-E6
Method	BLASTX
NCBI GI	g2459417
BLAST score	404
E value	2.0e-39
Match length	103
% identity	77
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	227742
Seq. ID	LIB3189-042-P1-K1-E7
Method	BLASTX
NCBI GI	g167367
BLAST score	617
E value	2.0e-64
Match length	153
% identity	79
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	227743
Seq. ID	LIB3189-042-P1-K1-F10
Method	BLASTX
NCBI GI	g1402833
BLAST score	225
E value	2.0e-18
Match length	81
% identity	57
NCBI Description	(U60147) plasma membrane major intrinsic protein 1 [Beta vulgaris]

Seq. No.	227744
Seq. ID	LIB3189-042-P1-K1-F4
Method	BLASTX
NCBI GI	g3925363
BLAST score	456
E value	1.0e-45
Match length	138
% identity	66
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	227745
Seq. ID	LIB3189-042-P1-K1-F5
Method	BLASTX
NCBI GI	g3158476
BLAST score	451
E value	5.0e-45
Match length	121
% identity	83
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	227746
Seq. ID	LIB3189-042-P1-K1-F7
Method	BLASTX
NCBI GI	g2765240
BLAST score	212
E value	6.0e-17
Match length	119
% identity	40
NCBI Description	(Y12805) invertase inhibitor [Nicotiana tabacum]

Seq. No.	227747
Seq. ID	LIB3189-042-P1-K1-F8
Method	BLASTX
NCBI GI	g2829204
BLAST score	502
E value	7.0e-51
Match length	120
% identity	85
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	227748
Seq. ID	LIB3189-042-P1-K1-G11
Method	BLASTX
NCBI GI	g3445200
BLAST score	147
E value	2.0e-09
Match length	106
% identity	40
NCBI Description	(AC004786) putative squalene epoxidase [Arabidopsis thaliana]

Seq. No.	227749
Seq. ID	LIB3189-042-P1-K1-G5
Method	BLASTX
NCBI GI	g3876865
BLAST score	172
E value	3.0e-12
Match length	96
% identity	36
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227750
Seq. ID	LIB3189-042-P1-K1-G6
Method	BLASTX
NCBI GI	g1350930
BLAST score	468
E value	6.0e-47
Match length	100
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	227751

Seq. ID	LIB3189-042-P1-K1-H2
Method	BLASTX
NCBI GI	g3150415
BLAST score	262
E value	3.0e-38
Match length	112
% identity	49
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	227752
Seq. ID	LIB3189-042-P1-K1-H4
Method	BLASTX
NCBI GI	g1170507
BLAST score	477
E value	6.0e-48
Match length	114
% identity	80
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Seq. No.	227753
Seq. ID	LIB3189-042-P1-K1-H5
Method	BLASTX
NCBI GI	g1345643
BLAST score	438
E value	2.0e-43
Match length	134
% identity	66
NCBI Description	FLAVONOID 3',5'-HYDROXYLASE 2 (F3'5'H) (CYTOCHROME P450 75A3) (CYPLXXVA3) >gi_629709_pir__S38984 flavonoid 3',5'-hydroxylase Hf2 - garden petunia >gi_311654_emb_CAA80265_ (Z22544) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_738771_prf__2001426A flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No.	227754
Seq. ID	LIB3189-042-P1-K1-H6
Method	BLASTX
NCBI GI	g4115376
BLAST score	199
E value	2.0e-15
Match length	138
% identity	16
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	227755
Seq. ID	LIB3189-042-P1-K1-H7
Method	BLASTX
NCBI GI	g3493172
BLAST score	508
E value	9.0e-52

Match length	111
% identity	90
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	227756
Seq. ID	LIB3189-042-P1-K1-H8
Method	BLASTX
NCBI GI	g1800281
BLAST score	709
E value	4.0e-75
Match length	147
% identity	22
NCBI Description	(U82086) polyubiquitin [Fragaria x ananassa]

Seq. No.	227757
Seq. ID	LIB3189-043-P1-K1-A11
Method	BLASTX
NCBI GI	g3688188
BLAST score	488
E value	3.0e-49
Match length	117
% identity	80
NCBI Description	(AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis thaliana]

Seq. No.	227758
Seq. ID	LIB3189-043-P1-K1-A12
Method	BLASTX
NCBI GI	g1856971
BLAST score	193
E value	1.0e-21
Match length	67
% identity	87
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	227759
Seq. ID	LIB3189-043-P1-K1-A3
Method	BLASTX
NCBI GI	g1350944
BLAST score	172
E value	8.0e-13
Match length	42
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	227760
Seq. ID	LIB3189-043-P1-K1-A4
Method	BLASTX
NCBI GI	g2879867
BLAST score	234
E value	1.0e-19
Match length	99
% identity	48
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	227761
Seq. ID	LIB3189-043-P1-K1-A7
Method	BLASTX
NCBI GI	g2497753
BLAST score	323
E value	5.0e-30
Match length	115
% identity	53
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	227762
Seq. ID	LIB3189-043-P1-K1-A8
Method	BLASTX
NCBI GI	g3334661
BLAST score	356
E value	9.0e-34
Match length	117
% identity	56
NCBI Description	(Y10490) putative cytochrome P450 [Glycine max]

Seq. No.	227763
Seq. ID	LIB3189-043-P1-K1-B1
Method	BLASTX
NCBI GI	g3914430
BLAST score	479
E value	3.0e-48
Match length	113
% identity	83
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No.	227764
Seq. ID	LIB3189-043-P1-K1-B10
Method	BLASTX
NCBI GI	g4337175
BLAST score	490
E value	2.0e-49
Match length	138
% identity	68
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	227765
Seq. ID	LIB3189-043-P1-K1-B2
Method	BLASTX
NCBI GI	g3935150
BLAST score	382
E value	8.0e-37
Match length	148
% identity	55

NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]
Seq. No.	227766
Seq. ID	LIB3189-043-P1-K1-B6
Method	BLASTX
NCBI GI	g2501494
BLAST score	160
E value	7.0e-11
Match length	76
% identity	47
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 5) >gi_542015_pir__S41951 UTP-glucose glucosyltransferase - cassava >gi_453249_emb_CAA54612_ (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]
Seq. No.	227767
Seq. ID	LIB3189-043-P1-K1-B7
Method	BLASTX
NCBI GI	g2443751
BLAST score	710
E value	3.0e-75
Match length	153
% identity	89
NCBI Description	(AF020303) fumarase [Arabidopsis thaliana] >gi_2529676 (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.	227768
Seq. ID	LIB3189-043-P1-K1-C11
Method	BLASTX
NCBI GI	g1694976
BLAST score	450
E value	9.0e-45
Match length	129
% identity	68
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]
Seq. No.	227769
Seq. ID	LIB3189-043-P1-K1-C2
Method	BLASTX
NCBI GI	g2842424
BLAST score	493
E value	7.0e-50
Match length	141
% identity	67
NCBI Description	(AJ223948) RNA helicase [Homo sapiens]
Seq. No.	227770
Seq. ID	LIB3189-043-P1-K1-C3
Method	BLASTX
NCBI GI	g4105269
BLAST score	237
E value	8.0e-20
Match length	148
% identity	39

NCBI Description	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]
Seq. No.	227771
Seq. ID	LIB3189-043-P1-K1-C5
Method	BLASTX
NCBI GI	g1771162
BLAST score	237
E value	7.0e-20
Match length	141
% identity	60
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]
Seq. No.	227772
Seq. ID	LIB3189-043-P1-K1-C8
Method	BLASTX
NCBI GI	g1854386
BLAST score	269
E value	1.0e-30
Match length	146
% identity	53
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]
Seq. No.	227773
Seq. ID	LIB3189-043-P1-K1-C9
Method	BLASTX
NCBI GI	g3334115
BLAST score	334
E value	3.0e-31
Match length	96
% identity	71
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]
Seq. No.	227774
Seq. ID	LIB3189-043-P1-K1-D10
Method	BLASTX
NCBI GI	g3202042
BLAST score	550
E value	2.0e-56
Match length	133
% identity	80
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]
Seq. No.	227775
Seq. ID	LIB3189-043-P1-K1-D12
Method	BLASTX
NCBI GI	g2662415
BLAST score	141
E value	1.0e-08
Match length	48

% identity	56
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No.	227776
Seq. ID	LIB3189-043-P1-K1-D2
Method	BLASTX
NCBI GI	g4240116
BLAST score	494
E value	5.0e-50
Match length	126
% identity	74
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	227777
Seq. ID	LIB3189-043-P1-K1-D4
Method	BLASTX
NCBI GI	g3461835
BLAST score	702
E value	2.0e-74
Match length	147
% identity	87
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	227778
Seq. ID	LIB3189-043-P1-K1-D7
Method	BLASTX
NCBI GI	g2623199
BLAST score	525
E value	1.0e-53
Match length	112
% identity	89
NCBI Description	(AF030290) protein phosphatase X isoform 2 [Arabidopsis thaliana]

Seq. No.	227779
Seq. ID	LIB3189-043-P1-K1-D8
Method	BLASTX
NCBI GI	g3128175
BLAST score	155
E value	2.0e-10
Match length	119
% identity	33
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	227780
Seq. ID	LIB3189-043-P1-K1-D9
Method	BLASTX
NCBI GI	g1332579
BLAST score	677
E value	2.0e-71
Match length	136
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	227781
Seq. ID	LIB3189-043-P1-K1-E10
Method	BLASTX
NCBI GI	g2982465
BLAST score	215
E value	3.0e-17
Match length	123
% identity	42
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	227782
Seq. ID	LIB3189-043-P1-K1-E11
Method	BLASTX
NCBI GI	g2062167
BLAST score	572
E value	4.0e-59
Match length	153
% identity	71
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	227783
Seq. ID	LIB3189-043-P1-K1-E12
Method	BLASTX
NCBI GI	g2811278
BLAST score	764
E value	1.0e-81
Match length	154
% identity	90
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227784
Seq. ID	LIB3189-043-P1-K1-E4
Method	BLASTX
NCBI GI	g2982465
BLAST score	178
E value	2.0e-13
Match length	75
% identity	48
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	227785
Seq. ID	LIB3189-043-P1-K1-E6
Method	BLASTX
NCBI GI	g167367
BLAST score	477
E value	5.0e-48
Match length	130
% identity	77
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	227786
Seq. ID	LIB3189-043-P1-K1-E7
Method	BLASTX
NCBI GI	g4105696
BLAST score	183

E value	4.0e-14
Match length	41
% identity	80
NCBI Description	(AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No.	227787
Seq. ID	LIB3189-043-P1-K1-E8
Method	BLASTX
NCBI GI	g1170507
BLAST score	471
E value	3.0e-47
Match length	114
% identity	79
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Seq. No.	227788
Seq. ID	LIB3189-043-P1-K1-F10
Method	BLASTX
NCBI GI	g4235430
BLAST score	618
E value	2.0e-64
Match length	143
% identity	81
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	227789
Seq. ID	LIB3189-043-P1-K1-F3
Method	BLASTX
NCBI GI	g4097579
BLAST score	499
E value	2.0e-50
Match length	105
% identity	87
NCBI Description	(U64922) NTGP1 [Nicotiana tabacum]

Seq. No.	227790
Seq. ID	LIB3189-043-P1-K1-F4
Method	BLASTX
NCBI GI	g567893
BLAST score	173
E value	3.0e-12
Match length	66
% identity	52
NCBI Description	(L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No.	227791
Seq. ID	LIB3189-043-P1-K1-F5
Method	BLASTX
NCBI GI	g4580460
BLAST score	523
E value	2.0e-53
Match length	152

% identity	72
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	227792
Seq. ID	LIB3189-043-P1-K1-F7
Method	BLASTX
NCBI GI	g2072986
BLAST score	720
E value	2.0e-76
Match length	152
% identity	84
NCBI Description	(U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi_2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana]

Seq. No.	227793
Seq. ID	LIB3189-043-P1-K1-F9
Method	BLASTX
NCBI GI	g2119937
BLAST score	437
E value	3.0e-43
Match length	90
% identity	93
NCBI Description	translation initiation factor eIF-4A.13 - common tobacco (fragment)

Seq. No.	227794
Seq. ID	LIB3189-043-P1-K1-G1
Method	BLASTX
NCBI GI	g498038
BLAST score	509
E value	1.0e-58
Match length	150
% identity	81
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	227795
Seq. ID	LIB3189-043-P1-K1-G3
Method	BLASTX
NCBI GI	g1710780
BLAST score	502
E value	6.0e-51
Match length	132
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	227796
Seq. ID	LIB3189-043-P1-K1-G4
Method	BLASTX
NCBI GI	g4544399
BLAST score	546
E value	5.0e-56
Match length	148
% identity	70

NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
Seq. No.	227797
Seq. ID	LIB3189-043-P1-K1-G8
Method	BLASTX
NCBI GI	g1362105
BLAST score	379
E value	2.0e-36
Match length	141
% identity	51
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - common tobacco (fragment) >gi_551257_emb_CAA57446_ (X81853) alcohol dehydrogenase [Nicotiana tabacum]
Seq. No.	227798
Seq. ID	LIB3189-043-P1-K1-G9
Method	BLASTX
NCBI GI	g4115925
BLAST score	305
E value	7.0e-28
Match length	137
% identity	36
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]
Seq. No.	227799
Seq. ID	LIB3189-043-P1-K1-H2
Method	BLASTX
NCBI GI	g3068704
BLAST score	619
E value	1.0e-64
Match length	149
% identity	79
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]
Seq. No.	227800
Seq. ID	LIB3189-043-P1-K1-H4
Method	BLASTX
NCBI GI	g3868853
BLAST score	183
E value	1.0e-13
Match length	60
% identity	63
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]
Seq. No.	227801
Seq. ID	LIB3189-043-P1-K1-H8
Method	BLASTX
NCBI GI	g3237190
BLAST score	170
E value	6.0e-12
Match length	60
% identity	55
NCBI Description	(AB014760) cystein proteinase inhibitor [Cucumis sativus]

Seq. No.	227802
Seq. ID	LIB3189-043-P1-K1-H9
Method	BLASTX
NCBI GI	g1944518
BLAST score	530
E value	3.0e-54
Match length	128
% identity	77
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	227803
Seq. ID	LIB3189-044-P1-K1-A4
Method	BLASTX
NCBI GI	g2497743
BLAST score	606
E value	4.0e-63
Match length	120
% identity	97
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	227804
Seq. ID	LIB3189-044-P1-K1-A5
Method	BLASTX
NCBI GI	g3876865
BLAST score	185
E value	9.0e-14
Match length	109
% identity	37
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227805
Seq. ID	LIB3189-044-P1-K1-A8
Method	BLASTX
NCBI GI	g3522937
BLAST score	351
E value	3.0e-33
Match length	133
% identity	56
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	227806
Seq. ID	LIB3189-044-P1-K1-B1
Method	BLASTX
NCBI GI	g3759184
BLAST score	372
E value	1.0e-35
Match length	150
% identity	53

NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	227807
Seq. ID	LIB3189-044-P1-K1-B11
Method	BLASTX
NCBI GI	g82620
BLAST score	526
E value	8.0e-54
Match length	127
% identity	73
NCBI Description	probable serine-type carboxypeptidase (EC 3.4.16.1) - wheat

Seq. No.	227808
Seq. ID	LIB3189-044-P1-K1-B12
Method	BLASTX
NCBI GI	g4006829
BLAST score	238
E value	6.0e-20
Match length	97
% identity	53
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	227809
Seq. ID	LIB3189-044-P1-K1-B3
Method	BLASTX
NCBI GI	g729470
BLAST score	360
E value	3.0e-34
Match length	99
% identity	72
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	227810
Seq. ID	LIB3189-044-P1-K1-B7
Method	BLASTX
NCBI GI	g4204281
BLAST score	231
E value	4.0e-19
Match length	133
% identity	37
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	227811
Seq. ID	LIB3189-044-P1-K1-B8
Method	BLASTX
NCBI GI	g2811031
BLAST score	485
E value	6.0e-49
Match length	143
% identity	68
NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi_2109299_gb_AAB58165.1_ (AF000132) betaine aldehyde

dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	227812
Seq. ID	LIB3189-044-P1-K1-C11
Method	BLASTX
NCBI GI	g2454182
BLAST score	355
E value	1.0e-33
Match length	131
% identity	60
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	227813
Seq. ID	LIB3189-044-P1-K1-C12
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	7.0e-20
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	227814
Seq. ID	LIB3189-044-P1-K1-C3
Method	BLASTX
NCBI GI	g3152576
BLAST score	177
E value	2.0e-13
Match length	65
% identity	63
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	227815
Seq. ID	LIB3189-044-P1-K1-C7
Method	BLASTX
NCBI GI	g4580460
BLAST score	165
E value	5.0e-12
Match length	45
% identity	78
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	227816
Seq. ID	LIB3189-044-P1-K1-C9
Method	BLASTX
NCBI GI	g3861068
BLAST score	155
E value	3.0e-10
Match length	52
% identity	54
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No. 227817

Seq. ID	LIB3189-044-P1-K1-D10
Method	BLASTX
NCBI GI	g728938
BLAST score	659
E value	2.0e-69
Match length	142
% identity	92
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472) inorganic pyrophosphatse ase' [Hordeum vulgare]

Seq. No.	227818
Seq. ID	LIB3189-044-P1-K1-D12
Method	BLASTX
NCBI GI	g3757514
BLAST score	217
E value	7.0e-18
Match length	74
% identity	64
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	227819
Seq. ID	LIB3189-044-P1-K1-D3
Method	BLASTX
NCBI GI	g3182981
BLAST score	547
E value	3.0e-56
Match length	132
% identity	80
NCBI Description	CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_ (D86494) diminuto [Pisum sativum]

Seq. No.	227820
Seq. ID	LIB3189-044-P1-K1-D5
Method	BLASTX
NCBI GI	g2245131
BLAST score	173
E value	2.0e-12
Match length	110
% identity	43
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227821
Seq. ID	LIB3189-044-P1-K1-E10
Method	BLASTX
NCBI GI	g124224
BLAST score	427
E value	3.0e-42
Match length	93
% identity	87
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	227822
Seq. ID	LIB3189-044-P1-K1-E11
Method	BLASTX
NCBI GI	g4185139
BLAST score	188
E value	2.0e-24
Match length	79
% identity	63
NCBI Description	(AC005724) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	227823
Seq. ID	LIB3189-044-P1-K1-E7
Method	BLASTX
NCBI GI	g586076
BLAST score	321
E value	4.0e-30
Match length	60
% identity	95
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	227824
Seq. ID	LIB3189-044-P1-K1-F11
Method	BLASTX
NCBI GI	g3600033
BLAST score	397
E value	1.0e-38
Match length	140
% identity	54
NCBI Description	(AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]

Seq. No.	227825
Seq. ID	LIB3189-044-P1-K1-F12
Method	BLASTX
NCBI GI	g267069
BLAST score	610
E value	1.0e-63
Match length	114
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227826
Seq. ID	LIB3189-044-P1-K1-F5
Method	BLASTX
NCBI GI	g531829
BLAST score	160
E value	7.0e-11
Match length	78
% identity	45

NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]
Seq. No.	227827
Seq. ID	LIB3189-044-P1-K1-H1
Method	BLASTX
NCBI GI	g1703380
BLAST score	479
E value	3.0e-48
Match length	93
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) ADP-ribosylation factor [Oryza sativa]
Seq. No.	227828
Seq. ID	LIB3189-044-P1-K1-H11
Method	BLASTX
NCBI GI	g3582328
BLAST score	158
E value	1.0e-10
Match length	118
% identity	14
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.	227829
Seq. ID	LIB3189-044-P1-K1-H5
Method	BLASTX
NCBI GI	g3702333
BLAST score	157
E value	1.0e-10
Match length	96
% identity	44
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.	227830
Seq. ID	LIB3189-044-P1-K1-H8
Method	BLASTX
NCBI GI	g3646340
BLAST score	695
E value	2.0e-73
Match length	149
% identity	91
NCBI Description	(AJ000763) MADS-box protein [Malus domestica]
Seq. No.	227831
Seq. ID	LIB3189-044-P1-K1-H9
Method	BLASTX
NCBI GI	g4455208
BLAST score	534
E value	9.0e-55
Match length	132
% identity	75
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	227832
Seq. ID	LIB3189-045-P1-K1-A11
Method	BLASTX

NCBI GI	g2191145
BLAST score	254
E value	6.0e-22
Match length	115
% identity	50
NCBI Description	(AF007269) A_IG002N01.4 gene product [Arabidopsis thaliana]

Seq. No.	227833
Seq. ID	LIB3189-045-P1-K1-A12
Method	BLASTX
NCBI GI	g123650
BLAST score	503
E value	4.0e-60
Match length	142
% identity	85
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat shock protein 70 (clone pMON9743) - garden petunia >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida]

Seq. No.	227834
Seq. ID	LIB3189-045-P1-K1-A9
Method	BLASTX
NCBI GI	g2213626
BLAST score	197
E value	2.0e-15
Match length	97
% identity	44
NCBI Description	(AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No.	227835
Seq. ID	LIB3189-045-P1-K1-B11
Method	BLASTX
NCBI GI	g1173218
BLAST score	664
E value	7.0e-70
Match length	130
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	227836
Seq. ID	LIB3189-045-P1-K1-B3
Method	BLASTX
NCBI GI	g508304
BLAST score	238
E value	6.0e-20
Match length	75
% identity	67
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	227837
Seq. ID	LIB3189-045-P1-K1-B8
Method	BLASTX
NCBI GI	g1370198
BLAST score	297

E value	7.0e-27
Match length	83
% identity	76
NCBI Description	(Z73948) RAB8E [Lotus japonicus]

Seq. No.	227838
Seq. ID	LIB3189-045-P1-K1-B9
Method	BLASTX
NCBI GI	g122007
BLAST score	452
E value	5.0e-45
Match length	117
% identity	79
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	227839
Seq. ID	LIB3189-045-P1-K1-C11
Method	BLASTX
NCBI GI	g2739044
BLAST score	581
E value	3.0e-60
Match length	145
% identity	73
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	227840
Seq. ID	LIB3189-045-P1-K1-C12
Method	BLASTX
NCBI GI	g4115925
BLAST score	453
E value	4.0e-45
Match length	99
% identity	44
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	227841
Seq. ID	LIB3189-045-P1-K1-C3
Method	BLASTX
NCBI GI	g99737
BLAST score	515
E value	2.0e-67
Match length	154
% identity	85
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	227842
Seq. ID	LIB3189-045-P1-K1-C7
Method	BLASTX
NCBI GI	g3914935

BLAST score	433
E value	8.0e-43
Match length	152
% identity	60
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_3204099_emb_CAA07226_ (AJ006759) ribosome-associated protein p40 [Cicer arietinum]

Seq. No.	227843
Seq. ID	LIB3189-045-P1-K1-D10
Method	BLASTX
NCBI GI	g3790102
BLAST score	747
E value	1.0e-79
Match length	155
% identity	95
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	227844
Seq. ID	LIB3189-045-P1-K1-D11
Method	BLASTX
NCBI GI	g1703115
BLAST score	504
E value	3.0e-51
Match length	95
% identity	97
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	227845
Seq. ID	LIB3189-045-P1-K1-D12
Method	BLASTX
NCBI GI	g3924823
BLAST score	254
E value	7.0e-22
Match length	118
% identity	46
NCBI Description	(Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST yk491a11.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	227846
Seq. ID	LIB3189-045-P1-K1-E11
Method	BLASTX
NCBI GI	g3694872
BLAST score	488
E value	3.0e-49
Match length	116
% identity	79
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	227847
Seq. ID	LIB3189-045-P1-K1-E12
Method	BLASTX
NCBI GI	g2760837

BLAST score 697
E value 9.0e-74
Match length 155
% identity 83
NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 227848
Seq. ID LIB3189-045-P1-K1-E3
Method BLASTX
NCBI GI g4457219
BLAST score 161
E value 6.0e-11
Match length 83
% identity 47
NCBI Description (AF127796) acyl carrier protein [Capsicum chinense]

Seq. No. 227849
Seq. ID LIB3189-045-P1-K1-E6
Method BLASTX
NCBI GI g1350956
BLAST score 511
E value 5.0e-52
Match length 108
% identity 93
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 227850
Seq. ID LIB3189-045-P1-K1-E8
Method BLASTX
NCBI GI g2462929
BLAST score 173
E value 7.0e-13
Match length 63
% identity 51
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 227851
Seq. ID LIB3189-045-P1-K1-E9
Method BLASTX
NCBI GI g2811278
BLAST score 196
E value 1.0e-15
Match length 36
% identity 94
NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 227852
Seq. ID LIB3189-045-P1-K1-F10
Method BLASTX
NCBI GI g4008006
BLAST score 450
E value 9.0e-45
Match length 155
% identity 57
NCBI Description (AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	227853
Seq. ID	LIB3189-045-P1-K1-F12
Method	BLASTX
NCBI GI	g3894158
BLAST score	326
E value	3.0e-30
Match length	119
% identity	48
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	227854
Seq. ID	LIB3189-045-P1-K1-F3
Method	BLASTX
NCBI GI	g1173187
BLAST score	607
E value	3.0e-63
Match length	120
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	227855
Seq. ID	LIB3189-045-P1-K1-F4
Method	BLASTX
NCBI GI	g464986
BLAST score	336
E value	8.0e-32
Match length	62
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	227856
Seq. ID	LIB3189-045-P1-K1-F5
Method	BLASTX
NCBI GI	g548847
BLAST score	168
E value	3.0e-13
Match length	46
% identity	96
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_1086182_pir__S39501 ribosomal protein S12 - curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	227857
Seq. ID	LIB3189-045-P1-K1-F9
Method	BLASTX
NCBI GI	g3169182
BLAST score	328
E value	1.0e-30
Match length	72
% identity	83
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	227858
Seq. ID	LIB3189-045-P1-K1-G1
Method	BLASTX
NCBI GI	g1553133
BLAST score	150
E value	1.0e-09
Match length	153
% identity	12
NCBI Description	(U64722) actin-fragmin kinase [Physarum polycephalum]

Seq. No.	227859
Seq. ID	LIB3189-045-P1-K1-G10
Method	BLASTX
NCBI GI	g3451069
BLAST score	290
E value	4.0e-26
Match length	122
% identity	44
NCBI Description	(AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227860
Seq. ID	LIB3189-045-P1-K1-G11
Method	BLASTX
NCBI GI	g4490733
BLAST score	210
E value	5.0e-17
Match length	98
% identity	46
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	227861
Seq. ID	LIB3189-045-P1-K1-G12
Method	BLASTX
NCBI GI	g4467151
BLAST score	413
E value	2.0e-40
Match length	144
% identity	60
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	227862
Seq. ID	LIB3189-045-P1-K1-G6
Method	BLASTX
NCBI GI	g3860272
BLAST score	329
E value	4.0e-31
Match length	76

% identity	87
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]
Seq. No.	227863
Seq. ID	LIB3189-045-P1-K1-G8
Method	BLASTX
NCBI GI	g4337210
BLAST score	159
E value	5.0e-11
Match length	57
% identity	56
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]
Seq. No.	227864
Seq. ID	LIB3189-045-P1-K1-G9
Method	BLASTX
NCBI GI	g2815246
BLAST score	218
E value	1.0e-17
Match length	55
% identity	71
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.	227865
Seq. ID	LIB3189-045-P1-K1-H11
Method	BLASTX
NCBI GI	g1703275
BLAST score	272
E value	6.0e-24
Match length	54
% identity	89
NCBI Description	METHIONINE AMINOPEPTIDASE 2 (METAP 2) (PEPTIDASE M 2) (INITIATION FACTOR 2 ASSOCIATED 67 KD GLYCOPROTEIN) (P67)
Seq. No.	227866
Seq. ID	LIB3189-045-P1-K1-H12
Method	BLASTX
NCBI GI	g123650
BLAST score	513
E value	2.0e-52
Match length	102
% identity	96
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat shock protein 70 (clone pMON9743) - garden petunia >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida]
Seq. No.	227867
Seq. ID	LIB3189-045-P1-K1-H5
Method	BLASTX
NCBI GI	g2497742
BLAST score	189
E value	1.0e-14
Match length	35
% identity	100

NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_995907 (U15153) nonspecific lipid transfer protein precursor [Gossypium hirsutum]
Seq. No.	227868
Seq. ID	LIB3189-045-P1-K1-H6
Method	BLASTX
NCBI GI	g3176669
BLAST score	178
E value	6.0e-13
Match length	118
% identity	38
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]
Seq. No.	227869
Seq. ID	LIB3189-045-P1-K1-H7
Method	BLASTX
NCBI GI	g2253583
BLAST score	160
E value	7.0e-11
Match length	74
% identity	53
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]
Seq. No.	227870
Seq. ID	LIB3189-046-P1-K1-A2
Method	BLASTX
NCBI GI	g1408471
BLAST score	521
E value	4.0e-53
Match length	136
% identity	74
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]
Seq. No.	227871
Seq. ID	LIB3189-046-P1-K1-A4
Method	BLASTX
NCBI GI	g3668082
BLAST score	451
E value	7.0e-45
Match length	129
% identity	71
NCBI Description	(AC004667) putative DAL1 protein [Arabidopsis thaliana]
Seq. No.	227872
Seq. ID	LIB3189-046-P1-K1-A7
Method	BLASTX
NCBI GI	g3599491
BLAST score	651
E value	2.0e-68
Match length	152
% identity	79
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]
Seq. No.	227873

Seq. ID	LIB3189-046-P1-K1-A8
Method	BLASTX
NCBI GI	g4165550
BLAST score	191
E value	8.0e-25
Match length	73
% identity	70
NCBI Description	(AJ004915) apgm [Malus domestica]

Seq. No.	227874
Seq. ID	LIB3189-046-P1-K1-B11
Method	BLASTX
NCBI GI	g3876865
BLAST score	171
E value	3.0e-12
Match length	99
% identity	36
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227875
Seq. ID	LIB3189-046-P1-K1-B12
Method	BLASTX
NCBI GI	g4567285
BLAST score	150
E value	3.0e-10
Match length	38
% identity	82
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227876
Seq. ID	LIB3189-046-P1-K1-B2
Method	BLASTX
NCBI GI	g2443878
BLAST score	255
E value	6.0e-22
Match length	126
% identity	49
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	227877
Seq. ID	LIB3189-046-P1-K1-B8
Method	BLASTX
NCBI GI	g3924596
BLAST score	278
E value	1.0e-24
Match length	78
% identity	73
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	227878
Seq. ID	LIB3189-046-P1-K1-C5
Method	BLASTX
NCBI GI	g1617036

BLAST score	250
E value	2.0e-21
Match length	70
% identity	74
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]

Seq. No.	227879
Seq. ID	LIB3189-046-P1-K1-D1
Method	BLASTX
NCBI GI	g2660664
BLAST score	532
E value	2.0e-54
Match length	151
% identity	70
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	227880
Seq. ID	LIB3189-046-P1-K1-D11
Method	BLASTX
NCBI GI	g267069
BLAST score	643
E value	2.0e-67
Match length	123
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227881
Seq. ID	LIB3189-046-P1-K1-D12
Method	BLASTX
NCBI GI	g2244971
BLAST score	261
E value	3.0e-23
Match length	65
% identity	74
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227882
Seq. ID	LIB3189-046-P1-K1-D3
Method	BLASTX
NCBI GI	g3851636
BLAST score	460
E value	3.0e-46
Match length	108
% identity	81
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	227883
Seq. ID	LIB3189-046-P1-K1-D4
Method	BLASTX
NCBI GI	g2894596
BLAST score	213
E value	2.0e-17
Match length	58

% identity	67
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	227884
Seq. ID	LIB3189-046-P1-K1-D7
Method	BLASTX
NCBI GI	g2149051
BLAST score	259
E value	4.0e-27
Match length	85
% identity	78
NCBI Description	(U73810) small Ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	227885
Seq. ID	LIB3189-046-P1-K1-D8
Method	BLASTX
NCBI GI	g2149051
BLAST score	252
E value	4.0e-22
Match length	49
% identity	98
NCBI Description	(U73810) small Ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	227886
Seq. ID	LIB3189-046-P1-K1-E1
Method	BLASTX
NCBI GI	g464621
BLAST score	151
E value	8.0e-10
Match length	38
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	227887
Seq. ID	LIB3189-046-P1-K1-E12
Method	BLASTX
NCBI GI	g303750
BLAST score	263
E value	3.0e-37
Match length	95
% identity	93
NCBI Description	(D12548) GTP-binding protein [Pisum sativum] >gi_738940_prf__2001457H GTP-binding protein [Pisum sativum]

Seq. No.	227888
Seq. ID	LIB3189-046-P1-K1-E7
Method	BLASTX
NCBI GI	g2911050
BLAST score	182
E value	2.0e-13
Match length	106

% identity	43
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	227889
Seq. ID	LIB3189-046-P1-K1-E9
Method	BLASTX
NCBI GI	g2511689
BLAST score	337
E value	1.0e-31
Match length	97
% identity	61
NCBI Description	(Z99952) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	227890
Seq. ID	LIB3189-046-P1-K1-F11
Method	BLASTX
NCBI GI	g232024
BLAST score	705
E value	9.0e-75
Match length	136
% identity	96
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	227891
Seq. ID	LIB3189-046-P1-K1-F12
Method	BLASTX
NCBI GI	g2924520
BLAST score	501
E value	7.0e-51
Match length	106
% identity	92
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	227892
Seq. ID	LIB3189-046-P1-K1-F2
Method	BLASTX
NCBI GI	g2811278
BLAST score	401
E value	3.0e-39
Match length	121
% identity	68
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227893
Seq. ID	LIB3189-046-P1-K1-F5
Method	BLASTX
NCBI GI	g2662343
BLAST score	357
E value	3.0e-34
Match length	74
% identity	93
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	227894
Seq. ID	LIB3189-046-P1-K1-F6
Method	BLASTX
NCBI GI	g1256771
BLAST score	186
E value	4.0e-15
Match length	68
% identity	68
NCBI Description	(U51270) COP9 [Spinacia oleracea]

Seq. No.	227895
Seq. ID	LIB3189-046-P1-K1-F7
Method	BLASTX
NCBI GI	g4204313
BLAST score	331
E value	5.0e-31
Match length	73
% identity	88
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	227896
Seq. ID	LIB3189-046-P1-K1-F9
Method	BLASTX
NCBI GI	g559005
BLAST score	406
E value	9.0e-40
Match length	106
% identity	75
NCBI Description	(U15933) ascorbate peroxidase [Nicotiana tabacum]

Seq. No.	227897
Seq. ID	LIB3189-046-P1-K1-G1
Method	BLASTX
NCBI GI	g399940
BLAST score	140
E value	4.0e-09
Match length	56
% identity	59
NCBI Description	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	227898
Seq. ID	LIB3189-046-P1-K1-G11
Method	BLASTX
NCBI GI	g3128228
BLAST score	589
E value	4.0e-61
Match length	128
% identity	87
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	227899
Seq. ID	LIB3189-046-P1-K1-G3
Method	BLASTX
NCBI GI	g3158376
BLAST score	479
E value	3.0e-48
Match length	131
% identity	74
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	227900
Seq. ID	LIB3189-046-P1-K1-G5
Method	BLASTX
NCBI GI	g1632831
BLAST score	531
E value	2.0e-54
Match length	114
% identity	91
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	227901
Seq. ID	LIB3189-046-P1-K1-G6
Method	BLASTX
NCBI GI	g2832649
BLAST score	603
E value	1.0e-62
Match length	154
% identity	73
NCBI Description	(AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]

Seq. No.	227902
Seq. ID	LIB3189-046-P1-K1-G7
Method	BLASTX
NCBI GI	g399940
BLAST score	339
E value	5.0e-33
Match length	100
% identity	82
NCBI Description	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	227903
Seq. ID	LIB3189-046-P1-K1-G8
Method	BLASTX
NCBI GI	g3913925
BLAST score	196
E value	5.0e-15
Match length	117
% identity	41
NCBI Description	ACID BETA-FRUCTOFURANOSIDASE AIV-18 (ACID SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) >gi_1857714 (U87849) acid beta-fructosidase [Capsicum annuum]

Seq. No.	227904

Seq. ID	LIB3189-046-P1-K1-H5
Method	BLASTX
NCBI GI	g1743354
BLAST score	177
E value	5.0e-13
Match length	39
% identity	82
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	227905
Seq. ID	LIB3189-046-P1-K1-H6
Method	BLASTX
NCBI GI	g3915031
BLAST score	271
E value	3.0e-24
Match length	80
% identity	66
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	227906
Seq. ID	LIB3189-046-P1-K1-H7
Method	BLASTX
NCBI GI	g3395436
BLAST score	261
E value	1.0e-22
Match length	128
% identity	39
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	227907
Seq. ID	LIB3189-047-P1-K1-A12
Method	BLASTX
NCBI GI	g169459
BLAST score	247
E value	6.0e-21
Match length	96
% identity	51
NCBI Description	(M18538) pop3 peptide [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No.	227908
Seq. ID	LIB3189-047-P1-K1-A3
Method	BLASTX
NCBI GI	g2811278
BLAST score	500
E value	1.0e-50
Match length	110
% identity	83
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227909
Seq. ID	LIB3189-047-P1-K1-A4
Method	BLASTX
NCBI GI	g2129473

09607-0960

BLAST score	259
E value	2.0e-22
Match length	94
% identity	52
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	227910
Seq. ID	LIB3189-047-P1-K1-A6
Method	BLASTX
NCBI GI	g1173018
BLAST score	260
E value	1.0e-22
Match length	84
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L2 >gi_1076399_pir__S54250 ribosomal protein L2 - Arabidopsis thaliana >gi_798818_emb_CAA60445_ (X86765) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	227911
Seq. ID	LIB3189-047-P1-K1-A7
Method	BLASTX
NCBI GI	g1431629
BLAST score	267
E value	6.0e-24
Match length	69
% identity	71
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	227912
Seq. ID	LIB3189-047-P1-K1-B11
Method	BLASTX
NCBI GI	g3169182
BLAST score	357
E value	3.0e-34
Match length	78
% identity	83
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	227913
Seq. ID	LIB3189-047-P1-K1-B2
Method	BLASTX
NCBI GI	g2811278
BLAST score	263
E value	1.0e-24
Match length	78
% identity	79
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227914
Seq. ID	LIB3189-047-P1-K1-B3
Method	BLASTX
NCBI GI	g3860323
BLAST score	355
E value	8.0e-34
Match length	78
% identity	83

NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	227915
Seq. ID	LIB3189-047-P1-K1-B5
Method	BLASTX
NCBI GI	g507275
BLAST score	178
E value	6.0e-13
Match length	105
% identity	40
NCBI Description	(L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama guanicoe]

Seq. No.	227916
Seq. ID	LIB3189-047-P1-K1-C10
Method	BLASTX
NCBI GI	g1174592
BLAST score	611
E value	1.0e-63
Match length	118
% identity	96
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	227917
Seq. ID	LIB3189-047-P1-K1-C12
Method	BLASTX
NCBI GI	g3426039
BLAST score	344
E value	2.0e-32
Match length	127
% identity	58
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	227918
Seq. ID	LIB3189-047-P1-K1-C4
Method	BLASTX
NCBI GI	g1174592
BLAST score	655
E value	2.0e-78
Match length	157
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	227919
Seq. ID	LIB3189-047-P1-K1-C7
Method	BLASTX
NCBI GI	g136739
BLAST score	379
E value	3.0e-46
Match length	120
% identity	81
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	227920
Seq. ID	LIB3189-047-P1-K1-C9
Method	BLASTX
NCBI GI	g3924823
BLAST score	219
E value	9.0e-18
Match length	71
% identity	54
NCBI Description	(Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST yk491a11.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	227921
Seq. ID	LIB3189-047-P1-K1-D12
Method	BLASTX
NCBI GI	g1352316
BLAST score	212
E value	5.0e-25
Match length	79
% identity	62
NCBI Description	DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1 [Arabidopsis thaliana]

Seq. No.	227922
Seq. ID	LIB3189-047-P1-K1-D2
Method	BLASTX
NCBI GI	g3894191
BLAST score	174
E value	2.0e-12
Match length	66
% identity	50
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	227923
Seq. ID	LIB3189-047-P1-K1-D3
Method	BLASTX
NCBI GI	g3080417
BLAST score	212
E value	4.0e-17
Match length	55
% identity	87
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	227924
Seq. ID	LIB3189-047-P1-K1-D4
Method	BLASTX
NCBI GI	g1086249
BLAST score	273
E value	5.0e-24
Match length	123
% identity	45
NCBI Description	subtilisin-like protease - Alnus glutinosa >gi_757522_emb_CAA59964_ (X85975) subtilisin-like protease [Alnus glutinosa]

Seq. No.	227925
Seq. ID	LIB3189-047-P1-K1-E10
Method	BLASTX
NCBI GI	g4185153
BLAST score	238
E value	5.0e-20
Match length	103
% identity	50
NCBI Description	(AC005724) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227926
Seq. ID	LIB3189-047-P1-K1-E11
Method	BLASTX
NCBI GI	g71634
BLAST score	716
E value	5.0e-76
Match length	135
% identity	99
NCBI Description	actin 1 - rice

Seq. No.	227927
Seq. ID	LIB3189-047-P1-K1-E12
Method	BLASTX
NCBI GI	g4538920
BLAST score	324
E value	4.0e-30
Match length	107
% identity	46
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	227928
Seq. ID	LIB3189-047-P1-K1-E2
Method	BLASTX
NCBI GI	g1168728
BLAST score	358
E value	4.0e-34
Match length	77
% identity	90
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	227929
Seq. ID	LIB3189-047-P1-K1-E3
Method	BLASTX
NCBI GI	g729974
BLAST score	468
E value	7.0e-47
Match length	121
% identity	71
NCBI Description	FLORAL HOMEOTIC PROTEIN PMADS1 (GREEN PETAL HOMEOTIC PROTEIN) >gi_322773_pir__S31693 transcription factor gp - garden petunia >gi_22665_emb_CAA49567_ (X69946) GP (green petal) [Petunia x hybrida]

Seq. No.	227930

Seq. ID	LIB3189-047-P1-K1-E4
Method	BLASTX
NCBI GI	g132944
BLAST score	524
E value	2.0e-53
Match length	115
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	227931
Seq. ID	LIB3189-047-P1-K1-E5
Method	BLASTX
NCBI GI	g3805845
BLAST score	233
E value	2.0e-19
Match length	83
% identity	60
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	227932
Seq. ID	LIB3189-047-P1-K1-E6
Method	BLASTX
NCBI GI	g4406774
BLAST score	192
E value	1.0e-14
Match length	55
% identity	67
NCBI Description	(AC006836) putative nonsense-mediated mRNA decay protein, 5' partial [Arabidopsis thaliana]

Seq. No.	227933
Seq. ID	LIB3189-047-P1-K1-F1
Method	BLASTX
NCBI GI	g3668089
BLAST score	374
E value	4.0e-38
Match length	132
% identity	59
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	227934
Seq. ID	LIB3189-047-P1-K1-F10
Method	BLASTX
NCBI GI	g3024017
BLAST score	380
E value	9.0e-40
Match length	94
% identity	91
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	227935
Seq. ID	LIB3189-047-P1-K1-F2
Method	BLASTX

NCBI GI	g2811278
BLAST score	756
E value	1.0e-80
Match length	155
% identity	90
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	227936
Seq. ID	LIB3189-047-P1-K1-F6
Method	BLASTX
NCBI GI	g231586
BLAST score	462
E value	2.0e-46
Match length	108
% identity	86
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	227937
Seq. ID	LIB3189-047-P1-K1-F7
Method	BLASTX
NCBI GI	g2995384
BLAST score	142
E value	2.0e-09
Match length	41
% identity	68
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	227938
Seq. ID	LIB3189-047-P1-K1-F8
Method	BLASTX
NCBI GI	g3600032
BLAST score	208
E value	1.0e-16
Match length	59
% identity	68
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	227939
Seq. ID	LIB3189-047-P1-K1-F9
Method	BLASTX
NCBI GI	g1176658
BLAST score	256
E value	3.0e-24
Match length	139
% identity	41
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	227940
Seq. ID	LIB3189-047-P1-K1-G5

Method	BLASTX
NCBI GI	g4337175
BLAST score	266
E value	1.0e-23
Match length	82
% identity	62
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	227941
Seq. ID	LIB3189-047-P1-K1-G7
Method	BLASTX
NCBI GI	g3334113
BLAST score	300
E value	2.0e-27
Match length	63
% identity	90
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	227942
Seq. ID	LIB3189-047-P1-K1-G9
Method	BLASTX
NCBI GI	g1703375
BLAST score	405
E value	8.0e-40
Match length	84
% identity	93
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	227943
Seq. ID	LIB3189-047-P1-K1-H1
Method	BLASTX
NCBI GI	g1213629
BLAST score	660
E value	2.0e-69
Match length	153
% identity	78
NCBI Description	(X95991) pectinesterase [Prunus persica]

Seq. No.	227944
Seq. ID	LIB3189-047-P1-K1-H2
Method	BLASTX
NCBI GI	g3264828
BLAST score	721
E value	1.0e-76
Match length	149
% identity	93
NCBI Description	(AF072404) cotton fiber expressed protein 1 [Gossypium hirsutum]

Seq. No.	227945
Seq. ID	LIB3189-047-P1-K1-H3
Method	BLASTX

NCBI GI g2702281
BLAST score 251
E value 8.0e-22
Match length 58
% identity 43
NCBI Description (AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No. 227946
Seq. ID LIB3189-047-P1-K1-H5
Method BLASTX
NCBI GI g1173218
BLAST score 271
E value 3.0e-24
Match length 55
% identity 96
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 227947
Seq. ID LIB3189-047-P1-K1-H6
Method BLASTX
NCBI GI g2244826
BLAST score 357
E value 5.0e-34
Match length 100
% identity 72
NCBI Description (Z97336) replication control protein homolog [Arabidopsis thaliana]

Seq. No. 227948
Seq. ID LIB3189-047-P1-K1-H8
Method BLASTX
NCBI GI g3264832
BLAST score 326
E value 9.0e-31
Match length 76
% identity 86
NCBI Description (AF072406) cotton fiber expressed protein 3 [Gossypium hirsutum]

Seq. No. 227949
Seq. ID LIB3189-047-P1-K1-H9
Method BLASTX
NCBI GI g2702281
BLAST score 183
E value 6.0e-14
Match length 49
% identity 43
NCBI Description (AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No. 227950
Seq. ID LIB3189-048-P1-K1-A1
Method BLASTX
NCBI GI g464986

BLAST score	242
E value	4.0e-39
Match length	82
% identity	95
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	227951
Seq. ID	LIB3189-048-P1-K1-A11
Method	BLASTX
NCBI GI	g131773
BLAST score	568
E value	1.0e-58
Match length	143
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	227952
Seq. ID	LIB3189-048-P1-K1-A2
Method	BLASTX
NCBI GI	g2244847
BLAST score	171
E value	1.0e-12
Match length	58
% identity	55
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	227953
Seq. ID	LIB3189-048-P1-K1-A5
Method	BLASTX
NCBI GI	g4559358
BLAST score	122
E value	1.0e-10
Match length	73
% identity	48
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	227954
Seq. ID	LIB3189-048-P1-K1-A6
Method	BLASTX
NCBI GI	g3377797
BLAST score	592
E value	2.0e-61
Match length	146

% identity	78
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara
Seq. No.	227955
Seq. ID	LIB3189-048-P1-K1-A8
Method	BLASTX
NCBI GI	g120669
BLAST score	557
E value	2.0e-57
Match length	120
% identity	88
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	227956
Seq. ID	LIB3189-048-P1-K1-A9
Method	BLASTX
NCBI GI	g3668089
BLAST score	230
E value	4.0e-19
Match length	85
% identity	48
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	227957
Seq. ID	LIB3189-048-P1-K1-B4
Method	BLASTX
NCBI GI	g267069
BLAST score	182
E value	2.0e-13
Match length	42
% identity	79
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	227958
Seq. ID	LIB3189-048-P1-K1-B9
Method	BLASTX
NCBI GI	g2462825
BLAST score	266
E value	3.0e-23
Match length	91
% identity	59
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]
Seq. No.	227959
Seq. ID	LIB3189-048-P1-K1-C10

Method	BLASTX
NCBI GI	g3876865
BLAST score	168
E value	1.0e-11
Match length	91
% identity	37
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227960
Seq. ID	LIB3189-048-P1-K1-C9
Method	BLASTX
NCBI GI	g465820
BLAST score	477
E value	6.0e-48
Match length	127
% identity	66
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi_280536_pir__S28301 hypothetical protein C40H1.6 - Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154) C40H1.6 [Caenorhabditis elegans]

Seq. No.	227961
Seq. ID	LIB3189-048-P1-K1-D10
Method	BLASTX
NCBI GI	g4371290
BLAST score	139
E value	1.0e-08
Match length	83
% identity	41
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	227962
Seq. ID	LIB3189-048-P1-K1-D11
Method	BLASTX
NCBI GI	g1702986
BLAST score	502
E value	7.0e-51
Match length	129
% identity	81
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	227963
Seq. ID	LIB3189-048-P1-K1-D12
Method	BLASTX
NCBI GI	g2129769
BLAST score	497
E value	2.0e-50
Match length	110
% identity	82
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	227964
Seq. ID	LIB3189-048-P1-K1-D6
Method	BLASTX
NCBI GI	g400054
BLAST score	172
E value	9.0e-13
Match length	59
% identity	58
NCBI Description	DIHYDROXY-ACID DEHYDRATASE (DAD) >gi_486729_pir__S35137 probable phosphogluconate dehydratase (EC 4.2.1.12) - Lactococcus lactis subsp. lactis >gi_2565156 (U92974) IlvD [Lactococcus lactis]

Seq. No.	227965
Seq. ID	LIB3189-048-P1-K1-D9
Method	BLASTX
NCBI GI	g3876865
BLAST score	161
E value	5.0e-11
Match length	73
% identity	40
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	227966
Seq. ID	LIB3189-048-P1-K1-E11
Method	BLASTX
NCBI GI	g2499710
BLAST score	270
E value	4.0e-24
Match length	82
% identity	44
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No.	227967
Seq. ID	LIB3189-048-P1-K1-E12
Method	BLASTX
NCBI GI	g1346735
BLAST score	665
E value	6.0e-70
Match length	149
% identity	81
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_1076562_pir__S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi_474170_emb_CAA49995_ (X70652) phosphoglycerate mutase [Ricinus communis]

Seq. No.	227968
Seq. ID	LIB3189-048-P1-K1-E2
Method	BLASTX
NCBI GI	g2833386

BLAST score	211
E value	5.0e-17
Match length	71
% identity	66
NCBI Description	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi_2129493_pir__S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi_3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi_1587969_prf__2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No.	227969
Seq. ID	LIB3189-048-P1-K1-E3
Method	BLASTX
NCBI GI	g2642238
BLAST score	211
E value	4.0e-17
Match length	66
% identity	67
NCBI Description	(AF031241) endoplasmic reticulum HSC70-cognate binding protein precursor [Glycine max]

Seq. No.	227970
Seq. ID	LIB3189-048-P1-K1-E8
Method	BLASTX
NCBI GI	g729618
BLAST score	552
E value	1.0e-62
Match length	143
% identity	81
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP 2) >gi_82172_pir__PQ0262 luminal binding protein BLP-2 - common tobacco (fragment) >gi_100338_pir__S21878 heat shock protein BiP homolog blp2 - common tobacco (fragment) >gi_19807_emb_CAA42661_ (X60059) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	227971
Seq. ID	LIB3189-048-P1-K1-F1
Method	BLASTX
NCBI GI	g267069
BLAST score	695
E value	1.0e-73
Match length	130
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	227972
Seq. ID	LIB3189-048-P1-K1-F3
Method	BLASTX
NCBI GI	g541951

BLAST score	169
E value	4.0e-12
Match length	86
% identity	42
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	227973
Seq. ID	LIB3189-048-P1-K1-F4
Method	BLASTX
NCBI GI	g4510347
BLAST score	221
E value	5.0e-18
Match length	77
% identity	60
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227974
Seq. ID	LIB3189-048-P1-K1-F5
Method	BLASTX
NCBI GI	g4510347
BLAST score	144
E value	1.0e-16
Match length	98
% identity	56
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227975
Seq. ID	LIB3189-048-P1-K1-G11
Method	BLASTX
NCBI GI	g3123271
BLAST score	477
E value	3.0e-49
Match length	106
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	227976
Seq. ID	LIB3189-048-P1-K1-G3
Method	BLASTX
NCBI GI	g231660
BLAST score	370
E value	2.0e-35
Match length	150
% identity	53
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	227977
Seq. ID	LIB3189-048-P1-K1-G6
Method	BLASTX
NCBI GI	g3650032
BLAST score	219
E value	4.0e-18
Match length	52
% identity	63
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No.	227978
Seq. ID	LIB3189-048-P1-K1-G7
Method	BLASTX
NCBI GI	g3122060
BLAST score	175
E value	4.0e-13
Match length	46
% identity	76
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2598657_emb_CAA10847_ (AJ222579) elongation factor 1-alpha (EF1-a) [Vicia faba]

Seq. No.	227979
Seq. ID	LIB3189-048-P1-K1-G8
Method	BLASTX
NCBI GI	g3834307
BLAST score	415
E value	1.0e-40
Match length	149
% identity	57
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	227980
Seq. ID	LIB3189-048-P1-K1-H3
Method	BLASTX
NCBI GI	g3299896
BLAST score	436
E value	3.0e-43
Match length	102
% identity	74
NCBI Description	(AF020390) beta-galactosidase [Lycopersicon esculentum]

Seq. No.	227981
Seq. ID	LIB3189-048-P1-K1-H6
Method	BLASTX
NCBI GI	g2851508
BLAST score	237
E value	2.0e-20
Match length	56
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	227982
Seq. ID	LIB3189-048-P1-K1-H9
Method	BLASTX
NCBI GI	g1332579
BLAST score	522
E value	3.0e-53

Match length	113
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	227983
Seq. ID	LIB3189-049-P1-K1-A11
Method	BLASTX
NCBI GI	g2651310
BLAST score	358
E value	5.0e-34
Match length	145
% identity	46
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	227984
Seq. ID	LIB3189-049-P1-K1-A12
Method	BLASTX
NCBI GI	g2244888
BLAST score	194
E value	5.0e-15
Match length	83
% identity	46
NGBI Description	(Z97338) similarity to cytochrome P450 [Arabidopsis thaliana]

Seq. No.	227985
Seq. ID	LIB3189-049-P1-K1-A2
Method	BLASTX
NCBI GI	g3522929
BLAST score	681
E value	5.0e-72
Match length	150
% identity	89
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	227986
Seq. ID	LIB3189-049-P1-K1-A3
Method	BLASTX
NCBI GI	g2493144
BLAST score	248
E value	1.0e-21
Match length	66
% identity	79
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	227987
Seq. ID	LIB3189-049-P1-K1-A6
Method	BLASTX
NCBI GI	g1545805

BLAST score	208
E value	9.0e-17
Match length	76
% identity	57
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	227988
Seq. ID	LIB3189-049-P1-K1-A7
Method	BLASTX
NCBI GI	g549061
BLAST score	405
E value	2.0e-39
Match length	112
% identity	71
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse >gi_468554_emb_CAA83432_ (Z31557) CCT (chaperonin containing TCP-1) zeta subunit [Mus musculus]

Seq. No.	227989
Seq. ID	LIB3189-049-P1-K1-A8
Method	BLASTX
NCBI GI	g1703318
BLAST score	536
E value	7.0e-55
Match length	148
% identity	30
NCBI Description	ANNEXIN-LIKE PROTEIN RJ4 >gi_1362037_pir__S56674 annexin homolog RJ4 (clone RJ4) - garden strawberry (fragment) >gi_643076 (U19941) annexin [Fragaria x ananassa]

Seq. No.	227990
Seq. ID	LIB3189-049-P1-K1-B10
Method	BLASTX
NCBI GI	g2245000
BLAST score	148
E value	2.0e-09
Match length	125
% identity	30
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	227991
Seq. ID	LIB3189-049-P1-K1-B12
Method	BLASTX
NCBI GI	g71498
BLAST score	391
E value	6.0e-38
Match length	113
% identity	67
NCBI Description	heat shock protein 17.7 - garden pea

Seq. No.	227992
Seq. ID	LIB3189-049-P1-K1-B4
Method	BLASTX
NCBI GI	g4337175
BLAST score	145

E value	1.0e-09
Match length	49
% identity	61
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.	227993
Seq. ID	LIB3189-049-P1-K1-B6
Method	BLASTX
NCBI GI	g267070
BLAST score	661
E value	1.0e-69
Match length	135
% identity	95
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699) TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana]
Seq. No.	227994
Seq. ID	LIB3189-049-P1-K1-B8
Method	BLASTX
NCBI GI	g2695861
BLAST score	139
E value	6.0e-09
Match length	42
% identity	67
NCBI Description	(Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum]
Seq. No.	227995
Seq. ID	LIB3189-049-P1-K1-C10
Method	BLASTX
NCBI GI	g2642215
BLAST score	254
E value	8.0e-22
Match length	75
% identity	69
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]
Seq. No.	227996
Seq. ID	LIB3189-049-P1-K1-C6
Method	BLASTX
NCBI GI	g3367576
BLAST score	497
E value	3.0e-50
Match length	127
% identity	70
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
Seq. No.	227997
Seq. ID	LIB3189-049-P1-K1-C7

Method	BLASTX
NCBI GI	g1931639
BLAST score	277
E value	1.0e-24
Match length	120
% identity	42
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	227998
Seq. ID	LIB3189-049-P1-K1-C8
Method	BLASTX
NCBI GI	g586076
BLAST score	375
E value	2.0e-36
Match length	73
% identity	93
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	227999
Seq. ID	LIB3189-049-P1-K1-D1
Method	BLASTX
NCBI GI	g3915031
BLAST score	659
E value	1.0e-77
Match length	147
% identity	96
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	228000
Seq. ID	LIB3189-049-P1-K1-D8
Method	BLASTX
NCBI GI	g542157
BLAST score	642
E value	3.0e-67
Match length	148
% identity	80
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	228001
Seq. ID	LIB3189-049-P1-K1-E11
Method	BLASTX
NCBI GI	g2982318
BLAST score	311
E value	5.0e-29
Match length	66
% identity	86
NCBI Description	(AF051244) probable 60S ribosomal protein L15 [Picea mariana]

Seq. No.	228002
Seq. ID	LIB3189-049-P1-K1-E2
Method	BLASTX

NCBI GI	g1702983
BLAST score	328
E value	1.0e-30
Match length	104
% identity	58
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein [Fragaria ananassa]

Seq. No.	228003
Seq. ID	LIB3189-049-P1-K1-E7
Method	BLASTX
NCBI GI	g586076
BLAST score	615
E value	3.0e-64
Match length	120
% identity	95
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	228004
Seq. ID	LIB3189-049-P1-K1-F10
Method	BLASTX
NCBI GI	g2341034
BLAST score	286
E value	5.0e-26
Match length	59
% identity	95
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	228005
Seq. ID	LIB3189-049-P1-K1-F6
Method	BLASTX
NCBI GI	g2498076
BLAST score	446
E value	2.0e-44
Match length	94
% identity	91
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE) >gi_1619958 (U72142) nucleoside diphosphate kinase [Helianthus annuus]

Seq. No.	228006
Seq. ID	LIB3189-049-P1-K1-F7
Method	BLASTX
NCBI GI	g3075394
BLAST score	350
E value	3.0e-33
Match length	106
% identity	69
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	228007
Seq. ID	LIB3189-049-P1-K1-G11
Method	BLASTX
NCBI GI	g3668097
BLAST score	159
E value	5.0e-11
Match length	34
% identity	82
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	228008
Seq. ID	LIB3189-049-P1-K1-G2
Method	BLASTX
NCBI GI	g3493172
BLAST score	219
E value	2.0e-18
Match length	57
% identity	75
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	228009
Seq. ID	LIB3189-049-P1-K1-G3
Method	BLASTX
NCBI GI	g2499488
BLAST score	342
E value	1.0e-32
Match length	71
% identity	90
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	228010
Seq. ID	LIB3189-049-P1-K1-G6
Method	BLASTX
NCBI GI	g3668097
BLAST score	266
E value	2.0e-23
Match length	74
% identity	74
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	228011
Seq. ID	LIB3189-049-P1-K1-H11
Method	BLASTX
NCBI GI	g1345673
BLAST score	270
E value	6.0e-24
Match length	65
% identity	78
NCBI Description	CATALASE ISOZYME 1 >gi_862452_dbj_BAA09506_ (D55645) catalase [Cucurbita pepo]

Seq. No.	228012
Seq. ID	LIB3189-049-P1-K1-H8
Method	BLASTX
NCBI GI	g1710151
BLAST score	608
E value	2.0e-63
Match length	127
% identity	87
NCBI Description	(U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No.	228013
Seq. ID	LIB3189-050-P1-K1-A11
Method	BLASTX
NCBI GI	g3850571
BLAST score	436
E value	3.0e-43
Match length	94
% identity	89
NCBI Description	(AC005278) Similar to gb_U85207 snRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb_AA612141 comes from this gene. [Arabidopsis thaliana]

Seq. No.	228014
Seq. ID	LIB3189-050-P1-K1-A12
Method	BLASTX
NCBI GI	g4454051
BLAST score	469
E value	4.0e-47
Match length	98
% identity	85
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	228015
Seq. ID	LIB3189-050-P1-K1-A3
Method	BLASTX
NCBI GI	g1169494
BLAST score	239
E value	4.0e-20
Match length	85
% identity	58
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_2119915_pir__S60659 EF-Tu protein precursor - soybean >gi_949873_emb_CAA61444_ (X89058) EF-Tu protein [Glycine max]

Seq. No.	228016
Seq. ID	LIB3189-050-P1-K1-A4
Method	BLASTX
NCBI GI	g3915826
BLAST score	373
E value	5.0e-52
Match length	134
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	228017
Seq. ID	LIB3189-050-P1-K1-A6
Method	BLASTX
NCBI GI	g3738257
BLAST score	500
E value	9.0e-51
Match length	105
% identity	93
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	228018
Seq. ID	LIB3189-050-P1-K1-A7
Method	BLASTX
NCBI GI	g2267567
BLAST score	394
E value	2.0e-38
Match length	85
% identity	87
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	228019
Seq. ID	LIB3189-050-P1-K1-A9
Method	BLASTX
NCBI GI	g2864614
BLAST score	187
E value	5.0e-14
Match length	80
% identity	51
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	228020
Seq. ID	LIB3189-050-P1-K1-B3
Method	BLASTX
NCBI GI	g3913791
BLAST score	161
E value	5.0e-19
Match length	56
% identity	89
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum]

Seq. No.	228021
Seq. ID	LIB3189-050-P1-K1-B4
Method	BLASTX
NCBI GI	g2244994
BLAST score	707
E value	6.0e-75
Match length	144
% identity	88
NCBI Description	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No.	228022
Seq. ID	LIB3189-050-P1-K1-B5
Method	BLASTX
NCBI GI	g4210948
BLAST score	239
E value	5.0e-30
Match length	74
% identity	87
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	228023
Seq. ID	LIB3189-050-P1-K1-B6
Method	BLASTX
NCBI GI	g2662343
BLAST score	590
E value	3.0e-61
Match length	112
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	228024
Seq. ID	LIB3189-050-P1-K1-B7
Method	BLASTX
NCBI GI	g3876865
BLAST score	150
E value	9.0e-10
Match length	66
% identity	41
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	228025
Seq. ID	LIB3189-050-P1-K1-C1
Method	BLASTX
NCBI GI	g2244931
BLAST score	153
E value	5.0e-10
Match length	118
% identity	33
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana] >gi_3426058_emb_CAA07572_ (AJ007585) IB1P8-4 protein [Arabidopsis thaliana]

Seq. No.	228026
Seq. ID	LIB3189-050-P1-K1-C10
Method	BLASTX
NCBI GI	g3334115
BLAST score	573
E value	3.0e-59
Match length	118
% identity	97
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	228027
Seq. ID	LIB3189-050-P1-K1-C12
Method	BLASTX
NCBI GI	g4191778
BLAST score	359
E value	4.0e-34
Match length	95
% identity	76
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	228028
Seq. ID	LIB3189-050-P1-K1-C4
Method	BLASTX
NCBI GI	g3668089
BLAST score	140
E value	4.0e-10
Match length	88
% identity	43
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	228029
Seq. ID	LIB3189-050-P1-K1-C6
Method	BLASTX
NCBI GI	g120669
BLAST score	450
E value	8.0e-45
Match length	102
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	228030
Seq. ID	LIB3189-050-P1-K1-C7
Method	BLASTX
NCBI GI	g401322
BLAST score	331
E value	7.0e-31
Match length	80
% identity	82
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	228031
Seq. ID	LIB3189-050-P1-K1-C8
Method	BLASTX
NCBI GI	g3759184
BLAST score	264
E value	5.0e-23
Match length	111
% identity	53
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	228032
Seq. ID	LIB3189-050-P1-K1-C9
Method	BLASTX
NCBI GI	g2245082
BLAST score	389
E value	8.0e-38
Match length	117
% identity	63
NCBI Description	(Z97343) SCARECROW homolog [Arabidopsis thaliana]

Seq. No.	228033
Seq. ID	LIB3189-050-P1-K1-D10
Method	BLASTX
NCBI GI	g586076
BLAST score	281
E value	1.0e-25
Match length	52
% identity	96
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	228034
Seq. ID	LIB3189-050-P1-K1-D12
Method	BLASTX
NCBI GI	g2980770
BLAST score	417
E value	5.0e-41
Match length	137
% identity	56
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	228035
Seq. ID	LIB3189-050-P1-K1-D2
Method	BLASTX
NCBI GI	g2500380
BLAST score	565
E value	2.0e-58
Match length	105
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	228036
Seq. ID	LIB3189-050-P1-K1-E11
Method	BLASTX
NCBI GI	g1688296
BLAST score	295
E value	3.0e-27
Match length	66
% identity	85
NCBI Description	(U78297) plasma membrane intrinsic protein PIP3 [Arabidopsis thaliana]

Seq. No.	228037
Seq. ID	LIB3189-050-P1-K1-E3
Method	BLASTX
NCBI GI	g4455208
BLAST score	596
E value	6.0e-62
Match length	138
% identity	84
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	228038
Seq. ID	LIB3189-050-P1-K1-E4
Method	BLASTX
NCBI GI	g4467359
BLAST score	596
E value	8.0e-69
Match length	145
% identity	88
NCBI Description	(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No.	228039
Seq. ID	LIB3189-050-P1-K1-E9
Method	BLASTX
NCBI GI	g3420006
BLAST score	312
E value	1.0e-28
Match length	93
% identity	61
NCBI Description	(AF000306) steroid sulfotransferase 2 [Brassica napus]

Seq. No.	228040
Seq. ID	LIB3189-050-P1-K1-F3
Method	BLASTX
NCBI GI	g1213450
BLAST score	535
E value	9.0e-55
Match length	141
% identity	76
NCBI Description	(U48963) isopentenyl pyrophosphate isomerase [Clarkia breweri]

Seq. No.	228041
Seq. ID	LIB3189-050-P1-K1-F5
Method	BLASTX
NCBI GI	g3327868
BLAST score	152
E value	7.0e-10
Match length	68
% identity	56
NCBI Description	(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana]

Seq. No.	228042
Seq. ID	LIB3189-050-P1-K1-F7
Method	BLASTX

NCBI GI g267069
BLAST score 574
E value 2.0e-59
Match length 112
% identity 95
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 228043
Seq. ID LIB3189-050-P1-K1-F8
Method BLASTX
NCBI GI g4038034
BLAST score 344
E value 2.0e-32
Match length 87
% identity 75
NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 228044
Seq. ID LIB3189-050-P1-K1-F9
Method BLASTX
NCBI GI g1706102
BLAST score 199
E value 1.0e-15
Match length 90
% identity 46
NCBI Description CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CPSF 160 KD SUBUNIT) >gi_1045574 (U37012) cleavage and polyadenylation specificity factor [Homo sapiens]

Seq. No. 228045
Seq. ID LIB3189-050-P1-K1-G10
Method BLASTX
NCBI GI g4490321
BLAST score 272
E value 6.0e-24
Match length 145
% identity 41
NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No. 228046
Seq. ID LIB3189-050-P1-K1-G11
Method BLASTX
NCBI GI g3885343
BLAST score 239
E value 4.0e-20
Match length 88
% identity 47
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No. 228047
Seq. ID LIB3189-050-P1-K1-G5
Method BLASTX
NCBI GI g3063396
BLAST score 356

E value 4.0e-34
Match length 72
% identity 90
NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 228048
Seq. ID LIB3189-050-P1-K1-G6
Method BLASTX
NCBI GI g3097321
BLAST score 208
E value 2.0e-16
Match length 111
% identity 39
NCBI Description (AB013289) Bd 30K [Glycine max]

Seq. No. 228049
Seq. ID LIB3189-050-P1-K1-G7
Method BLASTX
NCBI GI g2829869
BLAST score 644
E value 1.0e-67
Match length 126
% identity 94
NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No. 228050
Seq. ID LIB3189-050-P1-K1-G8
Method BLASTX
NCBI GI g1871185
BLAST score 258
E value 6.0e-23
Match length 57
% identity 81
NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No. 228051
Seq. ID LIB3189-050-P1-K1-H1
Method BLASTX
NCBI GI g2829204
BLAST score 186
E value 4.0e-14
Match length 35
% identity 97
NCBI Description (AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No. 228052
Seq. ID LIB3189-050-P1-K1-H10
Method BLASTX
NCBI GI g4567281
BLAST score 174
E value 2.0e-12
Match length 57
% identity 63
NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	228053
Seq. ID	LIB3189-050-P1-K1-H12
Method	BLASTX
NCBI GI	g3334115
BLAST score	649
E value	4.0e-68
Match length	146
% identity	82
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	228054
Seq. ID	LIB3189-050-P1-K1-H3
Method	BLASTX
NCBI GI	g3334113
BLAST score	459
E value	7.0e-46
Match length	89
% identity	98
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	228055
Seq. ID	LIB3189-050-P1-K1-H4
Method	BLASTX
NCBI GI	g113621
BLAST score	522
E value	3.0e-53
Match length	122
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays]

Seq. No.	228056
Seq. ID	LIB3189-050-P1-K1-H9
Method	BLASTX
NCBI GI	g1172874
BLAST score	213
E value	4.0e-17
Match length	45
% identity	78
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	228057
Seq. ID	LIB3189-051-P1-K1-A10
Method	BLASTX
NCBI GI	g3033400

BLAST score	570
E value	6.0e-59
Match length	132
% identity	80
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	228058
Seq. ID	LIB3189-051-P1-K1-A11
Method	BLASTX
NCBI GI	g4335745
BLAST score	353
E value	2.0e-33
Match length	142
% identity	49
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	228059
Seq. ID	LIB3189-051-P1-K1-A2
Method	BLASTX
NCBI GI	g1174592
BLAST score	731
E value	8.0e-78
Match length	137
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	228060
Seq. ID	LIB3189-051-P1-K1-A3
Method	BLASTX
NCBI GI	g417103
BLAST score	670
E value	1.0e-70
Match length	134
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	228061
Seq. ID	LIB3189-051-P1-K1-A6
Method	BLASTX
NCBI GI	g3915635
BLAST score	289
E value	4.0e-26
Match length	105
% identity	66
NCBI Description	CYCLIN DELTA-1 >gi_2995130_emb_CAA58285_ (X83369) cyclin delta-1 [Arabidopsis thaliana]

Seq. No.	228062
Seq. ID	LIB3189-051-P1-K1-A7
Method	BLASTX
NCBI GI	g2765837
BLAST score	243
E value	1.0e-20
Match length	83
% identity	64
NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No.	228063
Seq. ID	LIB3189-051-P1-K1-A8
Method	BLASTX
NCBI GI	g3264759
BLAST score	600
E value	2.0e-62
Match length	151
% identity	79
NCBI Description	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]

Seq. No.	228064
Seq. ID	LIB3189-051-P1-K1-A9
Method	BLASTX
NCBI GI	g3874447
BLAST score	181
E value	2.0e-13
Match length	122
% identity	32
NCBI Description	(Z81039) predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com

Seq. No.	228065
Seq. ID	LIB3189-051-P1-K1-B1
Method	BLASTX
NCBI GI	g2760322
BLAST score	240
E value	4.0e-20
Match length	92
% identity	52
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 228066

Seq. ID	LIB3189-051-P1-K1-B2
Method	BLASTX
NCBI GI	g1617270
BLAST score	433
E value	6.0e-43
Match length	103
% identity	73
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	228067
Seq. ID	LIB3189-051-P1-K1-B3
Method	BLASTX
NCBI GI	g4263771
BLAST score	352
E value	3.0e-33
Match length	120
% identity	59
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	228068
Seq. ID	LIB3189-051-P1-K1-B4
Method	BLASTX
NCBI GI	g2995953
BLAST score	287
E value	9.0e-26
Match length	103
% identity	56
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	228069
Seq. ID	LIB3189-051-P1-K1-B6
Method	BLASTX
NCBI GI	g3334115
BLAST score	526
E value	1.0e-53
Match length	124
% identity	85
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	228070
Seq. ID	LIB3189-051-P1-K1-B8
Method	BLASTX
NCBI GI	g3790359
BLAST score	196
E value	5.0e-15
Match length	67
% identity	55
NCBI Description	(AB013359) DPM2 [Rattus norvegicus]

Seq. No.	228071
Seq. ID	LIB3189-051-P1-K1-B9
Method	BLASTX
NCBI GI	g3252813

BLAST score	440
E value	1.0e-43
Match length	98
% identity	86
NCBI Description	(AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810586 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	228072
Seq. ID	LIB3189-051-P1-K1-C1
Method	BLASTX
NCBI GI	g4337175
BLAST score	414
E value	1.0e-40
Match length	118
% identity	66
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	228073
Seq. ID	LIB3189-051-P1-K1-C10
Method	BLASTX
NCBI GI	g267082
BLAST score	811
E value	4.0e-87
Match length	154
% identity	99
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	228074
Seq. ID	LIB3189-051-P1-K1-C12
Method	BLASTX
NCBI GI	g167367
BLAST score	642
E value	3.0e-67
Match length	154
% identity	81
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	228075
Seq. ID	LIB3189-051-P1-K1-C2
Method	BLASTX
NCBI GI	g4557062
BLAST score	175
E value	6.0e-13
Match length	61
% identity	64
NCBI Description	(AC007045) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228076
Seq. ID	LIB3189-051-P1-K1-C4
Method	BLASTX
NCBI GI	g2119045

BLAST score	424
E value	7.0e-42
Match length	111
% identity	43
NCBI Description	small nuclear ribonucleoprotein U1A - potato >gi_1050840_emb_CAA90282_ (Z49990) U1snRNP-specific protein, U1A [Solanum tuberosum]

Seq. No.	228077
Seq. ID	LIB3189-051-P1-K1-C7
Method	BLASTX
NCBI GI	g548847
BLAST score	210
E value	7.0e-17
Match length	47
% identity	87
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_1086182_pir__S39501 ribosomal protein S12 - curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	228078
Seq. ID	LIB3189-051-P1-K1-C9
Method	BLASTX
NCBI GI	g4567283
BLAST score	365
E value	8.0e-35
Match length	154
% identity	52
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	228079
Seq. ID	LIB3189-051-P1-K1-D1
Method	BLASTX
NCBI GI	g1351408
BLAST score	457
E value	1.0e-45
Match length	136
% identity	68
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	228080
Seq. ID	LIB3189-051-P1-K1-D10
Method	BLASTX
NCBI GI	g2879811
BLAST score	534
E value	1.0e-54
Match length	111
% identity	92
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	228081
Seq. ID	LIB3189-051-P1-K1-D11

Method	BLASTX
NCBI GI	g2827559
BLAST score	160
E value	8.0e-11
Match length	42
% identity	71
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	228082
Seq. ID	LIB3189-051-P1-K1-D12
Method	BLASTX
NCBI GI	g3451075
BLAST score	542
E value	1.0e-55
Match length	151
% identity	66
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	228083
Seq. ID	LIB3189-051-P1-K1-D2
Method	BLASTX
NCBI GI	g2244994
BLAST score	520
E value	2.0e-59
Match length	144
% identity	75
NCBI Description	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No.	228084
Seq. ID	LIB3189-051-P1-K1-D4
Method	BLASTX
NCBI GI	g4539399
BLAST score	453
E value	3.0e-45
Match length	108
% identity	88
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	228085
Seq. ID	LIB3189-051-P1-K1-D5
Method	BLASTX
NCBI GI	g4204313
BLAST score	559
E value	1.0e-57
Match length	125
% identity	85
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	228086
Seq. ID	LIB3189-051-P1-K1-D8
Method	BLASTX
NCBI GI	g2493895

BLAST score	553
E value	6.0e-57
Match length	132
% identity	81
NCBI Description	CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_1071911_pir__S46438 cysteine synthase (EC 4.2.99.8) - watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine synthase [Citrullus lanatus]

Seq. No.	228087
Seq. ID	LIB3189-051-P1-K1-D9
Method	BLASTX
NCBI GI	g1488043
BLAST score	274
E value	3.0e-24
Match length	84
% identity	68
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No.	228088
Seq. ID	LIB3189-051-P1-K1-E1
Method	BLASTX
NCBI GI	g1928981
BLAST score	565
E value	3.0e-58
Match length	121
% identity	62
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	228089
Seq. ID	LIB3189-051-P1-K1-E10
Method	BLASTX
NCBI GI	g4512653
BLAST score	230
E value	4.0e-19
Match length	51
% identity	86
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	228090
Seq. ID	LIB3189-051-P1-K1-E2
Method	BLASTX
NCBI GI	g4559356
BLAST score	151
E value	1.0e-09
Match length	150
% identity	9
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228091
Seq. ID	LIB3189-051-P1-K1-E3
Method	BLASTX
NCBI GI	g2440015
BLAST score	446
E value	7.0e-46

Match length	153
% identity	68
NCBI Description	(AF014960) multidrug resistance-associated protein 2; AtMRP2 [Arabidopsis thaliana]

Seq. No.	228092
Seq. ID	LIB3189-051-P1-K1-E4
Method	BLASTX
NCBI GI	g2129499
BLAST score	784
E value	6.0e-84
Match length	158
% identity	92
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	228093
Seq. ID	LIB3189-051-P1-K1-E8
Method	BLASTX
NCBI GI	g232024
BLAST score	791
E value	9.0e-85
Match length	149
% identity	99
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	228094
Seq. ID	LIB3189-051-P1-K1-F12
Method	BLASTX
NCBI GI	g3318611
BLAST score	216
E value	2.0e-17
Match length	41
% identity	100
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	228095
Seq. ID	LIB3189-051-P1-K1-F4
Method	BLASTX
NCBI GI	g3702333
BLAST score	245
E value	1.0e-20
Match length	131
% identity	42
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228096
Seq. ID	LIB3189-051-P1-K1-F6
Method	BLASTX
NCBI GI	g2129630
BLAST score	335
E value	3.0e-31

Match length	136
% identity	48
NCBI Description	lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750_ (X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721) unknown [Arabidopsis thaliana]

Seq. No.	228097
Seq. ID	LIB3189-051-P1-K1-F7
Method	BLASTX
NCBI GI	g3298548
BLAST score	360
E value	3.0e-34
Match length	115
% identity	61
NCBI Description	(AC004681) putative spliceosomal protein [Arabidopsis thaliana]

Seq. No.	228098
Seq. ID	LIB3189-051-P1-K1-F8
Method	BLASTX
NCBI GI	g464849
BLAST score	826
E value	7.0e-89
Match length	156
% identity	99
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	228099
Seq. ID	LIB3189-051-P1-K1-G10
Method	BLASTX
NCBI GI	g3449282
BLAST score	316
E value	3.0e-29
Match length	70
% identity	87
NCBI Description	(AB006139) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Arabidopsis thaliana] >gi_3449284_dbj_BAA32457_ (AB008929) N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase [Arabidopsis thaliana] >gi_4510353_gb_AAD21442.1_ (AC006921) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Arabidopsis thaliana]

Seq. No.	228100
Seq. ID	LIB3189-051-P1-K1-G3
Method	BLASTX
NCBI GI	g2244833
BLAST score	181
E value	3.0e-13
Match length	138
% identity	16
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No.	228101

Seq. ID	LIB3189-051-P1-K1-G4
Method	BLASTX
NCBI GI	g4106061
BLAST score	199
E value	7.0e-16
Match length	75
% identity	60
NCBI Description	(AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	228102
Seq. ID	LIB3189-051-P1-K1-H10
Method	BLASTX
NCBI GI	g1710838
BLAST score	559
E value	1.0e-57
Match length	127
% identity	84
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_535584 (L36119) adenosylhomocysteinase [Medicago sativa]

Seq. No.	228103
Seq. ID	LIB3189-051-P1-K1-H11
Method	BLASTX
NCBI GI	g1706318
BLAST score	193
E value	2.0e-31
Match length	92
% identity	69
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) (ERT D1) >gi_1362098_pir__S56177 probable glutamate decarboxylase - tomato >gi_995555_emb_CAA56812_ (X80840) homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon [Lycopersicon esculentum]

Seq. No.	228104
Seq. ID	LIB3189-051-P1-K1-H2
Method	BLASTX
NCBI GI	g3024013
BLAST score	358
E value	4.0e-34
Match length	114
% identity	61
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA) >gi_2706460_emb_CAA15918.1_ (AL021046) translational initiation factor 2 alpha [Schizosaccharomyces pombe]

Seq. No.	228105
Seq. ID	LIB3189-051-P1-K1-H3
Method	BLASTX
NCBI GI	g2129499
BLAST score	429
E value	6.0e-80
Match length	160
% identity	93
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton

>gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	228106
Seq. ID	LIB3189-051-P1-K1-H4
Method	BLASTX
NCBI GI	g1718097
BLAST score	474
E value	1.0e-47
Match length	130
% identity	64
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	228107
Seq. ID	LIB3189-051-P1-K1-H6
Method	BLASTX
NCBI GI	g2832625
BLAST score	465
E value	9.0e-47
Match length	113
% identity	76
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	228108
Seq. ID	LIB3189-051-P1-K1-H8
Method	BLASTX
NCBI GI	g82263
BLAST score	755
E value	1.0e-80
Match length	148
% identity	97
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	228109
Seq. ID	LIB3189-051-P1-K1-H9
Method	BLASTX
NCBI GI	g1297190
BLAST score	428
E value	3.0e-42
Match length	112
% identity	72
NCBI Description	(U53501) Theoretical protein with similarity to GenBank Accession Number L22302 serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	228110
Seq. ID	LIB3189-052-P1-K1-A2
Method	BLASTX
NCBI GI	g1351279
BLAST score	416
E value	7.0e-41
Match length	122
% identity	67

NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase [Petunia x hybrida]
Seq. No.	228111
Seq. ID	LIB3189-052-P1-K1-A4
Method	BLASTX
NCBI GI	g2648032
BLAST score	637
E value	3.0e-78
Match length	162
% identity	80
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]
Seq. No.	228112
Seq. ID	LIB3189-052-P1-K1-B12
Method	BLASTX
NCBI GI	g1170567
BLAST score	655
E value	7.0e-69
Match length	146
% identity	89
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.	228113
Seq. ID	LIB3189-052-P1-K1-B5
Method	BLASTX
NCBI GI	g2811278
BLAST score	711
E value	2.0e-75
Match length	149
% identity	87
NCBI Description	(AF043284) expansin [Gossypium hirsutum]
Seq. No.	228114
Seq. ID	LIB3189-052-P1-K1-B6
Method	BLASTX
NCBI GI	g1170567
BLAST score	295
E value	5.0e-27
Match length	69
% identity	84
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.	228115
Seq. ID	LIB3189-052-P1-K1-B7
Method	BLASTX
NCBI GI	g4204300
BLAST score	430
E value	2.0e-42
Match length	138
% identity	64
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	228116
Seq. ID	LIB3189-052-P1-K1-B9
Method	BLASTX
NCBI GI	g1703375
BLAST score	460
E value	1.0e-45
Match length	97
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	228117
Seq. ID	LIB3189-052-P1-K1-C10
Method	BLASTX
NCBI GI	g1617274
BLAST score	410
E value	4.0e-40
Match length	132
% identity	62
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	228118
Seq. ID	LIB3189-052-P1-K1-C12
Method	BLASTX
NCBI GI	g3193303
BLAST score	304
E value	9.0e-28
Match length	92
% identity	61
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	228119
Seq. ID	LIB3189-052-P1-K1-C5
Method	BLASTX
NCBI GI	g3851670
BLAST score	144
E value	2.0e-13
Match length	62
% identity	65
NCBI Description	(AF099906) J8 [Arabidopsis thaliana]

Seq. No.	228120
Seq. ID	LIB3189-052-P1-K1-C6
Method	BLASTX
NCBI GI	g3928150
BLAST score	462
E value	4.0e-46
Match length	117
% identity	79
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	228121
Seq. ID	LIB3189-052-P1-K1-C8

Method	BLASTX
NCBI GI	g3377764
BLAST score	233
E value	5.0e-26
Match length	67
% identity	88
NCBI Description	(AF079851) nodule-enhanced sucrose synthase [Pisum sativum]

Seq. No.	228122
Seq. ID	LIB3189-052-P1-K1-C9
Method	BLASTX
NCBI GI	g2736147
BLAST score	312
E value	7.0e-29
Match length	70
% identity	79
NCBI Description	(AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No.	228123
Seq. ID	LIB3189-052-P1-K1-D12
Method	BLASTX
NCBI GI	g1332579
BLAST score	695
E value	2.0e-73
Match length	142
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	228124
Seq. ID	LIB3189-052-P1-K1-D2
Method	BLASTX
NCBI GI	g1091678
BLAST score	152
E value	8.0e-10
Match length	98
% identity	35
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	228125
Seq. ID	LIB3189-052-P1-K1-D3
Method	BLASTX
NCBI GI	g1170747
BLAST score	338
E value	1.0e-31
Match length	79
% identity	84
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	228126
Seq. ID	LIB3189-052-P1-K1-D5
Method	BLASTX
NCBI GI	g2286153

BLAST score 527
E value 7.0e-54
Match length 109
% identity 96
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 228127
Seq. ID LIB3189-052-P1-K1-D6
Method BLASTX
NCBI GI g2829204
BLAST score 217
E value 8.0e-24
Match length 80
% identity 81
NCBI Description (AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No. 228128
Seq. ID LIB3189-052-P1-K1-E1
Method BLASTX
NCBI GI g4574320
BLAST score 225
E value 2.0e-18
Match length 78
% identity 64
NCBI Description (AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]

Seq. No. 228129
Seq. ID LIB3189-052-P1-K1-E10
Method BLASTX
NCBI GI g1916807
BLAST score 247
E value 3.0e-21
Match length 73
% identity 73
NCBI Description (U81162) auxin-binding protein [Prunus persica]

Seq. No. 228130
Seq. ID LIB3189-052-P1-K1-E12
Method BLASTX
NCBI GI g3876865
BLAST score 164
E value 3.0e-11
Match length 113
% identity 35
NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 228131
Seq. ID LIB3189-052-P1-K1-E2
Method BLASTX
NCBI GI g626009
BLAST score 378
E value 7.0e-38

Match length	110
% identity	72
NCBI Description	capsanthin-capsorubin synthase (EC 1.-.-.-) - pepper >gi_468748_emb_CAA54495_ (X77289) capsanthin/capsorubin synthase [Capsicum annuum] >gi_522120_emb_CAA53759_ (X76165) capsanthin/capsorubin sythase [Capsicum annuum]

Seq. No.	228132
Seq. ID	LIB3189-052-P1-K1-E4
Method	BLASTX
NCBI GI	g1174592
BLAST score	620
E value	6.0e-65
Match length	116
% identity	98
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	228133
Seq. ID	LIB3189-052-P1-K1-E6
Method	BLASTX
NCBI GI	g4102861
BLAST score	394
E value	2.0e-38
Match length	79
% identity	91
NCBI Description	(AF016893) copper/zinc-superoxide dismutase [Populus tremuloides]

Seq. No.	228134
Seq. ID	LIB3189-052-P1-K1-F10
Method	BLASTX
NCBI GI	g2129473
BLAST score	288
E value	9.0e-26
Match length	135
% identity	44
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	228135
Seq. ID	LIB3189-052-P1-K1-F11
Method	BLASTX
NCBI GI	g1928981
BLAST score	446
E value	1.0e-44
Match length	101
% identity	89
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	228136
Seq. ID	LIB3189-052-P1-K1-F12
Method	BLASTX
NCBI GI	g2462748
BLAST score	187

E value 2.0e-14
Match length 45
% identity 89
NCBI Description (AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No. 228137
Seq. ID LIB3189-052-P1-K1-F4
Method BLASTX
NCBI GI g3123745
BLAST score 143
E value 9.0e-09
Match length 84
% identity 36
NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 228138
Seq. ID LIB3189-052-P1-K1-G10
Method BLASTX
NCBI GI g1545805
BLAST score 214
E value 9.0e-18
Match length 51
% identity 80
NCBI Description (D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No. 228139
Seq. ID LIB3189-052-P1-K1-G11
Method BLASTX
NCBI GI g99801
BLAST score 346
E value 1.0e-32
Match length 110
% identity 70
NCBI Description chaperonine 60K alpha chain - rape plastid (fragment)

Seq. No. 228140
Seq. ID LIB3189-052-P1-K1-G12
Method BLASTX
NCBI GI g4512664
BLAST score 530
E value 4.0e-54
Match length 136
% identity 79
NCBI Description (AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
>gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No. 228141
Seq. ID LIB3189-052-P1-K1-G2
Method BLASTX
NCBI GI g544424
BLAST score 323
E value 3.0e-30
Match length 72
% identity 81

NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	228142
Seq. ID	LIB3189-052-P1-K1-G3
Method	BLASTX
NCBI GI	g115492
BLAST score	676
E value	3.0e-71
Match length	136
% identity	57
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	228143
Seq. ID	LIB3189-052-P1-K1-G8
Method	BLASTX
NCBI GI	g2191168
BLAST score	357
E value	7.0e-34
Match length	120
% identity	57
NCBI Description	(AF007270) contains similarity to myosin heavy chain [Arabidopsis thaliana]

Seq. No.	228144
Seq. ID	LIB3189-052-P1-K1-G9
Method	BLASTX
NCBI GI	g132675
BLAST score	280
E value	5.0e-25
Match length	80
% identity	71
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi_71222_pir__R5NT14 ribosomal protein L14 - common tobacco chloroplast >gi_11864_emb_CAA77379_ (Z00044) ribosomal protein L14 [Nicotiana tabacum] >gi_225233_prf__1211235BQ ribosomal protein L14 [Nicotiana tabacum]

Seq. No.	228145
Seq. ID	LIB3189-052-P1-K1-H1
Method	BLASTX
NCBI GI	g544075
BLAST score	494
E value	6.0e-50
Match length	122
% identity	29
NCBI Description	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_486768_pir__S35312 coatomer complex chain beta' - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop [Bos taurus]

Seq. No.	228146
Seq. ID	LIB3189-052-P1-K1-H11
Method	BLASTX
NCBI GI	g2129955
BLAST score	404
E value	2.0e-39
Match length	110
% identity	67
NCBI Description	photoassimilate-responsive protein PAR-1b precursor - common tobacco >gi_871487_emb_CAA58731_ (X83851) mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Nicotiana tabacum]

Seq. No.	228147
Seq. ID	LIB3189-052-P1-K1-H2
Method	BLASTX
NCBI GI	g3413170
BLAST score	363
E value	1.0e-34
Match length	107
% identity	70
NCBI Description	(AJ010227) 40S ribosomal protein S6 [Cicer arietinum]

Seq. No.	228148
Seq. ID	LIB3189-053-P1-K1-A11
Method	BLASTX
NCBI GI	g2369714
BLAST score	381
E value	3.0e-61
Match length	132
% identity	88
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	228149
Seq. ID	LIB3189-053-P1-K1-A3
Method	BLASTX
NCBI GI	g3914431
BLAST score	555
E value	3.0e-57
Match length	123
% identity	84
NCBI Description	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha subunit [Spinacia oleracea]

Seq. No.	228150
Seq. ID	LIB3189-053-P1-K1-A7
Method	BLASTX
NCBI GI	g3334138
BLAST score	352
E value	2.0e-33
Match length	82
% identity	79
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	228151
Seq. ID	LIB3189-053-P1-K1-A8
Method	BLASTX
NCBI GI	g115492
BLAST score	494
E value	4.0e-50
Match length	96
% identity	53
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	228152
Seq. ID	LIB3189-053-P1-K1-A9
Method	BLASTX
NCBI GI	g3694872
BLAST score	507
E value	2.0e-51
Match length	120
% identity	80
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	228153
Seq. ID	LIB3189-053-P1-K1-B1
Method	BLASTX
NCBI GI	g3024126
BLAST score	539
E value	2.0e-55
Match length	124
% identity	85
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	228154
Seq. ID	LIB3189-053-P1-K1-B10
Method	BLASTX
NCBI GI	g1710585
BLAST score	352
E value	2.0e-33
Match length	81
% identity	85
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1143507_emb_CAA63786_ (X93587) P0 ribosomal protein [Lupinus luteus]

Seq. No.	228155
Seq. ID	LIB3189-053-P1-K1-B12
Method	BLASTX
NCBI GI	g441457
BLAST score	530
E value	3.0e-54
Match length	99
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	228156

Seq. ID	LIB3189-053-P1-K1-B2
Method	BLASTX
NCBI GI	g1752734
BLAST score	475
E value	7.0e-48
Match length	104
% identity	75
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	228157
Seq. ID	LIB3189-053-P1-K1-B3
Method	BLASTX
NCBI GI	g2493133
BLAST score	250
E value	2.0e-21
Match length	101
% identity	49
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) >gi_2183244 (AF002134) Vma8p [Candida albicans]

Seq. No.	228158
Seq. ID	LIB3189-053-P1-K1-B4
Method	BLASTX
NCBI GI	g1084321
BLAST score	475
E value	7.0e-48
Match length	118
% identity	78
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) - cucumber >gi_2244614_dbj_BAA21089_ (D50085) NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]

Seq. No.	228159
Seq. ID	LIB3189-053-P1-K1-B5
Method	BLASTX
NCBI GI	g3643611
BLAST score	353
E value	1.0e-33
Match length	96
% identity	65
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	228160
Seq. ID	LIB3189-053-P1-K1-B8
Method	BLASTX
NCBI GI	g232024
BLAST score	773
E value	1.0e-82
Match length	148
% identity	97
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	228161

Seq. ID	LIB3189-053-P1-K1-B9
Method	BLASTX
NCBI GI	g2088651
BLAST score	206
E value	2.0e-16
Match length	112
% identity	38
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	228162
Seq. ID	LIB3189-053-P1-K1-C1
Method	BLASTX
NCBI GI	g1076809
BLAST score	554
E value	5.0e-57
Match length	150
% identity	76
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays]

Seq. No.	228163
Seq. ID	LIB3189-053-P1-K1-C11
Method	BLASTX
NCBI GI	g2982303
BLAST score	346
E value	1.0e-32
Match length	85
% identity	79
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	228164
Seq. ID	LIB3189-053-P1-K1-C2
Method	BLASTX
NCBI GI	g2459445
BLAST score	195
E value	7.0e-15
Match length	52
% identity	36
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	228165
Seq. ID	LIB3189-053-P1-K1-C6
Method	BLASTX
NCBI GI	g70644
BLAST score	589
E value	4.0e-61
Match length	119
% identity	19
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	228166
Seq. ID	LIB3189-053-P1-K1-C7
Method	BLASTX
NCBI GI	g586797

BLAST score	229
E value	6.0e-19
Match length	101
% identity	43
NCBI Description	HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III

Seq. No.	228167
Seq. ID	LIB3189-053-P1-K1-D1
Method	BLASTX
NCBI GI	g2792297
BLAST score	261
E value	1.0e-22
Match length	77
% identity	58
NCBI Description	(AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No.	228168
Seq. ID	LIB3189-053-P1-K1-D10
Method	BLASTX
NCBI GI	g1170711
BLAST score	111
E value	8.0e-09
Match length	89
% identity	45
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-ALPHA >gi_541901_pir__S41596 protein kinase ASK-alpha (EC 2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_ (X75432) shaggy related kinase [Arabidopsis thaliana] >gi_1769889_emb_CAA48538_ (X68525) serine /threonine protein kinase [Arabidopsis thaliana]

Seq. No.	228169
Seq. ID	LIB3189-053-P1-K1-D12
Method	BLASTX
NCBI GI	g3334115
BLAST score	446
E value	2.0e-44
Match length	108
% identity	84
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	228170
Seq. ID	LIB3189-053-P1-K1-D5
Method	BLASTX
NCBI GI	g2648032
BLAST score	164
E value	2.0e-11
Match length	36
% identity	81
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	228171
Seq. ID	LIB3189-053-P1-K1-D6
Method	BLASTX

NCBI GI g3913633
BLAST score 306
E value 4.0e-28
Match length 96
% identity 66
NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No. 228172
Seq. ID LIB3189-053-P1-K1-D9
Method BLASTX
NCBI GI g3885343
BLAST score 176
E value 8.0e-13
Match length 64
% identity 45
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No. 228173
Seq. ID LIB3189-053-P1-K1-E1
Method BLASTX
NCBI GI g967125
BLAST score 689
E value 7.0e-73
Match length 136
% identity 93
NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No. 228174
Seq. ID LIB3189-053-P1-K1-E10
Method BLASTX
NCBI GI g1498330
BLAST score 678
E value 1.0e-71
Match length 143
% identity 94
NCBI Description (U60498) actin [Glycine max]

Seq. No. 228175
Seq. ID LIB3189-053-P1-K1-E11
Method BLASTX
NCBI GI g464981
BLAST score 553
E value 6.0e-57
Match length 111
% identity 92
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 228176
Seq. ID LIB3189-053-P1-K1-E12
Method BLASTX
NCBI GI g267082
BLAST score 676
E value 2.0e-71
Match length 126

% identity	98
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	228177
Seq. ID	LIB3189-053-P1-K1-E2
Method	BLASTX
NCBI GI	g3204106
BLAST score	503
E value	5.0e-51
Match length	155
% identity	64
NCBI Description	(AJ006763) putative beta-amilase [Cicer arietinum]

Seq. No.	228178
Seq. ID	LIB3189-053-P1-K1-E3
Method	BLASTX
NCBI GI	g2708747
BLAST score	268
E value	1.0e-23
Match length	114
% identity	47
NCBI Description	(AC003952) putative glycine-rich, zinc-finger DNA-binding protein [Arabidopsis thaliana]

Seq. No.	228179
Seq. ID	LIB3189-053-P1-K1-E5
Method	BLASTX
NCBI GI	g2829204
BLAST score	189
E value	1.0e-14
Match length	35
% identity	100
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	228180
Seq. ID	LIB3189-053-P1-K1-E9
Method	BLASTX
NCBI GI	g4455209
BLAST score	335
E value	2.0e-31
Match length	91
% identity	74
NCBI Description	(AL035440) putative Proline synthetase associated protein [Arabidopsis thaliana]

Seq. No.	228181
Seq. ID	LIB3189-053-P1-K1-F2
Method	BLASTX
NCBI GI	g1076510
BLAST score	654
E value	1.0e-68
Match length	140
% identity	86
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean

>gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No.	228182
Seq. ID	LIB3189-053-P1-K1-F3
Method	BLASTX
NCBI GI	g3776084
BLAST score	190
E value	2.0e-14
Match length	60
% identity	58
NCBI Description	(Y18251) NtN2 [Medicago truncatula]

Seq. No.	228183
Seq. ID	LIB3189-053-P1-K1-F5
Method	BLASTX
NCBI GI	g4432866
BLAST score	258
E value	2.0e-22
Match length	101
% identity	45
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	228184
Seq. ID	LIB3189-053-P1-K1-F7
Method	BLASTX
NCBI GI	g267069
BLAST score	301
E value	9.0e-28
Match length	54
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	228185
Seq. ID	LIB3189-053-P1-K1-G1
Method	BLASTX
NCBI GI	g2829204
BLAST score	520
E value	5.0e-53
Match length	120
% identity	88
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	228186
Seq. ID	LIB3189-053-P1-K1-G2
Method	BLASTX
NCBI GI	g3152576
BLAST score	291
E value	2.0e-26
Match length	83
% identity	71
NCBI Description	(AC002986) Similar to liver-specific transport protein

gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	228187
Seq. ID	LIB3189-053-P1-K1-G3
Method	BLASTX
NCBI GI	g2829927
BLAST score	262
E value	8.0e-23
Match length	134
% identity	45
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	228188
Seq. ID	LIB3189-053-P1-K1-G5
Method	BLASTX
NCBI GI	g3687243
BLAST score	245
E value	6.0e-21
Match length	61
% identity	79
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	228189
Seq. ID	LIB3189-053-P1-K1-H5
Method	BLASTX
NCBI GI	g2924777
BLAST score	237
E value	3.0e-20
Match length	86
% identity	3
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	228190
Seq. ID	LIB3189-053-P1-K1-H6
Method	BLASTX
NCBI GI	g1703478
BLAST score	409
E value	3.0e-40
Match length	99
% identity	78
NCBI Description	(U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana]

Seq. No.	228191
Seq. ID	LIB3189-053-P1-K1-H7
Method	BLASTX
NCBI GI	g1841462
BLAST score	312
E value	4.0e-29
Match length	77
% identity	79
NCBI Description	(Y10991) Elongation factor 2 [Nicotiana tabacum]

Seq. No.	228192
Seq. ID	LIB3189-053-P1-K1-H9

Method	BLASTX
NCBI GI	g3915847
BLAST score	192
E value	8.0e-15
Match length	52
% identity	75
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	228193
Seq. ID	LIB3196-001-P1-M1-A1
Method	BLASTX
NCBI GI	g1848277
BLAST score	479
E value	2.0e-48
Match length	99
% identity	97
NCBI Description	(U86136) telomerase-associated protein TP-1 [Homo sapiens]

Seq. No.	228194
Seq. ID	LIB3196-001-P1-M1-A9
Method	BLASTX
NCBI GI	g632962
BLAST score	312
E value	1.0e-28
Match length	101
% identity	60
NCBI Description	(L29222) clk1-136; putative [Homo sapiens]

Seq. No.	228195
Seq. ID	LIB3196-001-P1-M1-B11
Method	BLASTX
NCBI GI	g2493416
BLAST score	170
E value	5.0e-12
Match length	88
% identity	38
NCBI Description	S100 CALCIUM-BINDING PROTEIN A13 >gi_2134853_pir__JC5064 calcium-binding protein S100 A13 - human >gi_1694828_emb_CAA68188_ (X99920) S100 calcium-binding protein A13 (S100A13) [Homo sapiens]

Seq. No.	228196
Seq. ID	LIB3196-001-P1-M1-B12
Method	BLASTX
NCBI GI	g685073
BLAST score	461
E value	4.0e-46
Match length	108
% identity	78
NCBI Description	SPRC=small proline-rich protein [human, odontogenic keratocysts, Peptide Partial, 161 aa]

Seq. No.	228197
Seq. ID	LIB3196-001-P1-M1-B2
Method	BLASTX
NCBI GI	g1351173

BLAST score	664
E value	6.0e-70
Match length	134
% identity	98
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_1050527_emb_CAA62635_ (X91257) seryl-tRNA synthetase [Homo sapiens]

Seq. No.	228198
Seq. ID	LIB3196-001-P1-M1-B3
Method	BLASTX
NCBI GI	g3283994
BLAST score	143
E value	5.0e-09
Match length	48
% identity	60
NCBI Description	(AF073293) M962 protein spliced isoform 2 [Homo sapiens]

Seq. No.	228199
Seq. ID	LIB3196-001-P1-M1-B4
Method	BLASTX
NCBI GI	g113944
BLAST score	572
E value	4.0e-59
Match length	120
% identity	60
NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi_71756_pir__LUHU annexin I - human >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I (lipocortin I)

Seq. No.	228200
Seq. ID	LIB3196-001-P1-M1-B6
Method	BLASTX
NCBI GI	g602467
BLAST score	554
E value	3.0e-57
Match length	103
% identity	60
NCBI Description	(M27445) nidogen [Homo sapiens]

Seq. No.	228201
Seq. ID	LIB3196-001-P1-M1-B7
Method	BLASTX
NCBI GI	g417570
BLAST score	565
E value	2.0e-58
Match length	133
% identity	85
NCBI Description	DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE OXIDASE) (DHODEHASE) >gi_478676_pir__S23762 dihydroorotate oxidase (EC 1.3.3.1) - Arabidopsis thaliana >gi_16449_emb_CAA44695_ (X62909) dihydroorotate dehydrogenase [Arabidopsis thaliana]

Seq. No.	228202
Seq. ID	LIB3196-001-P1-M1-B8
Method	BLASTX
NCBI GI	g88044
BLAST score	661
E value	1.0e-69
Match length	138
% identity	96
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	228203
Seq. ID	LIB3196-001-P1-M1-B9
Method	BLASTX
NCBI GI	g50823
BLAST score	637
E value	8.0e-67
Match length	125
% identity	100
NCBI Description	(X12507) initiation factor 4AII (AA 1 - 407) [Mus musculus]

Seq. No.	228204
Seq. ID	LIB3196-001-P1-M1-C1
Method	BLASTX
NCBI GI	g2501432
BLAST score	544
E value	6.0e-56
Match length	107
% identity	96
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir__JC4894 ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating enzyme E2 UbcH-ben [Homo sapiens] >gi_4507793_ref_NP_003339.1_pUBE2N_ ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)

Seq. No.	228205
Seq. ID	LIB3196-001-P1-M1-C10
Method	BLASTX
NCBI GI	g266690
BLAST score	306
E value	4.0e-28
Match length	95
% identity	67
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	228206
Seq. ID	LIB3196-001-P1-M1-C12
Method	BLASTX
NCBI GI	g121116
BLAST score	367
E value	3.0e-35

Match length	126
% identity	51
NCBI Description	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi_71649_pir__FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf__1211330A gelsolin [Homo sapiens] >gi_4504165_ref_NP_000168.1_pGSN_ gelsolin (amyloidosis, Finnish type)

Seq. No.	228207
Seq. ID	LIB3196-001-P1-M1-C2
Method	BLASTX
NCBI GI	g121009
BLAST score	658
E value	3.0e-69
Match length	126
% identity	38
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2 (TRANSDUCIN BETA CHAIN 2) >gi_71872_pir__RGBOB2 GTP-binding regulatory protein beta-2 chain - bovine (fragment) >gi_163113 (M16480) guanine nucleotide-binding regulatory protein-beta-2 subunit [Bos taurus] >gi_163785 (M36431) transducin beta-2 subunit [Bos taurus]

Seq. No.	228208
Seq. ID	LIB3196-001-P1-M1-C6
Method	BLASTX
NCBI GI	g120649
BLAST score	450
E value	5.0e-45
Match length	102
% identity	89
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_182863 (J02642) glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_224880_prf__1203217A dehydrogenase,glyceraldehydephosphate [Homo sapiens]

Seq. No.	228209
Seq. ID	LIB3196-001-P1-M1-D12
Method	BLASTX
NCBI GI	g4204275
BLAST score	329
E value	1.0e-30
Match length	132
% identity	50
NCBI Description	(AC004146) Unknown protein [Arabidopsis thaliana]

Seq. No.	228210
Seq. ID	LIB3196-001-P1-M1-D2
Method	BLASTX

NCBI GI	g2738949
BLAST score	440
E value	9.0e-44
Match length	94
% identity	87
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	228211
Seq. ID	LIB3196-001-P1-M1-D6
Method	BLASTX
NCBI GI	g3879734
BLAST score	175
E value	3.0e-13
Match length	46
% identity	70
NCBI Description	(Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727

Seq. No.	228212
Seq. ID	LIB3196-001-P1-M1-D7
Method	BLASTX
NCBI GI	g4539660
BLAST score	461
E value	3.0e-46
Match length	132
% identity	66
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	228213
Seq. ID	LIB3196-001-P1-M1-E1
Method	BLASTX
NCBI GI	g539636
BLAST score	420
E value	2.0e-41
Match length	108
% identity	76
NCBI Description	membrane glycoprotein CLA-1 protein long form precursor - human >gi_397607_emb_CAA80277_ (Z22555) CLA-1 [Homo sapiens]

Seq. No.	228214
Seq. ID	LIB3196-001-P1-M1-E11
Method	BLASTX
NCBI GI	g1706566
BLAST score	694
E value	2.0e-73
Match length	140
% identity	98
NCBI Description	MITOCHONDRIAL TRIFUNCTONAL ENZYME BETA SUBUNIT PRECURSOR (TP-BETA) [CONTAINS: 3-KETOACYL-COA THIOLASE (ACETYL-COA ACYLTRANSFERASE) (BETA-KETOTHIOLASE)] >gi_543065_pir__JC2109 long-chain-fatty-acid beta-oxidation multienzyme complex beta chain precursor, mitochondrial - human >gi_862458_dbj_BAA03942_ (D16481) 3-ketoacyl-CoA

	thiolase beta-subunit of trifunctional protein [Homo sapiens] >gi_4504327_ref_NP_000174.1_pHADHB_ hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
Seq. No.	228215
Seq. ID	LIB3196-001-P1-M1-E7
Method	BLASTX
NCBI GI	g3462807
BLAST score	472
E value	2.0e-47
Match length	113
% identity	81
NCBI Description	(AF082516) I-1 receptor candidate protein [Homo sapiens]
Seq. No.	228216
Seq. ID	LIB3196-001-P1-M1-E8
Method	BLASTX
NCBI GI	g2605714
BLAST score	231
E value	3.0e-19
Match length	60
% identity	80
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]
Seq. No.	228217
Seq. ID	LIB3196-001-P1-M1-F1
Method	BLASTX
NCBI GI	g135422
BLAST score	615
E value	3.0e-64
Match length	120
% identity	95
NCBI Description	TUBULIN ALPHA-4 CHAIN >gi_88945_pir__A25873 tubulin alpha chain (version 2) - human >gi_2119265_pir__I77427 alpha-tubulin isotype M-alpha-6 - mouse >gi_202215 (M13444) alpha-tubulin isotype M-alpha-6 [Mus musculus]
Seq. No.	228218
Seq. ID	LIB3196-001-P1-M1-F10
Method	BLASTX
NCBI GI	g133867
BLAST score	481
E value	2.0e-48
Match length	112
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]
Seq. No.	228219
Seq. ID	LIB3196-001-P1-M1-F7
Method	BLASTX
NCBI GI	g1929449
BLAST score	163

E value	9.0e-12
Match length	44
% identity	70
NCBI Description	(L63543) endodermin [Xenopus laevis]

Seq. No.	228220
Seq. ID	LIB3196-001-P1-M1-F9
Method	BLASTX
NCBI GI	g547753
BLAST score	184
E value	4.0e-15
Match length	78
% identity	63
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	228221
Seq. ID	LIB3196-001-P1-M1-G1
Method	BLASTX
NCBI GI	g3024812
BLAST score	238
E value	2.0e-20
Match length	60
% identity	78
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_2599050 (AF027705) vacuolar ATPase 16kDa subunit c [Ovis aries]

Seq. No.	228222
Seq. ID	LIB3196-001-P1-M1-G12
Method	BLASTX
NCBI GI	g435480
BLAST score	249
E value	1.0e-21
Match length	71
% identity	70
NCBI Description	(X76679) MAL-b [Homo sapiens]

Seq. No.	228223
Seq. ID	LIB3196-001-P1-M1-G8
Method	BLASTX
NCBI GI	g3152603
BLAST score	364
E value	8.0e-35
Match length	104
% identity	59
NCBI Description	(AC004482) unknown protein [Arabidopsis thaliana]

Seq. No.	228224
Seq. ID	LIB3196-001-P1-M1-H1
Method	BLASTX
NCBI GI	g1346348
BLAST score	153
E value	4.0e-10
Match length	101
% identity	38
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E) (K6E KERATIN) >gi_2119223_pir__I61770 keratin type II - human >gi_908803 (L42611) keratin type II [Homo sapiens]

Seq. No.	228225
Seq. ID	LIB3196-001-P1-M1-H10
Method	BLASTX
NCBI GI	g120649
BLAST score	597
E value	4.0e-62
Match length	118
% identity	97
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_182863 (J02642) glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_224880_prf__1203217A dehydrogenase,glyceraldehydephosphate [Homo sapiens]

Seq. No.	228226
Seq. ID	LIB3196-001-P1-M1-H4
Method	BLASTX
NCBI GI	g3122072
BLAST score	645
E value	1.0e-67
Match length	125
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]

Seq. No.	228227
Seq. ID	LIB3196-001-P1-M1-H8
Method	BLASTX
NCBI GI	g3811347
BLAST score	168
E value	8.0e-12
Match length	78
% identity	47
NCBI Description	(AF065215) cytosolic phospholipase A2 beta [Homo sapiens]

Seq. No.	228228
Seq. ID	LIB3196-001-P1-M1-H9
Method	BLASTX
NCBI GI	g4559312
BLAST score	360
E value	9.0e-35
Match length	80
% identity	89
NCBI Description	(AF134149) 2-pore K+ channel subunit TOSS [Homo sapiens] >gi_4574322_gb_AAD24000.1_AF117708_1 (AF117708) tandem pore domain potassium channel TWIK-2 [Homo sapiens]

Seq. No.	228229

Seq. ID	LIB3196-002-P1-M1-A12
Method	BLASTX
NCBI GI	g121116
BLAST score	277
E value	5.0e-25
Match length	77
% identity	74
NCBI Description	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi_71649_pir__FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf__1211330A gelsolin [Homo sapiens] >gi_4504165_ref_NP_000168.1_pGSN_ gelsolin (amyloidosis, Finnish type)

Seq. No.	228230
Seq. ID	LIB3196-002-P1-M1-A4
Method	BLASTX
NCBI GI	g114312
BLAST score	422
E value	1.0e-41
Match length	83
% identity	95
NCBI Description	CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE, CLASS 2 ISOFORM (ENDOPLASMIC RETICULUM CLASS 2 CA(2+) ATPASE) (CALCIUM PUMP) (SERCA2) (HK1) >gi_86991_pir__A31981 Ca2+-transporting ATPase (EC 3.6.1.38) 1, renal - human >gi_306850 (M23114) HK1 [Homo sapiens]

Seq. No.	228231
Seq. ID	LIB3196-002-P1-M1-A7
Method	BLASTX
NCBI GI	g3914685
BLAST score	526
E value	8.0e-54
Match length	117
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No.	228232
Seq. ID	LIB3196-002-P1-M1-B2
Method	BLASTX
NCBI GI	g3482913
BLAST score	235
E value	9.0e-23
Match length	87
% identity	67
NCBI Description	(AC003970) Similar to MtN21, gi_2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No.	228233
Seq. ID	LIB3196-002-P1-M1-B4
Method	BLASTX
NCBI GI	g1854386
BLAST score	521
E value	3.0e-53
Match length	132

% identity	73
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	228234
Seq. ID	LIB3196-002-P1-M1-B7
Method	BLASTX
NCBI GI	g3335226
BLAST score	405
E value	1.0e-39
Match length	87
% identity	25
NCBI Description	(AF077374) small proline-rich protein [Homo sapiens]

Seq. No.	228235
Seq. ID	LIB3196-002-P1-M1-B8
Method	BLASTX
NCBI GI	g3293537
BLAST score	471
E value	2.0e-47
Match length	93
% identity	97
NCBI Description	(AF071059) zinc finger RNA binding protein [Mus musculus]

Seq. No.	228236
Seq. ID	LIB3196-002-P1-M1-B9
Method	BLASTX
NCBI GI	g4240147
BLAST score	293
E value	2.0e-26
Match length	66
% identity	94
NCBI Description	(AB020636) KIAA0829 protein [Homo sapiens]

Seq. No.	228237
Seq. ID	LIB3196-002-P1-M1-C12
Method	BLASTX
NCBI GI	g113289
BLAST score	233
E value	3.0e-19
Match length	117
% identity	53
NCBI Description	ACTIN >gi_100988_pir__S24408 actin - Achlya bisexualis >gi_2290_emb_CAA42559_ (X59936) actin [Achlya bisexualis]

Seq. No.	228238
Seq. ID	LIB3196-002-P1-M1-C4
Method	BLASTX
NCBI GI	g432359
BLAST score	560
E value	2.0e-60
Match length	124
% identity	95
NCBI Description	(D23660) ribosomal protein [Homo sapiens]

Seq. No.	228239
Seq. ID	LIB3196-002-P1-M1-C9

Method	BLASTX
NCBI GI	g405194
BLAST score	442
E value	6.0e-44
Match length	117
% identity	78
NCBI Description	(L10911) splicing factor [Homo sapiens]

Seq. No.	228240
Seq. ID	LIB3196-002-P1-M1-D12
Method	BLASTX
NCBI GI	g113944
BLAST score	663
E value	8.0e-70
Match length	137
% identity	56
NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi_71756_pir__LUHU annexin I - human >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I (lipocortin I)

Seq. No.	228241
Seq. ID	LIB3196-002-P1-M1-D6
Method	BLASTX
NCBI GI	g4539330
BLAST score	418
E value	3.0e-41
Match length	115
% identity	70
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	228242
Seq. ID	LIB3196-002-P1-M1-D7
Method	BLASTX
NCBI GI	g671865
BLAST score	252
E value	8.0e-22
Match length	109
% identity	40
NCBI Description	(X78801) ovomacroglobulin, ovostatin [Gallus gallus]

Seq. No.	228243
Seq. ID	LIB3196-002-P1-M1-D8
Method	BLASTX
NCBI GI	g2496887
BLAST score	264
E value	4.0e-23
Match length	114
% identity	52
NCBI Description	HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III >gi_732538 (U22832) C09F5.2 gene product [Caenorhabditis elegans]

Seq. No.	228244
Seq. ID	LIB3196-002-P1-M1-D9
Method	BLASTX
NCBI GI	g2522261
BLAST score	248
E value	2.0e-21
Match length	52
% identity	92
NCBI Description	(D88492) CPE-receptor [Chlorocebus aethiops]

Seq. No.	228245
Seq. ID	LIB3196-002-P1-M1-E10
Method	BLASTX
NCBI GI	g2224565
BLAST score	529
E value	3.0e-54
Match length	120
% identity	85
NCBI Description	(AB002310) KIAA0312 [Homo sapiens]

Seq. No.	228246
Seq. ID	LIB3196-002-P1-M1-E2
Method	BLASTX
NCBI GI	g1001708
BLAST score	214
E value	3.0e-17
Match length	80
% identity	57
NCBI Description	(D64004) NifS [Synechocystis sp.]

Seq. No.	228247
Seq. ID	LIB3196-002-P1-M1-E8
Method	BLASTX
NCBI GI	g1293563
BLAST score	347
E value	3.0e-33
Match length	82
% identity	83
NCBI Description	(U49188) Diff33 gene product [Homo sapiens]

Seq. No.	228248
Seq. ID	LIB3196-002-P1-M1-F1
Method	BLASTX
NCBI GI	g1351222
BLAST score	596
E value	5.0e-62
Match length	125
% identity	93
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945087 (U31097) transcription factor TFIIB [Glycine max]

Seq. No.	228249
Seq. ID	LIB3196-002-P1-M1-F10
Method	BLASTX
NCBI GI	g2118384
BLAST score	610
E value	1.0e-63

Match length	133
% identity	90
NCBI Description	squamous cell carcinoma antigen 2 - human

Seq. No.	228250
Seq. ID	LIB3196-002-P1-M1-F12
Method	BLASTX
NCBI GI	g294668
BLAST score	321
E value	9.0e-30
Match length	120
% identity	63
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	228251
Seq. ID	LIB3196-002-P1-M1-F4
Method	BLASTX
NCBI GI	g1363944
BLAST score	320
E value	1.0e-29
Match length	70
% identity	93
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	228252
Seq. ID	LIB3196-002-P1-M1-F5
Method	BLASTX
NCBI GI	g3914935
BLAST score	203
E value	3.0e-16
Match length	63
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_3204099_emb_CAA07226_ (AJ006759) ribosome-associated protein p40 [Cicer arietinum]

Seq. No.	228253
Seq. ID	LIB3196-002-P1-M1-F7
Method	BLASTX
NCBI GI	g3108187
BLAST score	277
E value	4.0e-25
Match length	55
% identity	96
NCBI Description	(AC004663) Notch 3 [Homo sapiens]

Seq. No.	228254
Seq. ID	LIB3196-002-P1-M1-F8
Method	BLASTX
NCBI GI	g4185792
BLAST score	392
E value	4.0e-38
Match length	77
% identity	97
NCBI Description	(AF095890) transcription factor E1AF [Homo sapiens]

Seq. No.	228255
Seq. ID	LIB3196-002-P1-M1-F9
Method	BLASTX
NCBI GI	g113950
BLAST score	494
E value	5.0e-50
Match length	116
% identity	52
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II - human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo sapiens]

Seq. No.	228256
Seq. ID	LIB3196-002-P1-M1-G1
Method	BLASTX
NCBI GI	g280816
BLAST score	152
E value	2.0e-10
Match length	60
% identity	60
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin

Seq. No.	228257
Seq. ID	LIB3196-002-P1-M1-G10
Method	BLASTX
NCBI GI	g2137308
BLAST score	276
E value	1.0e-24
Match length	73
% identity	77
NCBI Description	G protein beta subuit like - mouse >gi_475012_dbj_BAA06185_ (D29802) G protein beta subuit like [Mus musculus]

Seq. No.	228258
Seq. ID	LIB3196-002-P1-M1-G4
Method	BLASTX
NCBI GI	g548710
BLAST score	351
E value	2.0e-33
Match length	114
% identity	40
NCBI Description	RETICULOCALBIN 1 PRECURSOR >gi_346940_pir__A45337 reticulocalbin - mouse >gi_220582_dbj_BAA02366_ (D13003) reticulocalbin [Mus musculus] >gi_968894_dbj_BAA07896_ (D43956) reticulocalbin [Mus musculus] >gi_1581021_prf__2116329A reticulocalbin [Mus musculus]

Seq. No.	228259
Seq. ID	LIB3196-002-P1-M1-G7
Method	BLASTX
NCBI GI	g2500527

BLAST score	610
E value	1.0e-63
Match length	116
% identity	99
NCBI Description	PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX PROTEIN P68) (DEAD BOX PROTEIN 5) >gi_2137742_pir__I48385 RNA helicase TNZ2 - mouse >gi_51263_emb_CAA46581_ (X65627) p68 RNA helicase [Mus musculus]

Seq. No.	228260
Seq. ID	LIB3196-002-P1-M1-G8
Method	BLASTX
NCBI GI	g3777596
BLAST score	223
E value	6.0e-26
Match length	112
% identity	51
NCBI Description	(AF095791) TACC2 protein [Homo sapiens]

Seq. No.	228261
Seq. ID	LIB3196-002-P1-M1-H10
Method	BLASTX
NCBI GI	g1170636
BLAST score	136
E value	5.0e-19
Match length	77
% identity	70
NCBI Description	DIACYLGLYCEROL KINASE, ALPHA (DIGLYCERIDE KINASE) (DGK-ALPHA) (DAG KINASE ALPHA) (80 KD DIACYLGLYCEROL KINASE) >gi_105839_pir__S12969 diacylglycerol kinase (EC 2.7.1.107) alpha - human >gi_30823_emb_CAA44396_ (X62535) diacylglycerol kinase [Homo sapiens] >gi_227338_prf__1702222A diacylglycerol kinase [Homo sapiens]

Seq. No.	228262
Seq. ID	LIB3196-002-P1-M1-H11
Method	BLASTX
NCBI GI	g132573
BLAST score	363
E value	1.0e-34
Match length	80
% identity	14
NCBI Description	PLACENTAL RIBONUCLEASE INHIBITOR (RIBONUCLEASE/ANGIOGENIN INHIBITOR) (RAI) (RI) >gi_88562_pir__A31858 ribonuclease-angiogenin inhibitor - human >gi_307040 (M22414) ribonuclease inhibitor precursor [Homo sapiens] >gi_226786_prf__1605207A RNase inhibitor [Homo sapiens]

Seq. No.	228263
Seq. ID	LIB3196-002-P1-M1-H12
Method	BLASTX
NCBI GI	g1082318
BLAST score	516
E value	1.0e-52
Match length	102
% identity	91

NCBI Description	cystathionine beta-synthase (EC 4.2.1.22) - human

Seq. No.	228264
Seq. ID	LIB3196-002-P1-M1-H3
Method	BLASTX
NCBI GI	g1754538
BLAST score	470
E value	3.0e-47
Match length	96
% identity	94
NCBI Description	(U66894) ESX [Homo sapiens] >gi_1841523 (U73843) ESE-1b [Homo sapiens] >gi_2338756 (AF017307) Ets-related transcription factor [Homo sapiens] >gi_2384740 (AF016295) Ets transcription factor [Homo sapiens] >gi_2459797 (U97156) epthelial-specific ets protein [Homo sapiens]

Seq. No.	228265
Seq. ID	LIB3196-002-P1-M1-H5
Method	BLASTX
NCBI GI	g337999
BLAST score	596
E value	1.0e-66
Match length	134
% identity	93
NCBI Description	(M63573) secreted cyclophilin-like protein [Homo sapiens]

Seq. No.	228266
Seq. ID	LIB3196-002-P1-M1-H7
Method	BLASTX
NCBI GI	g1617312
BLAST score	365
E value	7.0e-35
Match length	126
% identity	57
NCBI Description	(X92689) UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferas [Homo sapiens]

Seq. No.	228267
Seq. ID	LIB3196-002-P1-M1-H8
Method	BLASTX
NCBI GI	g399012
BLAST score	299
E value	3.0e-27
Match length	100
% identity	65
NCBI Description	ADP,ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) >gi_280900_pir__B43646 ADP,ATP carrier protein T2 - bovine >gi_529417 (M24103) translocase [Bos taurus]

Seq. No.	228268
Seq. ID	LIB3196-002-P1-M1-H9
Method	BLASTX
NCBI GI	g477138
BLAST score	526
E value	6.0e-54
Match length	108

% identity	90
NCBI Description	carcinoma-associated antigen GA733-1 precursor - human >gi_31591_emb_CAA31781_ (X13425) GA733-1 protein (AA 1-323) [Homo sapiens]
Seq. No.	228269
Seq. ID	LIB3196-003-P1-M1-A1
Method	BLASTX
NCBI GI	g130224
BLAST score	441
E value	6.0e-44
Match length	115
% identity	74
NCBI Description	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148) >gi_89333_pir__S00666 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) isozyme II - bovine >gi_639_emb_CAA68406_ (Y00301) phosphatidylinositol-specific phospholipase C. [Bos taurus] >gi_225974_prf__1404383A phospholipase C [Bos taurus]
Seq. No.	228270
Seq. ID	LIB3196-003-P1-M1-A2
Method	BLASTX
NCBI GI	g2244974
BLAST score	147
E value	2.0e-09
Match length	90
% identity	44
NCBI Description	(Z97340) similarity to pore protein Pisum sativum [Arabidopsis thaliana]
Seq. No.	228271
Seq. ID	LIB3196-003-P1-M1-A4
Method	BLASTX
NCBI GI	g226728
BLAST score	298
E value	4.0e-27
Match length	102
% identity	67
NCBI Description	transcription factor ATF3 [Homo sapiens]
Seq. No.	228272
Seq. ID	LIB3196-003-P1-M1-A6
Method	BLASTX
NCBI GI	g539663
BLAST score	450
E value	6.0e-45
Match length	98
% identity	88
NCBI Description	PR264/SC35 protein - human >gi_35597_emb_CAA44307_ (X62447) PR 264 [Homo sapiens] >gi_455419_emb_CAA53383_ (X75755) PR264/SC35 [Homo sapiens] >gi_3335676 (AF077858) splicing factor SC35 [Mus musculus] >gi_228504_prf__1805195B RNA-binding protein PR264 [Homo sapiens]

Seq. No.	228273
Seq. ID	LIB3196-003-P1-M1-A7
Method	BLASTX
NCBI GI	g3329390
BLAST score	605
E value	4.0e-63
Match length	117
% identity	98
NCBI Description	(AF038960) SKD1 homolog [Homo sapiens]

Seq. No.	228274
Seq. ID	LIB3196-003-P1-M1-B1
Method	BLASTX
NCBI GI	g119540
BLAST score	662
E value	9.0e-70
Match length	128
% identity	100
NCBI Description	DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2) >gi_105956_pir__S10888 ERCC2 protein - human

Seq. No.	228275
Seq. ID	LIB3196-003-P1-M1-B12
Method	BLASTX
NCBI GI	g2605714
BLAST score	351
E value	2.0e-33
Match length	89
% identity	79
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	228276
Seq. ID	LIB3196-003-P1-M1-B2
Method	BLASTX
NCBI GI	g125077
BLAST score	639
E value	4.0e-67
Match length	129
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	228277
Seq. ID	LIB3196-003-P1-M1-B4
Method	BLASTX
NCBI GI	g1730836
BLAST score	208
E value	1.0e-16
Match length	120
% identity	43
NCBI Description	HYPOTHETICAL 54.2 KD PROTEIN IN ZWF1-BLH1/LAP3 INTERGENIC REGION >gi_2131939_pir__S63206 hypothetical protein YNL240c

	- yeast (Saccharomyces cerevisiae) >gi_1183974_emb_CAA93358_ (Z69381) N1114 [Saccharomyces cerevisiae] >gi_1302274_emb_CAA96145_ (Z71516) ORF YNL240c [Saccharomyces cerevisiae]
Seq. No.	228278
Seq. ID	LIB3196-003-P1-M1-B8
Method	BLASTX
NCBI GI	g127148
BLAST score	561
E value	6.0e-58
Match length	108
% identity	99
NCBI Description	MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM (MLC3SM) (LC17B) (LC17-GI) >gi_108819_pir__S13671 myosin catalytic light chain A - bovine >gi_1360691_pir__MOHU6N myosin alkali light chain 6, nonmuscle form - human >gi_578_emb_CAA38721_ (X54977) 17,000 dalton myosin light chain [Bos taurus] >gi_189018 (M22919) non-muscle myosin light chain [Homo sapiens]
Seq. No.	228279
Seq. ID	LIB3196-003-P1-M1-B9
Method	BLASTX
NCBI GI	g3024101
BLAST score	353
E value	1.0e-33
Match length	87
% identity	76
NCBI Description	CHLORIDE CONDUCTANCE INDUCER PROTEIN MAT-8 PRECURSOR >gi_1082298_pir__A55571 chloride conductance inducer Mat-8 - human >gi_1085026_emb_CAA63604_ (X93036) MAT8 protein [Homo sapiens]
Seq. No.	228280
Seq. ID	LIB3196-003-P1-M1-C1
Method	BLASTX
NCBI GI	g1905874
BLAST score	546
E value	4.0e-56
Match length	111
% identity	95
NCBI Description	(U90878) carboxyl terminal LIM domain protein [Homo sapiens]
Seq. No.	228281
Seq. ID	LIB3196-003-P1-M1-C2
Method	BLASTX
NCBI GI	g207905
BLAST score	541
E value	1.0e-55
Match length	122
% identity	89
NCBI Description	(M18027) alpha globulin B [Artificial gene]
Seq. No.	228282
Seq. ID	LIB3196-003-P1-M1-C4

Method	BLASTX
NCBI GI	g3319958
BLAST score	663
E value	7.0e-70
Match length	126
% identity	8
NCBI Description	(AJ228139) VAKTI precursor [Homo sapiens]

Seq. No.	228283
Seq. ID	LIB3196-003-P1-M1-C5
Method	BLASTX
NCBI GI	g137578
BLAST score	474
E value	9.0e-48
Match length	122
% identity	78
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228284
Seq. ID	LIB3196-003-P1-M1-C7
Method	BLASTX
NCBI GI	g1785488
BLAST score	158
E value	1.0e-10
Match length	80
% identity	40
NCBI Description	(D14590) flavonoid 3',5'-hydroxylase [Campanula medium]

Seq. No.	228285
Seq. ID	LIB3196-003-P1-M1-C8
Method	BLASTX
NCBI GI	g116075
BLAST score	188
E value	3.0e-14
Match length	80
% identity	55
NCBI Description	CCAAT/ENHANCER BINDING PROTEIN BETA (C/EBP BETA) (NUCLEAR FACTOR NF-IL6) (TRANSCRIPTION FACTOR 5) >gi_107921_pir__S12788 transcription factor NF-IL6 - human >gi_35036_emb_CAA36794_ (X52560) nuclear factor NF-IL6 (AA 1-345) [Homo sapiens]

Seq. No.	228286
Seq. ID	LIB3196-003-P1-M1-C9
Method	BLASTX
NCBI GI	g207905
BLAST score	509
E value	7.0e-52
Match length	120
% identity	85
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	228287
Seq. ID	LIB3196-003-P1-M1-D1
Method	BLASTX
NCBI GI	g547712
BLAST score	592
E value	1.0e-61
Match length	121
% identity	96
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	228288
Seq. ID	LIB3196-003-P1-M1-D11
Method	BLASTX
NCBI GI	g1928981
BLAST score	500
E value	8.0e-51
Match length	105
% identity	94
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	228289
Seq. ID	LIB3196-003-P1-M1-D12
Method	BLASTX
NCBI GI	g416877
BLAST score	356
E value	9.0e-61
Match length	126
% identity	91
NCBI Description	TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE (HIGH-AFFINITY HEPATIC BILE ACID-BINDING PROTEIN) (HBAB) >gi_1071804_pir__A53436 3-alpha-hydroxysteroid/dihydrodiol dehydrogenase (EC 1.1.1.-) - human >gi_181549 (M86609) dihydrodiol dehydrogenase [Homo sapiens] >gi_452484_gb_AAA16227.1_ (U05684) dihydrodiol dehydrogenase [Homo sapiens] >gi_487135 (U05861) hepatic dihydrodiol dehydrogenase [Homo sapiens]

Seq. No.	228290
Seq. ID	LIB3196-003-P1-M1-D2
Method	BLASTX
NCBI GI	g542184
BLAST score	206
E value	2.0e-16
Match length	108
% identity	40
NCBI Description	globulin-1S, GLB1S - maize

Seq. No.	228291
Seq. ID	LIB3196-003-P1-M1-D4
Method	BLASTX
NCBI GI	g4406775
BLAST score	220
E value	5.0e-18

Match length 77
% identity 58
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 228292
Seq. ID LIB3196-003-P1-M1-D9
Method BLASTX
NCBI GI g1504040
BLAST score 143
E value 6.0e-09
Match length 118
% identity 16
NCBI Description (D86983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens]

Seq. No. 228293
Seq. ID LIB3196-003-P1-M1-E1
Method BLASTX
NCBI GI g3915737
BLAST score 471
E value 2.0e-47
Match length 120
% identity 43
NCBI Description IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon esculentum]

Seq. No. 228294
Seq. ID LIB3196-003-P1-M1-E10
Method BLASTX
NCBI GI g4417309
BLAST score 166
E value 1.0e-11
Match length 106
% identity 37
NCBI Description (AC006446) putative pol polyprotein with a reverse transcriptase domain [Arabidopsis thaliana]

Seq. No. 228295
Seq. ID LIB3196-003-P1-M1-E11
Method BLASTX
NCBI GI g3746127
BLAST score 307
E value 4.0e-28
Match length 81
% identity 75
NCBI Description (U76253) E25B protein [Mus musculus]

Seq. No. 228296
Seq. ID LIB3196-003-P1-M1-E2
Method BLASTX
NCBI GI g3024665
BLAST score 202
E value 7.0e-16
Match length 114
% identity 41
NCBI Description STRICTOSIDINE SYNTHASE 3 PRECURSOR >gi_1754987 (U43946)

strictosidine synthase [Arabidopsis thaliana]

Seq. No.	228297
Seq. ID	LIB3196-003-P1-M1-E4
Method	BLASTX
NCBI GI	g115502
BLAST score	585
E value	9.0e-61
Match length	120
% identity	49
NCBI Description	CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) >gi_71690_pir__MCHUNB calmodulin-related protein NB-1 - human >gi_29650_emb_CAA31809_ (X13461) hGH6 calmodulin-like protein [Homo sapiens] >gi_189081 (M58026) NB-1 [Homo sapiens]

Seq. No.	228298
Seq. ID	LIB3196-003-P1-M1-E9
Method	BLASTX
NCBI GI	g2146982
BLAST score	449
E value	8.0e-45
Match length	93
% identity	100
NCBI Description	UDP-galactose translocator protein - human >gi_1526438_dbj_BAA12673_ (D84454) UDP-galactose translocator [Homo sapiens]

Seq. No.	228299
Seq. ID	LIB3196-003-P1-M1-F1
Method	BLASTX
NCBI GI	g2494144
BLAST score	209
E value	9.0e-17
Match length	118
% identity	7
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	228300
Seq. ID	LIB3196-003-P1-M1-F10
Method	BLASTX
NCBI GI	g3915742
BLAST score	580
E value	3.0e-60
Match length	121
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228301
Seq. ID	LIB3196-003-P1-M1-F11
Method	BLASTX
NCBI GI	g4336349
BLAST score	526

E value	8.0e-54
Match length	110
% identity	91
NCBI Description	(AF082871) arsenate resistance protein ARS2 [Homo sapiens]

Seq. No.	228302
Seq. ID	LIB3196-003-P1-M1-F12
Method	BLASTX
NCBI GI	g586120
BLAST score	231
E value	3.0e-19
Match length	102
% identity	49
NCBI Description	TRICHOHYALIN >gi_539701_pir__A45973 trichohyalin - human >gi_292836 (L09190) trichohyalin [Homo sapiens]

Seq. No.	228303
Seq. ID	LIB3196-003-P1-M1-F4
Method	BLASTX
NCBI GI	g729391
BLAST score	634
E value	2.0e-66
Match length	128
% identity	98
NCBI Description	MITOCHONDRIAL TRIFUNCTONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [CONTAINS: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE] >gi_543064_pir__JC2108 long-chain-fatty-acid beta-oxidation multienzyme complex alpha chain precursor, mitochondrial - human >gi_862457_dbj_BAA03941_ (D16480) enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein [Homo sapiens] >gi_4504325_ref_NP_000173.1_pHADHA_ hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su

Seq. No.	228304
Seq. ID	LIB3196-003-P1-M1-F7
Method	BLASTX
NCBI GI	g3646373
BLAST score	534
E value	8.0e-55
Match length	105
% identity	92
NCBI Description	(AJ011078) RGP1 protein [Oryza sativa]

Seq. No.	228305
Seq. ID	LIB3196-003-P1-M1-F8
Method	BLASTX
NCBI GI	g3337351
BLAST score	161
E value	4.0e-11
Match length	50
% identity	58
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228306

Seq. ID	LIB3196-003-P1-M1-G12
Method	BLASTX
NCBI GI	g4467804
BLAST score	625
E value	2.0e-65
Match length	117
% identity	95
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No.	228307
Seq. ID	LIB3196-003-P1-M1-G3
Method	BLASTX
NCBI GI	g547753
BLAST score	348
E value	6.0e-33
Match length	115
% identity	70
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	228308
Seq. ID	LIB3196-003-P1-M1-G4
Method	BLASTX
NCBI GI	g549063
BLAST score	316
E value	3.0e-29
Match length	81
% identity	74
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	228309
Seq. ID	LIB3196-003-P1-M1-G5
Method	BLASTX
NCBI GI	g872116
BLAST score	305
E value	6.0e-28
Match length	122
% identity	44
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	228310
Seq. ID	LIB3196-003-P1-M1-G6
Method	BLASTX
NCBI GI	g4337025
BLAST score	351
E value	2.0e-33
Match length	123
% identity	59
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	228311
Seq. ID	LIB3196-003-P1-M1-G7
Method	BLASTX

NCBI GI	g120669
BLAST score	561
E value	5.0e-58
Match length	110
% identity	95
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	228312
Seq. ID	LIB3196-003-P1-M1-G9
Method	BLASTX
NCBI GI	g125105
BLAST score	623
E value	3.0e-65
Match length	126
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	228313
Seq. ID	LIB3196-003-P1-M1-H1
Method	BLASTX
NCBI GI	g399888
BLAST score	619
E value	1.0e-64
Match length	126
% identity	97
NCBI Description	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN (HLA-DR ANTIGENS ASSOCIATED INVARIANT CHAIN) (P33) (CD74 ANTIGEN)

Seq. No.	228314
Seq. ID	LIB3196-003-P1-M1-H10
Method	BLASTX
NCBI GI	g3237306
BLAST score	625
E value	2.0e-65
Match length	126
% identity	97
NCBI Description	(U92715) breast cancer antiestrogen resistance 3 protein [Homo sapiens] >gi_4502371_ref_NP_003558.1_pBCAR3_ breast cancer antiestrogen resistance

Seq. No.	228315
Seq. ID	LIB3196-003-P1-M1-H12
Method	BLASTX
NCBI GI	g228298
BLAST score	215
E value	2.0e-17
Match length	64
% identity	69

NCBI Description	transcription factor IIE:SUBUNIT=small 34kD [Homo sapiens]
Seq. No.	228316
Seq. ID	LIB3196-003-P1-M1-H2
Method	BLASTX
NCBI GI	g2347187
BLAST score	295
E value	9.0e-27
Match length	74
% identity	81
NCBI Description	(AC002338) putative malonyl-CoA:Acyl carrier protein transacylase, 3' partial [Arabidopsis thaliana]
Seq. No.	228317
Seq. ID	LIB3196-003-P1-M1-H4
Method	BLASTX
NCBI GI	g386850
BLAST score	650
E value	2.0e-68
Match length	129
% identity	100
NCBI Description	(M19723) keratin K5 [Homo sapiens]
Seq. No.	228318
Seq. ID	LIB3196-003-P1-M1-H5
Method	BLASTX
NCBI GI	g117528
BLAST score	309
E value	2.0e-28
Match length	90
% identity	81
NCBI Description	LAMBDA-CRYSTALLIN >gi_90077_pir__A31992 lambda-crystallin - rabbit >gi_164905 (M22743) lambda-crystallin precursor [Oryctolagus cuniculus]
Seq. No.	228319
Seq. ID	LIB3196-003-P1-M1-H7
Method	BLASTX
NCBI GI	g125080
BLAST score	616
E value	2.0e-64
Match length	125
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.	228320
Seq. ID	LIB3196-003-P1-M1-H8
Method	BLASTX
NCBI GI	g4091080
BLAST score	262
E value	6.0e-23
Match length	60
% identity	80

NCBI Description	(AF045571) nucleic acid binding protein [Oryza sativa]

Seq. No.	228321
Seq. ID	LIB3196-004-P1-M1-A9
Method	BLASTX
NCBI GI	g113944
BLAST score	605
E value	4.0e-63
Match length	124
% identity	55
NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi_71756_pir__LUHU annexin I - human >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I (lipocortin I)

Seq. No.	228322
Seq. ID	LIB3196-004-P1-M1-B1
Method	BLASTX
NCBI GI	g4455217
BLAST score	220
E value	5.0e-18
Match length	119
% identity	44
NCBI Description	(AL035440) Avr9 elicitor response like protein [Arabidopsis thaliana]

Seq. No.	228323
Seq. ID	LIB3196-004-P1-M1-B11
Method	BLASTX
NCBI GI	g2494305
BLAST score	281
E value	1.0e-52
Match length	116
% identity	97
NCBI Description	TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) >gi_1363072_pir__S56172 translation initiation factor eIF-2B beta chain - rabbit >gi_1061200_emb_CAA88255_ (Z48222) protein synthesis initiation factor eIF-2B beta subunit [Oryctolagus cuniculus]

Seq. No.	228324
Seq. ID	LIB3196-004-P1-M1-B3
Method	BLASTX
NCBI GI	g4127947
BLAST score	650
E value	2.0e-68
Match length	126
% identity	97
NCBI Description	(AJ010046) guanine nucleotide-exchange factor [Homo sapiens]

Seq. No.	228325
Seq. ID	LIB3196-004-P1-M1-C12

Method	BLASTX
NCBI GI	g1877202
BLAST score	543
E value	7.0e-56
Match length	120
% identity	90
NCBI Description	(Y08915) alpha 4 protein [Homo sapiens] >gi_4557663_ref_NP_001542.1_pIGBP1_ immunoglobulin-binding protein

Seq. No.	228326
Seq. ID	LIB3196-004-P1-M1-C2
Method	BLASTX
NCBI GI	g125080
BLAST score	616
E value	2.0e-64
Match length	125
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228327
Seq. ID	LIB3196-004-P1-M1-C3
Method	BLASTX
NCBI GI	g547753
BLAST score	322
E value	3.0e-55
Match length	124
% identity	96
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	228328
Seq. ID	LIB3196-004-P1-M1-C6
Method	BLASTX
NCBI GI	g631131
BLAST score	534
E value	1.0e-54
Match length	109
% identity	98
NCBI Description	epithelial cell marker protein 1 - human >gi_187302 (M93010) epithelial cell marker protein 1 [Homo sapiens]

Seq. No.	228329
Seq. ID	LIB3196-004-P1-M1-C8
Method	BLASTX
NCBI GI	g2961346
BLAST score	143
E value	4.0e-14
Match length	54
% identity	76
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	228330

Seq. ID	LIB3196-004-P1-M1-C9
Method	BLASTX
NCBI GI	g1346344
BLAST score	620
E value	7.0e-65
Match length	123
% identity	100
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II - human >gi_908779 (L42583) keratin type II [Homo sapiens]

Seq. No.	228331
Seq. ID	LIB3196-004-P1-M1-D10
Method	BLASTX
NCBI GI	g70753
BLAST score	262
E value	5.0e-23
Match length	78
% identity	68
NCBI Description	histone H3 - garden pea >gi_82610_pir__S00373 histone H3 - wheat

Seq. No.	228332
Seq. ID	LIB3196-004-P1-M1-D3
Method	BLASTX
NCBI GI	g1710015
BLAST score	643
E value	1.0e-67
Match length	125
% identity	98
NCBI Description	RAS-RELATED PROTEIN RAB-12 >gi_631513_pir__S40207 rab12 protein - dog >gi_437985_emb_CAA80471_ (Z22818) Rab12 protein [Canis familiaris]

Seq. No.	228333
Seq. ID	LIB3196-004-P1-M1-D7
Method	BLASTX
NCBI GI	g1346344
BLAST score	393
E value	2.0e-38
Match length	109
% identity	76
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II - human >gi_908779 (L42583) keratin type II [Homo sapiens]

Seq. No.	228334
Seq. ID	LIB3196-004-P1-M1-E1
Method	BLASTX
NCBI GI	g4099482
BLAST score	550
E value	1.0e-56
Match length	125
% identity	86
NCBI Description	(U87791) eRFS [Homo sapiens]

Seq. No.	228335

Seq. ID	LIB3196-004-P1-M1-E2
Method	BLASTX
NCBI GI	g1170499
BLAST score	586
E value	8.0e-61
Match length	125
% identity	89
NCBI Description	TRANSLATION INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR (IF-2MT) >gi_1082869_pir__A55628 translation initiation factor IF-2 precursor, mitochondrial - human >gi_609492 (L34600) initiation factor 2 [Homo sapiens] >gi_4505277_ref_NP_002444.1_pMTIF2_ mitochondrial translational initiation factor

Seq. No.	228336
Seq. ID	LIB3196-004-P1-M1-F1
Method	BLASTX
NCBI GI	g125080
BLAST score	612
E value	5.0e-64
Match length	124
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228337
Seq. ID	LIB3196-004-P1-M1-F2
Method	BLASTX
NCBI GI	g1922935
BLAST score	558
E value	1.0e-57
Match length	120
% identity	98
NCBI Description	(U47924) B-cell receptor associated protein [Homo sapiens] >gi_2289906 (AC002397) BAP [Mus musculus]

Seq. No.	228338
Seq. ID	LIB3196-004-P1-M1-F5
Method	BLASTX
NCBI GI	g3176690
BLAST score	279
E value	7.0e-25
Match length	119
% identity	55
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	228339
Seq. ID	LIB3196-004-P1-M1-F6
Method	BLASTX
NCBI GI	g3882081
BLAST score	594
E value	8.0e-62

Match length	119
% identity	33
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	228340
Seq. ID	LIB3196-004-P1-M1-G3
Method	BLASTX
NCBI GI	g4262292
BLAST score	312
E value	1.0e-28
Match length	123
% identity	50
NCBI Description	(AF072506) envelope protein precursor [Homo sapiens]

Seq. No.	228341
Seq. ID	LIB3196-004-P1-M1-G5
Method	BLASTX
NCBI GI	g167311
BLAST score	501
E value	6.0e-51
Match length	108
% identity	90
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	228342
Seq. ID	LIB3196-004-P1-M1-G7
Method	BLASTX
NCBI GI	g4218961
BLAST score	513
E value	3.0e-52
Match length	121
% identity	87
NCBI Description	(AF093130) caspase 9 short isoform [Homo sapiens]

Seq. No.	228343
Seq. ID	LIB3196-004-P1-M1-H11
Method	BLASTX
NCBI GI	g3776021
BLAST score	579
E value	4.0e-60
Match length	114
% identity	97
NCBI Description	(AJ010472) RNA helicase [Arabidopsis thaliana]

Seq. No.	228344
Seq. ID	LIB3196-004-P1-M1-H12
Method	BLASTX
NCBI GI	g88044
BLAST score	605
E value	4.0e-63
Match length	125
% identity	97
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	228345

Seq. ID	LIB3196-004-P1-M1-H2
Method	BLASTX
NCBI GI	g137578
BLAST score	470
E value	3.0e-47
Match length	95
% identity	94
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228346
Seq. ID	LIB3196-004-P1-M1-H4
Method	BLASTX
NCBI GI	g1076668
BLAST score	606
E value	3.0e-63
Match length	119
% identity	95
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	228347
Seq. ID	LIB3196-005-P1-M1-A1
Method	BLASTX
NCBI GI	g1596167
BLAST score	334
E value	3.0e-31
Match length	117
% identity	56
NCBI Description	(D87953) RTP [Homo sapiens] >gi_3046386 (AF004162) nickel-specific induction protein [Homo sapiens]

Seq. No.	228348
Seq. ID	LIB3196-005-P1-M1-A10
Method	BLASTX
NCBI GI	g346219
BLAST score	298
E value	4.0e-27
Match length	124
% identity	59
NCBI Description	keratin K4a - human (fragment)

Seq. No.	228349
Seq. ID	LIB3196-005-P1-M1-A12
Method	BLASTX
NCBI GI	g1173209
BLAST score	532
E value	1.0e-54
Match length	106
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton

	>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
Seq. No.	228350
Seq. ID	LIB3196-005-P1-M1-A4
Method	BLASTX
NCBI GI	g3869127
BLAST score	230
E value	4.0e-19
Match length	66
% identity	64
NCBI Description	(AB019527) LDOC1 protein [Homo sapiens]
Seq. No.	228351
Seq. ID	LIB3196-005-P1-M1-A6
Method	BLASTX
NCBI GI	g579930
BLAST score	563
E value	4.0e-58
Match length	112
% identity	96
NCBI Description	(X68314) glutathione peroxidase-GI [Homo sapiens] >gi_4504103_ref_NP_002074.1_pGPX2_ glutathione peroxidase 2 (gastrointestinal)
Seq. No.	228352
Seq. ID	LIB3196-005-P1-M1-A8
Method	BLASTX
NCBI GI	g137578
BLAST score	378
E value	2.0e-36
Match length	129
% identity	57
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	228353
Seq. ID	LIB3196-005-P1-M1-A9
Method	BLASTX
NCBI GI	g421989
BLAST score	302
E value	1.0e-27
Match length	94
% identity	61
NCBI Description	serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx [Hordeum vulgare]
Seq. No.	228354
Seq. ID	LIB3196-005-P1-M1-B1
Method	BLASTX
NCBI GI	g2501446
BLAST score	512

E value	4.0e-52
Match length	98
% identity	100
NCBI Description	UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) >gi_1518694 (U61397) ubiquitin-homology domain protein PIC1 [Homo sapiens] >gi_1574948 (U38784) similar to ubiquitin and to yeast Smt3p (suppressor of MIF2); Method: conceptual translation supplied by author [Homo sapiens] >gi_1703503 (U72722) gap modifying protein 1 [Homo sapiens] >gi_1762973 (U67122) SUMO-1 [Homo sapiens] >gi_1769602 (U83117) sentrin [Homo sapiens] >gi_1770521_emb_CAA67898_ (X99586) SMT3C protein [Homo sapiens] >gi_2645737 (AF033353) ubiquitin-homology domain protein [Mus musculus] >gi_4507801_ref_NP_003343.1_pUBL1_ ubiquitin-like 1 (sentrin)

Seq. No.	228355
Seq. ID	LIB3196-005-P1-M1-B10
Method	BLASTX
NCBI GI	g2501494
BLAST score	315
E value	4.0e-29
Match length	107
% identity	57
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 5) >gi_542015_pir__S41951 UTP-glucose glucosyltransferase - cassava >gi_453249_emb_CAA54612_ (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	228356
Seq. ID	LIB3196-005-P1-M1-B11
Method	BLASTX
NCBI GI	g1703290
BLAST score	143
E value	2.0e-11
Match length	86
% identity	45
NCBI Description	ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN-ASSOCIATED PROTEIN 1) (RAP) (HEPARIN BINDING PROTEIN-44) (HBP-44) >gi_478425_pir__JX0281 heparin-binding protein-44 precursor - mouse >gi_460892_bbs_142288 (S67967) heparin binding protein-44, HBP-44 [mice, Peptide, 360 aa] [Mus sp.]

Seq. No.	228357
Seq. ID	LIB3196-005-P1-M1-B12
Method	BLASTX
NCBI GI	g1488647
BLAST score	480
E value	2.0e-48
Match length	116
% identity	82
NCBI Description	(X99937) RNA helicase [Spinacia oleracea]

Seq. No.	228358
Seq. ID	LIB3196-005-P1-M1-B3
Method	BLASTX
NCBI GI	g3023847
BLAST score	654
E value	8.0e-69
Match length	130
% identity	27
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	228359
Seq. ID	LIB3196-005-P1-M1-B4
Method	BLASTX
NCBI GI	g125080
BLAST score	668
E value	2.0e-70
Match length	135
% identity	99
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848_(J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228360
Seq. ID	LIB3196-005-P1-M1-B5
Method	BLASTX
NCBI GI	g3676473
BLAST score	270
E value	8.0e-24
Match length	119
% identity	48
NCBI Description	(AF053886) (R)-(+)-mandelonitrile lyase isoform MDL5 precursor [Prunus serotina]

Seq. No.	228361
Seq. ID	LIB3196-005-P1-M1-B6
Method	BLASTX
NCBI GI	g137578
BLAST score	500
E value	7.0e-51
Match length	118
% identity	86
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228362
Seq. ID	LIB3196-005-P1-M1-B7
Method	BLASTX
NCBI GI	g3122072

BLAST score	603
E value	8.0e-63
Match length	121
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]

Seq. No.	228363
Seq. ID	LIB3196-005-P1-M1-B8
Method	BLASTX
NCBI GI	g137578
BLAST score	453
E value	2.0e-45
Match length	109
% identity	84
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228364
Seq. ID	LIB3196-005-P1-M1-C10
Method	BLASTX
NCBI GI	g586120
BLAST score	148
E value	1.0e-09
Match length	46
% identity	57
NCBI Description	TRICHOHYALIN >gi_539701_pir__A45973 trichohyalin - human >gi_292836 (L09190) trichohyalin [Homo sapiens]

Seq. No.	228365
Seq. ID	LIB3196-005-P1-M1-C12
Method	BLASTX
NCBI GI	g2500376
BLAST score	466
E value	9.0e-47
Match length	95
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]

Seq. No.	228366
Seq. ID	LIB3196-005-P1-M1-C3
Method	BLASTX
NCBI GI	g3834310
BLAST score	549
E value	2.0e-56
Match length	105
% identity	100
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

Seq. No.	228367
Seq. ID	LIB3196-005-P1-M1-C4
Method	BLASTX
NCBI GI	g3043548
BLAST score	340
E value	5.0e-32
Match length	131
% identity	50
NCBI Description	(AB011084) KIAA0512 protein [Homo sapiens]

Seq. No.	228368
Seq. ID	LIB3196-005-P1-M1-C5
Method	BLASTX
NCBI GI	g1632831
BLAST score	347
E value	8.0e-33
Match length	74
% identity	93
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	228369
Seq. ID	LIB3196-005-P1-M1-C8
Method	BLASTX
NCBI GI	g3395429
BLAST score	172
E value	3.0e-12
Match length	94
% identity	41
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228370
Seq. ID	LIB3196-005-P1-M1-D1
Method	BLASTX
NCBI GI	g4008441
BLAST score	214
E value	3.0e-17
Match length	62
% identity	63
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	228371
Seq. ID	LIB3196-005-P1-M1-D2
Method	BLASTX
NCBI GI	g631131
BLAST score	272
E value	3.0e-48
Match length	107
% identity	98
NCBI Description	epithelial cell marker protein 1 - human >gi_187302 (M93010) epithelial cell marker protein 1 [Homo sapiens]

Seq. No. 228372

Seq. ID	LIB3196-005-P1-M1-D4
Method	BLASTX
NCBI GI	g2498629
BLAST score	598
E value	3.0e-62
Match length	135
% identity	31
NCBI Description	TRANSCRIPTIONAL REPRESSOR NF-X1 >gi_2135825_pir__I38869 NFX1 - human >gi_563217 (U15306) NFX1 [Homo sapiens] >gi_4505387_ref_NP_002495.1_pNFX1_ nuclear transcription factor, X-box binding

Seq. No.	228373
Seq. ID	LIB3196-005-P1-M1-E3
Method	BLASTX
NCBI GI	g114374
BLAST score	583
E value	1.0e-60
Match length	120
% identity	99
NCBI Description	SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN (SODIUM PUMP) (NA+/K+ ATPASE) >gi_88220_pir__A24414 Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha-1 chain - human >gi_28927_emb_CAA27840_ (X04297) ATPase alpha subunit (aa 1-1023) [Homo sapiens] >gi_219942_dbj_BAA00061_ (D00099) Na,K-ATPase alpha-subunit [Homo sapiens] >gi_356169_prf__1208322A ATPase alpha,Na/K [Homo sapiens]

Seq. No.	228374
Seq. ID	LIB3196-005-P1-M1-E5
Method	BLASTX
NCBI GI	g1346347
BLAST score	661
E value	1.0e-69
Match length	134
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	228375
Seq. ID	LIB3196-005-P1-M1-E6
Method	BLASTX
NCBI GI	g3746127
BLAST score	348
E value	6.0e-33
Match length	88
% identity	77
NCBI Description	(U76253) E25B protein [Mus musculus]

Seq. No.	228376
Seq. ID	LIB3196-005-P1-M1-E7
Method	BLASTX
NCBI GI	g399365
BLAST score	502
E value	5.0e-51

Match length	117
% identity	85
NCBI Description	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (CLASS 3) >gi_178402 (M74542) aldehyde dehydrogenase type III [Homo sapiens] >gi_4502035_ref_NP_000682.1_pALDH3_ aldehyde dehydrogenase
Seq. No.	228377
Seq. ID	LIB3196-005-P1-M1-E9
Method	BLASTX
NCBI GI	g683553
BLAST score	151
E value	6.0e-10
Match length	93
% identity	41
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
Seq. No.	228378
Seq. ID	LIB3196-005-P1-M1-F10
Method	BLASTX
NCBI GI	g1173055
BLAST score	611
E value	9.0e-64
Match length	122
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]
Seq. No.	228379
Seq. ID	LIB3196-005-P1-M1-F11
Method	BLASTX
NCBI GI	g1174470
BLAST score	457
E value	1.0e-45
Match length	124
% identity	69
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]
Seq. No.	228380
Seq. ID	LIB3196-005-P1-M1-F6
Method	BLASTX
NCBI GI	g4049480
BLAST score	145
E value	4.0e-09
Match length	58
% identity	57
NCBI Description	(Y18001) ATPase subunit 8 [Papio hamadryas]
Seq. No.	228381
Seq. ID	LIB3196-005-P1-M1-F7
Method	BLASTX

NCBI GI	g3396098
BLAST score	160
E value	6.0e-11
Match length	51
% identity	57
NCBI Description	(AF080236) pyridoxamine 5'-phosphate oxidase [Schizophyllum commune]

Seq. No.	228382
Seq. ID	LIB3196-005-P1-M1-F8
Method	BLASTX
NCBI GI	g4056459
BLAST score	114
E value	1.0e-09
Match length	95
% identity	45
NCBI Description	(AC005990) Contains similarity to gb_L26505 Met30p from Saccharomyces cerevisiae. [Arabidopsis thaliana]

Seq. No.	228383
Seq. ID	LIB3196-005-P1-M1-F9
Method	BLASTX
NCBI GI	g113950
BLAST score	562
E value	5.0e-58
Match length	113
% identity	59
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II - human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo sapiens]

Seq. No.	228384
Seq. ID	LIB3196-005-P1-M1-G1
Method	BLASTX
NCBI GI	g4490330
BLAST score	623
E value	3.0e-65
Match length	129
% identity	96
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	228385
Seq. ID	LIB3196-005-P1-M1-G3
Method	BLASTX
NCBI GI	g3915742
BLAST score	498
E value	2.0e-50
Match length	98
% identity	94
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228386
Seq. ID	LIB3196-005-P1-M1-G5
Method	BLASTX
NCBI GI	g126156
BLAST score	419
E value	3.0e-41
Match length	130
% identity	65
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228387
Seq. ID	LIB3196-005-P1-M1-H10
Method	BLASTX
NCBI GI	g4469023
BLAST score	437
E value	2.0e-43
Match length	98
% identity	86
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	228388
Seq. ID	LIB3196-005-P1-M1-H12
Method	BLASTX
NCBI GI	g1076398
BLAST score	148
E value	1.0e-09
Match length	39
% identity	69
NCBI Description	ribosomal protein L2 - Arabidopsis thaliana >gi_572523_emb_CAA57902_ (X82556) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	228389
Seq. ID	LIB3196-005-P1-M1-H3
Method	BLASTX
NCBI GI	g730165
BLAST score	305
E value	7.0e-28
Match length	95
% identity	67
NCBI Description	EARLY NODULIN 93 (N-93) >gi_486679_pir__S34801 nodulin (clone GmN93) - soybean >gi_218262_dbj_BAA02724_ (D13506) early nodulin [Glycine max] >gi_3763851_dbj_BAA33816_ (AB018378) early nodulin [Glycine max] >gi_447138_prf__1913422D nodulin [Glycine max]

Seq. No.	228390
Seq. ID	LIB3196-005-P1-M1-H4
Method	BLASTX
NCBI GI	g3435086
BLAST score	572
E value	3.0e-59

Match length	130
% identity	89
NCBI Description	(AF004222) RTN2-A [Homo sapiens]

Seq. No.	228391
Seq. ID	LIB3196-005-P1-M1-H7
Method	BLASTX
NCBI GI	g88044
BLAST score	625
E value	2.0e-65
Match length	132
% identity	97
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	228392
Seq. ID	LIB3196-005-P1-M1-H8
Method	BLASTX
NCBI GI	g124224
BLAST score	580
E value	4.0e-60
Match length	114
% identity	95
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	228393
Seq. ID	LIB3196-006-P1-M1-A1
Method	BLASTX
NCBI GI	g4539405
BLAST score	489
E value	1.0e-49
Match length	116
% identity	81
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	228394
Seq. ID	LIB3196-006-P1-M1-A11
Method	BLASTX
NCBI GI	g1872200
BLAST score	180
E value	2.0e-13
Match length	82
% identity	50
NCBI Description	(U22376) alternatively spliced product using exon 13A [Homo sapiens]

Seq. No.	228395
Seq. ID	LIB3196-006-P1-M1-A7
Method	BLASTX
NCBI GI	g337358
BLAST score	404
E value	1.0e-39

Match length	82
% identity	99
NCBI Description	(L03357) RET tyrosine kinase/cAMP protein kinase A subunit RI [Homo sapiens]

Seq. No.	228396
Seq. ID	LIB3196-006-P1-M1-B1
Method	BLASTX
NCBI GI	g1346344
BLAST score	156
E value	1.0e-10
Match length	31
% identity	97
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II - human >gi_908779 (L42583) keratin type II [Homo sapiens]

Seq. No.	228397
Seq. ID	LIB3196-006-P1-M1-B11
Method	BLASTX
NCBI GI	g3445201
BLAST score	281
E value	4.0e-25
Match length	61
% identity	80
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	228398
Seq. ID	LIB3196-006-P1-M1-B12
Method	BLASTX
NCBI GI	g137578
BLAST score	533
E value	1.0e-54
Match length	122
% identity	89
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228399
Seq. ID	LIB3196-006-P1-M1-B2
Method	BLASTX
NCBI GI	g125105
BLAST score	195
E value	3.0e-18
Match length	78
% identity	72
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	228400

Seq. ID	LIB3196-006-P1-M1-B3
Method	BLASTX
NCBI GI	g2924781
BLAST score	537
E value	4.0e-55
Match length	125
% identity	81
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	228401
Seq. ID	LIB3196-006-P1-M1-B4
Method	BLASTX
NCBI GI	g116075
BLAST score	437
E value	2.0e-43
Match length	89
% identity	99
NCBI Description	CCAAT/ENHANCER BINDING PROTEIN BETA (C/EBP BETA) (NUCLEAR FACTOR NF-IL6) (TRANSCRIPTION FACTOR 5) >gi_107921_pir__S12788 transcription factor NF-IL6 - human >gi_35036_emb_CAA36794_ (X52560) nuclear factor NF-IL6 (AA 1-345) [Homo sapiens]

Seq. No.	228402
Seq. ID	LIB3196-006-P1-M1-B6
Method	BLASTX
NCBI GI	g4176446
BLAST score	241
E value	2.0e-20
Match length	120
% identity	36
NCBI Description	(AL022238) dJ1042K10.2.1 (novel protein with probable rabGAP domains and Src homology domain 3) (isoform 1) [Homo sapiens]

Seq. No.	228403
Seq. ID	LIB3196-006-P1-M1-B8
Method	BLASTX
NCBI GI	g133014
BLAST score	471
E value	2.0e-47
Match length	91
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L7A (PLA-X POLYPEPTIDE) (SURF-3) >gi_71116_pir__R5HU7A ribosomal protein L7a - human >gi_71117_pir__R5RT7A ribosomal protein L7a - rat >gi_34203_emb_CAA36383_ (X52138) L7a protein [Homo sapiens] >gi_35512_emb_CAA29889_ (X06705) PLA-X polypeptide [Homo sapiens] >gi_36647_emb_CAA43925_ (X61923) ribosomal protein L7a [Homo sapiens] >gi_56956_emb_CAA33117_ (X15013) ribosomal protein L7a (AA 1-266) [Rattus rattus] >gi_337495 (M36072) ribosomal protein L7a large subunit [Homo sapiens] >gi_1584354_prf__2122395A nuclear hormone receptor-associated protein [Homo sapiens] >gi_4506661_ref_NP_000963.1_pRPL7A_ ribosomal protein L7a

Seq. No.	228404
Seq. ID	LIB3196-006-P1-M1-C1
Method	BLASTX
NCBI GI	g125077
BLAST score	496
E value	2.0e-50
Match length	119
% identity	87
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	228405
Seq. ID	LIB3196-006-P1-M1-C10
Method	BLASTX
NCBI GI	g3746541
BLAST score	201
E value	1.0e-15
Match length	46
% identity	87
NCBI Description	(AF059273) glucocorticoid modulatory element binding protein 2 [Rattus norvegicus]

Seq. No.	228406
Seq. ID	LIB3196-006-P1-M1-C11
Method	BLASTX
NCBI GI	g1346342
BLAST score	347
E value	8.0e-33
Match length	118
% identity	65
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo sapiens]

Seq. No.	228407
Seq. ID	LIB3196-006-P1-M1-C3
Method	BLASTX
NCBI GI	g2662341
BLAST score	579
E value	4.0e-60
Match length	114
% identity	98
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	228408
Seq. ID	LIB3196-006-P1-M1-C4
Method	BLASTX
NCBI GI	g1173256
BLAST score	525
E value	1.0e-53
Match length	100
% identity	100

NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]
Seq. No.	228409
Seq. ID	LIB3196-006-P1-M1-C5
Method	BLASTX
NCBI GI	g464621
BLAST score	319
E value	1.0e-29
Match length	108
% identity	58
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]
Seq. No.	228410
Seq. ID	LIB3196-006-P1-M1-C9
Method	BLASTX
NCBI GI	g2435521
BLAST score	411
E value	2.0e-40
Match length	120
% identity	14
NCBI Description	(AF024504) contains similarity to Nicotiana tabacum membrane-associated salt-inducible protein (GB:U08285) [Arabidopsis thaliana]
Seq. No.	228411
Seq. ID	LIB3196-006-P1-M1-D1
Method	BLASTX
NCBI GI	g2662415
BLAST score	216
E value	1.0e-17
Match length	51
% identity	71
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]
Seq. No.	228412
Seq. ID	LIB3196-006-P1-M1-D3
Method	BLASTX
NCBI GI	g541675
BLAST score	535
E value	6.0e-55
Match length	119
% identity	89
NCBI Description	(X76342) alternative ORF [Homo sapiens]
Seq. No.	228413
Seq. ID	LIB3196-006-P1-M1-D4
Method	BLASTX
NCBI GI	g1172995
BLAST score	262
E value	7.0e-23
Match length	108

% identity	55
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]
Seq. No.	228414
Seq. ID	LIB3196-006-P1-M1-D5
Method	BLASTX
NCBI GI	g416917
BLAST score	212
E value	6.0e-30
Match length	86
% identity	77
NCBI Description	DESMOGLEIN 1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN 1) (DG1) >gi_319948_pir__IJHUG1 desmoglein 1 precursor - human >gi_30506_emb_CAA39976_ (X56654) desmoglein type 1 [Homo sapiens] >gi_3983129 (AF097935) desmoglein 1 [Homo sapiens] >gi_4503401_ref_NP_001933.1_pDSG1_ desmoglein
Seq. No.	228415
Seq. ID	LIB3196-006-P1-M1-D6
Method	BLASTX
NCBI GI	g3915742
BLAST score	346
E value	1.0e-32
Match length	127
% identity	57
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]
Seq. No.	228416
Seq. ID	LIB3196-006-P1-M1-D8
Method	BLASTX
NCBI GI	g120649
BLAST score	576
E value	1.0e-59
Match length	112
% identity	98
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_182863 (J02642) glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_224880_prf__1203217A dehydrogenase,glyceraldehydephosphate [Homo sapiens]
Seq. No.	228417
Seq. ID	LIB3196-006-P1-M1-E11
Method	BLASTX

NCBI GI	g629693
BLAST score	180
E value	3.0e-13
Match length	74
% identity	50
NCBI Description	probable integrase - common tobacco (fragment). >gi_530742_emb_CAA56791_ (X80830) integrase [Nicotiana tabacum]

Seq. No.	228418
Seq. ID	LIB3196-006-P1-M1-E12
Method	BLASTX
NCBI GI	g3915742
BLAST score	580
E value	3.0e-60
Match length	121
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228419
Seq. ID	LIB3196-006-P1-M1-E2
Method	BLASTX
NCBI GI	g544129
BLAST score	433
E value	5.0e-43
Match length	114
% identity	74
NCBI Description	VIGNAIN PRECURSOR (BEAN ENDOPEPTIDASE) (CYSTEINE PROTEINASE EP-C1) >gi_20994_emb_CAA44816_ (X63102) endopeptidase [Phaseolus vulgaris]

Seq. No.	228420
Seq. ID	LIB3196-006-P1-M1-E7
Method	BLASTX
NCBI GI	g1245046
BLAST score	607
E value	3.0e-63
Match length	130
% identity	87
NCBI Description	(U45285) specific 116-kDa vacuolar proton pump subunit [Homo sapiens]

Seq. No.	228421
Seq. ID	LIB3196-006-P1-M1-E8
Method	BLASTX
NCBI GI	g479532
BLAST score	457
E value	1.0e-45
Match length	94
% identity	99
NCBI Description	GTP-binding regulatory protein Gs alpha chain - human >gi_1335091_emb_CAA39484_ (X56009) alpha subunit of GsGTP binding protein [Homo sapiens]

Seq. No.	228422
Seq. ID	LIB3196-006-P1-M1-E9
Method	BLASTX
NCBI GI	g207905
BLAST score	609
E value	1.0e-63
Match length	127
% identity	91
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	228423
Seq. ID	LIB3196-006-P1-M1-F10
Method	BLASTX
NCBI GI	g2136189
BLAST score	586
E value	7.0e-61
Match length	115
% identity	97
NCBI Description	specific granule protein, 28K, precusor - human >gi_1213613_emb_CAA63984_ (X94323) SGP28 protein [Homo sapiens] >gi_1587691_prf__2207217A SGP28 protein [Homo sapiens]

Seq. No.	228424
Seq. ID	LIB3196-006-P1-M1-F11
Method	BLASTX
NCBI GI	g4457221
BLAST score	184
E value	1.0e-13
Match length	56
% identity	62
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No.	228425
Seq. ID	LIB3196-006-P1-M1-F12
Method	BLASTX
NCBI GI	g4335763
BLAST score	250
E value	2.0e-21
Match length	88
% identity	51
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	228426
Seq. ID	LIB3196-006-P1-M1-F2
Method	BLASTX
NCBI GI	g3043584
BLAST score	643
E value	2.0e-67
Match length	132
% identity	96
NCBI Description	(AB011102) KIAA0530 protein [Homo sapiens]

Seq. No.	228427
Seq. ID	LIB3196-006-P1-M1-F5
Method	BLASTX

NCBI GI	g3885334
BLAST score	554
E value	4.0e-57
Match length	126
% identity	82
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	228428
Seq. ID	LIB3196-006-P1-M1-F6
Method	BLASTX
NCBI GI	g113339
BLAST score	651
E value	2.0e-68
Match length	131
% identity	95
NCBI Description	ADENOSINE DEAMINASE (ADENOSINE AMINOHYDROLASE) >gi_67782_pir__DUHUA adenosine deaminase (EC 3.5.4.4) - human >gi_28380_emb_CAA26734_ (X02994) adenosine deaminase [Homo sapiens] >gi_178077 (M13792) adenosine deaminase [Homo sapiens]

Seq. No.	228429
Seq. ID	LIB3196-006-P1-M1-G12
Method	BLASTX
NCBI GI	g547751
BLAST score	625
E value	2.0e-65
Match length	127
% identity	99
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (39.1) (VERSION 1) >gi_422802_pir__S30433 keratin 17, cytoskeletal - human >gi_30379_emb_CAA79626_ (Z19574) cytokeratin 17 [Homo sapiens] >gi_34075_emb_CAA44451_ (X62571) keratin related product [Homo sapiens] >gi_4557701_ref_NP_000413.1_pKRT17_ keratin

Seq. No.	228430
Seq. ID	LIB3196-006-P1-M1-G8
Method	BLASTX
NCBI GI	g137578
BLAST score	545
E value	4.0e-56
Match length	125
% identity	89
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228431
Seq. ID	LIB3196-006-P1-M1-G9
Method	BLASTX
NCBI GI	g547753
BLAST score	619

E value	8.0e-65
Match length	130
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	228432
Seq. ID	LIB3196-006-P1-M1-H1
Method	BLASTX
NCBI GI	g125080
BLAST score	387
E value	2.0e-37
Match length	76
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228433
Seq. ID	LIB3196-006-P1-M1-H3
Method	BLASTX
NCBI GI	g1346349
BLAST score	611
E value	8.0e-64
Match length	123
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II - human >gi_908805 (L42612) keratin type II [Homo sapiens]

Seq. No.	228434
Seq. ID	LIB3196-006-P1-M1-H4
Method	BLASTX
NCBI GI	g337760
BLAST score	520
E value	3.0e-53
Match length	107
% identity	38
NCBI Description	(M60255) cerebroside sulfate activator protein [Homo sapiens]

Seq. No.	228435
Seq. ID	LIB3196-006-P1-M1-H8
Method	BLASTX
NCBI GI	g1711507
BLAST score	378
E value	2.0e-36
Match length	91
% identity	76
NCBI Description	SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) >gi_624221 (U19030) signal recognition particle 19 kDa protein subunit SRP19 [Oryza sativa]

Seq. No.	228436
Seq. ID	LIB3196-006-P1-M1-H9
Method	BLASTX

Doc No = 4004000

NCBI GI	g3894178
BLAST score	428
E value	2.0e-42
Match length	125
% identity	68
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	228437
Seq. ID	LIB3196-007-P1-M1-A10
Method	BLASTX
NCBI GI	g129951
BLAST score	409
E value	2.0e-42
Match length	94
% identity	83
NCBI Description	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) >gi_72060_pir__NBHUC8 decorin precursor - human >gi_181170 (M14219) proteoglycan core protein [Homo sapiens] >gi_4503271_ref_NP_001911.1_pDCN_ decorin

Seq. No.	228438
Seq. ID	LIB3196-007-P1-M1-A2
Method	BLASTX
NCBI GI	g125080
BLAST score	529
E value	2.0e-54
Match length	108
% identity	99
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228439
Seq. ID	LIB3196-007-P1-M1-A6
Method	BLASTX
NCBI GI	g3970680
BLAST score	222
E value	4.0e-18
Match length	68
% identity	59
NCBI Description	(AL034388) 67A9.b [Drosophila melanogaster]

Seq. No.	228440
Seq. ID	LIB3196-007-P1-M1-A8
Method	BLASTX
NCBI GI	g730832
BLAST score	174
E value	1.0e-12
Match length	53
% identity	58
NCBI Description	8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN) (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi_18748_emb_CAA78359_ (Z13956) a protein similar to

potato tuber protein p322 homolgous to Bowman-Birk Proteinase Inhibitor [Glycine max]

Seq. No.	228441
Seq. ID	LIB3196-007-P1-M1-B10
Method	BLASTX
NCBI GI	g4263711
BLAST score	277
E value	2.0e-24
Match length	63
% identity	76
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	228442
Seq. ID	LIB3196-007-P1-M1-B12
Method	BLASTX
NCBI GI	g1653702
BLAST score	204
E value	2.0e-16
Match length	61
% identity	66
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	228443
Seq. ID	LIB3196-007-P1-M1-B2
Method	BLASTX
NCBI GI	g2500378
BLAST score	419
E value	3.0e-41
Match length	83
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	228444
Seq. ID	LIB3196-007-P1-M1-B3
Method	BLASTX
NCBI GI	g4539292
BLAST score	244
E value	9.0e-21
Match length	47
% identity	91
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	228445
Seq. ID	LIB3196-007-P1-M1-B5
Method	BLASTX
NCBI GI	g167367
BLAST score	489
E value	2.0e-49
Match length	128
% identity	76
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No. 228446

Seq. ID LIB3196-007-P1-M1-C1
Method BLASTX
NCBI GI g423072
BLAST score 198
E value 3.0e-15
Match length 136
% identity 35
NCBI Description ribosomal protein L7 - human >gi_1335288_emb_CAA41026_ (X57958) ribosomal protein L7 [Homo sapiens]

Seq. No. 228447
Seq. ID LIB3196-007-P1-M1-C11
Method BLASTX
NCBI GI g87774
BLAST score 628
E value 9.0e-66
Match length 128
% identity 99
NCBI Description hypothetical protein - human (clone 266) (fragment) >gi_34081_emb_CAA29248_ (X05803) gene product (clone 266) (266 AA) [Homo sapiens]

Seq. No. 228448
Seq. ID LIB3196-007-P1-M1-C12
Method BLASTX
NCBI GI g136479
BLAST score 502
E value 5.0e-51
Match length 99
% identity 99
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23) >gi_88948_pir__S06590 IgE-dependent histamine-releasing factor - human >gi_37496_emb_CAA34200_ (X16064) tumor protein (AA 1 - 172) [Homo sapiens] >gi_4507669_ref_NP_003286.1_pTPT1_ tumor protein, translationally-controlled

Seq. No. 228449
Seq. ID LIB3196-007-P1-M1-C2
Method BLASTX
NCBI GI g81546
BLAST score 522
E value 2.0e-53
Match length 119
% identity 88
NCBI Description alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No. 228450
Seq. ID LIB3196-007-P1-M1-C3
Method BLASTX
NCBI GI g163412
BLAST score 550
E value 1.0e-56
Match length 105
% identity 97
NCBI Description (M63009) NADH dehydrogenase [Bos taurus]

Seq. No.	228451
Seq. ID	LIB3196-007-P1-M1-C6
Method	BLASTX
NCBI GI	g1658197
BLAST score	591
E value	2.0e-61
Match length	125
% identity	86
NCBI Description	(U74630) calreticulin [Ricinus communis] >gi_1763297 (U74631) calreticulin [Ricinus communis]

Seq. No.	228452
Seq. ID	LIB3196-007-P1-M1-C8
Method	BLASTX
NCBI GI	g1362093
BLAST score	452
E value	4.0e-45
Match length	108
% identity	75
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	228453
Seq. ID	LIB3196-007-P1-M1-C9
Method	BLASTX
NCBI GI	g3298540
BLAST score	564
E value	2.0e-58
Match length	119
% identity	87
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No.	228454
Seq. ID	LIB3196-007-P1-M1-D2
Method	BLASTX
NCBI GI	g3688598
BLAST score	530
E value	3.0e-54
Match length	115
% identity	83
NCBI Description	(AB009029) Cycloartenol Synthase [Panax ginseng]

Seq. No.	228455
Seq. ID	LIB3196-007-P1-M1-D6
Method	BLASTX
NCBI GI	g133041
BLAST score	520
E value	4.0e-53
Match length	100
% identity	100
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi_71137_pir__R5HUP0 acidic ribosomal protein P0 - human >gi_190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041) [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_

ribosomal protein, large, P0

Seq. No.	228456
Seq. ID	LIB3196-007-P1-M1-D7
Method	BLASTX
NCBI GI	g133041
BLAST score	182
E value	5.0e-14
Match length	50
% identity	74
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi_71137_pir__R5HUP0 acidic ribosomal protein P0 - human >gi_190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041) [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_ ribosomal protein, large, P0

Seq. No.	228457
Seq. ID	LIB3196-007-P1-M1-D9
Method	BLASTX
NCBI GI	g1076316
BLAST score	162
E value	3.0e-11
Match length	74
% identity	45
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	228458
Seq. ID	LIB3196-007-P1-M1-E11
Method	BLASTX
NCBI GI	g224877
BLAST score	502
E value	5.0e-51
Match length	99
% identity	96
NCBI Description	deaminase a,adenosine [Homo sapiens]

Seq. No.	228459
Seq. ID	LIB3196-007-P1-M1-E2
Method	BLASTX
NCBI GI	g2352925
BLAST score	138
E value	4.0e-19
Match length	113
% identity	56
NCBI Description	(AF012864) plastidic 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2 [Petroselinum crispum]

Seq. No.	228460
Seq. ID	LIB3196-007-P1-M1-E4
Method	BLASTX
NCBI GI	g1723292
BLAST score	245
E value	8.0e-21

Match length	130
% identity	42
NCBI Description	HYPOTHETICAL 60.5 KD PROTEIN C13D6.04C IN CHROMOSOME I >gi_1204166_emb_CAA93544_ (Z69725) unknown [Schizosaccharomyces pombe]

Seq. No.	228461
Seq. ID	LIB3196-007-P1-M1-E9
Method	BLASTX
NCBI GI	g4558591
BLAST score	430
E value	1.0e-42
Match length	112
% identity	71
NCBI Description	(AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	228462
Seq. ID	LIB3196-007-P1-M1-F1
Method	BLASTX
NCBI GI	g2736151
BLAST score	215
E value	3.0e-17
Match length	82
% identity	50
NCBI Description	(AF021935) mytonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]

Seq. No.	228463
Seq. ID	LIB3196-007-P1-M1-F10
Method	BLASTX
NCBI GI	g115492
BLAST score	475
E value	8.0e-48
Match length	94
% identity	52
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	228464
Seq. ID	LIB3196-007-P1-M1-F3
Method	BLASTX
NCBI GI	g2129636
BLAST score	248
E value	3.0e-21
Match length	110
% identity	52
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	228465
Seq. ID	LIB3196-007-P1-M1-F4
Method	BLASTX
NCBI GI	g4415996
BLAST score	676
E value	2.0e-71
Match length	130

% identity	98
NCBI Description	(AF059290) beta-tubulin 4 [Eleusine indica]

Seq. No.	228466
Seq. ID	LIB3196-007-P1-M1-F5
Method	BLASTX
NCBI GI	g3212854
BLAST score	164
E value	2.0e-11
Match length	128
% identity	38
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	228467
Seq. ID	LIB3196-007-P1-M1-F6
Method	BLASTX
NCBI GI	g1483218
BLAST score	547
E value	3.0e-56
Match length	129
% identity	75
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	228468
Seq. ID	LIB3196-007-P1-M1-G10
Method	BLASTX
NCBI GI	g1170097
BLAST score	569
E value	8.0e-59
Match length	118
% identity	89
NCBI Description	GLUTATHIONE S-TRANSFERASE MU 5 (GSTM5-5) (CLASS-MU) >gi_423000_pir__A46048 glutathione transferase (EC 2.5.1.18) class mu, GSTM5 - human >gi_468260 (L02321) glutathione S-transferase GSTM5-5 [Homo sapiens] >gi_4504181_ref_NP_000842.1_pGSTM5_ glutathione S-transferase M5

Seq. No.	228469
Seq. ID	LIB3196-007-P1-M1-G11
Method	BLASTX
NCBI GI	g125077
BLAST score	158
E value	1.0e-10
Match length	31
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	228470
Seq. ID	LIB3196-007-P1-M1-G2
Method	BLASTX
NCBI GI	g3023858
BLAST score	615

E value	3.0e-64
Match length	128
% identity	55
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	228471
Seq. ID	LIB3196-007-P1-M1-G3
Method	BLASTX
NCBI GI	g232031
BLAST score	220
E value	6.0e-18
Match length	67
% identity	60
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	228472
Seq. ID	LIB3196-007-P1-M1-G6
Method	BLASTX
NCBI GI	g461776
BLAST score	304
E value	1.0e-27
Match length	53
% identity	96
NCBI Description	CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) >gi_251369_bbs_108679 (S40060) spr1=small proline rich squamous cell marker [Rhesus monkeys, tracheobronchial epithelium, Peptide, 89 aa] [Rhesus monkeys] >gi_342297 (M83999) small proline-rich protein [Macaca mulatta]

Seq. No.	228473
Seq. ID	LIB3196-007-P1-M1-H1
Method	BLASTX
NCBI GI	g3861488
BLAST score	324
E value	4.0e-30
Match length	77
% identity	82
NCBI Description	(AF060902) vesicle soluble NSF attachment protein receptor VTI2 [Homo sapiens]

Seq. No.	228474
Seq. ID	LIB3196-007-P1-M1-H11
Method	BLASTX
NCBI GI	g4406656
BLAST score	434
E value	5.0e-43
Match length	98
% identity	86
NCBI Description	(AF131820) Unknown [Homo sapiens]

Seq. No.	228475

Seq. ID	LIB3196-007-P1-M1-H3
Method	BLASTX
NCBI GI	g547008
BLAST score	279
E value	7.0e-25
Match length	122
% identity	52
NCBI Description	(S70314) alpha-adducin=calmodulin-binding protein {alternatively spliced, clone IT10C1} [human, frontal cortex, Peptide Partial, 207 aa] [Homo sapiens]

Seq. No.	228476
Seq. ID	LIB3196-007-P1-M1-H5
Method	BLASTX
NCBI GI	g2244898
BLAST score	247
E value	4.0e-21
Match length	69
% identity	68
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	228477
Seq. ID	LIB3196-007-P1-M1-H6
Method	BLASTX
NCBI GI	g2160694
BLAST score	205
E value	3.0e-16
Match length	72
% identity	58
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	228478
Seq. ID	LIB3196-007-P1-M1-H8
Method	BLASTX
NCBI GI	g1717824
BLAST score	372
E value	1.0e-35
Match length	84
% identity	50
NCBI Description	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN) >gi_950004 (U25147) citrate transporter protein [Homo sapiens]

Seq. No.	228479
Seq. ID	LIB3196-008-P1-M1-A11
Method	BLASTX
NCBI GI	g3294467
BLAST score	226
E value	1.0e-22
Match length	63
% identity	90
NCBI Description	(U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 228480

Seq. ID	LIB3196-008-P1-M1-A12
Method	BLASTX
NCBI GI	g1843399
BLAST score	258
E value	2.0e-22
Match length	61
% identity	87
NCBI Description	(AB000467) unnamed protein product [Homo sapiens]

Seq. No.	228481
Seq. ID	LIB3196-008-P1-M1-A3
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	9.0e-20
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	228482
Seq. ID	LIB3196-008-P1-M1-A4
Method	BLASTX
NCBI GI	g119530
BLAST score	651
E value	2.0e-68
Match length	128
% identity	98
NCBI Description	PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) >gi_87320_pir__A23723 protein disulfide-isomerase (EC 5.3.4.1) ERp72 precursor - human >gi_181508 (J05016) protein disulfide isomerase-related protein [Homo sapiens]

Seq. No.	228483
Seq. ID	LIB3196-008-P1-M1-A5
Method	BLASTX
NCBI GI	g87653
BLAST score	273
E value	3.0e-24
Match length	78
% identity	76
NCBI Description	heterogeneous ribonuclear particle protein C - human >gi_306875 (M16342) C protein [Homo sapiens]

Seq. No.	228484
Seq. ID	LIB3196-008-P1-M1-B11
Method	BLASTX
NCBI GI	g125077
BLAST score	442
E value	2.0e-44
Match length	92
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	228485
Seq. ID	LIB3196-008-P1-M1-B12
Method	BLASTX
NCBI GI	g1346347
BLAST score	427
E value	2.0e-42
Match length	107
% identity	85
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	228486
Seq. ID	LIB3196-008-P1-M1-B2
Method	BLASTX
NCBI GI	g1885356
BLAST score	205
E value	9.0e-17
Match length	45
% identity	82
NCBI Description	(U59323) type 1 RNA helicase pNORF1 [Homo sapiens]

Seq. No.	228487
Seq. ID	LIB3196-008-P1-M1-B3
Method	BLASTX
NCBI GI	g346219
BLAST score	245
E value	7.0e-21
Match length	124
% identity	51
NCBI Description	keratin K4a - human (fragment)

Seq. No.	228488
Seq. ID	LIB3196-008-P1-M1-B4
Method	BLASTX
NCBI GI	g137578
BLAST score	596
E value	5.0e-62
Match length	117
% identity	97
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228489
Seq. ID	LIB3196-008-P1-M1-B9
Method	BLASTX
NCBI GI	g284779
BLAST score	184
E value	3.0e-26
Match length	76
% identity	73
NCBI Description	Ras guanine nucleotide exchange factor son-of-sevenless

(sos) 1 - mouse >gi_54135_emb_CAA77662_ (Z11574) mouse Son of sevenless 1 [Mus musculus]

Seq. No.	228490
Seq. ID	LIB3196-008-P1-M1-C1
Method	BLASTX
NCBI GI	g3868758
BLAST score	235
E value	5.0e-20
Match length	59
% identity	75
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	228491
Seq. ID	LIB3196-008-P1-M1-C11
Method	BLASTX
NCBI GI	g3334405
BLAST score	432
E value	5.0e-43
Match length	91
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	228492
Seq. ID	LIB3196-008-P1-M1-C12
Method	BLASTX
NCBI GI	g484102
BLAST score	227
E value	8.0e-19
Match length	97
% identity	52
NCBI Description	(U02082) guanine nucleotide regulatory protein [Homo sapiens] >gi_3041860 (AC004534) guanine nucleotide regulatory protein [Homo sapiens]

Seq. No.	228493
Seq. ID	LIB3196-008-P1-M1-C2
Method	BLASTX
NCBI GI	g3334115
BLAST score	335
E value	2.0e-31
Match length	84
% identity	80
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	228494
Seq. ID	LIB3196-008-P1-M1-C6
Method	BLASTX
NCBI GI	g2315449
BLAST score	190
E value	2.0e-14
Match length	84

% identity	45
NCBI Description	(AF016448) similar to Saccharomyces cerevisiae nuclear protein SNF7 (SP:P39929)in one region and the chromosome segregation protein SMC2 (SP:P38989) in another [Caenorhabditis elegans]

Seq. No.	228495
Seq. ID	LIB3196-008-P1-M1-D10
Method	BLASTX
NCBI GI	g1703121
BLAST score	646
E value	7.0e-68
Match length	127
% identity	99
NCBI Description	ACTIN, CYTOPLASMIC TYPE 5 >gi_63007_emb_CAA26486_ (X02648) put. type 5 nonmuscle actin [Gallus gallus]

Seq. No.	228496
Seq. ID	LIB3196-008-P1-M1-D11
Method	BLASTX
NCBI GI	g3935151
BLAST score	307
E value	2.0e-28
Match length	89
% identity	61
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	228497
Seq. ID	LIB3196-008-P1-M1-D9
Method	BLASTX
NCBI GI	g462013
BLAST score	565
E value	2.0e-58
Match length	125
% identity	90
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	228498
Seq. ID	LIB3196-008-P1-M1-E12
Method	BLASTX
NCBI GI	g4510347
BLAST score	155
E value	2.0e-10
Match length	60
% identity	55
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228499
Seq. ID	LIB3196-008-P1-M1-E2
Method	BLASTX
NCBI GI	g2995405
BLAST score	357
E value	5.0e-34
Match length	118

% identity	58
NCBI Description	(Y12432) polyprotein [Ananas comosus]
Seq. No.	228500
Seq. ID	LIB3196-008-P1-M1-E4
Method	BLASTX
NCBI GI	g119165
BLAST score	411
E value	3.0e-41
Match length	127
% identity	72
NCBI Description	ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) >gi_105918_pir__S22655 translation elongation factor eEF-1 gamma chain - human >gi_31102_emb_CAA45089_ (X63526) homologue to elongation factor 1-gamma from A.salina [Homo sapiens] >gi_31104_emb_CAA77630_ (Z11531) elongation factor-1-gamma [Homo sapiens] >gi_4503481_ref_NP_001395.1_pEEF1G_ eukaryotic translation elongation factor 1 gamma
Seq. No.	228501
Seq. ID	LIB3196-008-P1-M1-E5
Method	BLASTX
NCBI GI	g2252630
BLAST score	142
E value	3.0e-09
Match length	45
% identity	64
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]
Seq. No.	228502
Seq. ID	LIB3196-008-P1-M1-E6
Method	BLASTX
NCBI GI	g1663567
BLAST score	364
E value	8.0e-35
Match length	72
% identity	92
NCBI Description	(U60800) semaphorin [Homo sapiens]
Seq. No.	228503
Seq. ID	LIB3196-008-P1-M1-E8
Method	BLASTX
NCBI GI	g167367
BLAST score	425
E value	3.0e-42
Match length	101
% identity	82
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	228504
Seq. ID	LIB3196-008-P1-M1-F1
Method	BLASTX
NCBI GI	g113950
BLAST score	355
E value	4.0e-34
Match length	70

% identity	66
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II - human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo sapiens]
Seq. No.	228505
Seq. ID	LIB3196-008-P1-M1-F11
Method	BLASTX
NCBI GI	g4325372
BLAST score	227
E value	7.0e-19
Match length	99
% identity	42
NCBI Description	(AF128396) contains similarity to protein disulfide isomerases [Arabidopsis thaliana]
Seq. No.	228506
Seq. ID	LIB3196-008-P1-M1-F2
Method	BLASTX
NCBI GI	g423485
BLAST score	151
E value	4.0e-10
Match length	55
% identity	64
NCBI Description	interferon response element-binding factor IREBF-2 - mouse (fragment) >gi_293675 (L13610) IFN-response element binding factor 2 [Mus musculus]
Seq. No.	228507
Seq. ID	LIB3196-008-P1-M1-F7
Method	BLASTX
NCBI GI	g1362009
BLAST score	429
E value	1.0e-42
Match length	106
% identity	50
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana
Seq. No.	228508
Seq. ID	LIB3196-008-P1-M1-F8
Method	BLASTX
NCBI GI	g137578
BLAST score	456
E value	7.0e-46
Match length	90
% identity	98
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	228509
Seq. ID	LIB3196-008-P1-M1-G1

Method	BLASTX
NCBI GI	g1350984
BLAST score	314
E value	5.0e-29
Match length	71
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S3A >gi_469248 (L31645) ribosomal protein S3a [Helianthus annuus]

Seq. No.	228510
Seq. ID	LIB3196-008-P1-M1-G10
Method	BLASTX
NCBI GI	g3776005
BLAST score	165
E value	1.0e-11
Match length	40
% identity	82
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	228511
Seq. ID	LIB3196-008-P1-M1-G11
Method	BLASTX
NCBI GI	g2224549
BLAST score	557
E value	1.0e-57
Match length	104
% identity	99
NCBI Description	(AB002302) KIAA0304 [Homo sapiens]

Seq. No.	228512
Seq. ID	LIB3196-008-P1-M1-G12
Method	BLASTX
NCBI GI	g1709233
BLAST score	314
E value	5.0e-29
Match length	94
% identity	67
NCBI Description	NADH-CYTOCHROME B5 REDUCTASE >gi_162941 (M83104) cytochrome b-5 reductase [Bos taurus]

Seq. No.	228513
Seq. ID	LIB3196-008-P1-M1-G5
Method	BLASTX
NCBI GI	g129881
BLAST score	576
E value	1.0e-59
Match length	126
% identity	90
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_482294_pir__A36094 pyrophosphate--fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - potato (cv. Kennebec) >gi_169538 (M55190) pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No.	228514
Seq. ID	LIB3196-008-P1-M1-H12
Method	BLASTX
NCBI GI	g137578
BLAST score	518
E value	5.0e-53
Match length	99
% identity	98
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228515
Seq. ID	LIB3196-008-P1-M1-H2
Method	BLASTX
NCBI GI	g1731146
BLAST score	191
E value	2.0e-14
Match length	49
% identity	71
NCBI Description	HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein [Caenorhabditis elegans]

Seq. No.	228516
Seq. ID	LIB3196-008-P1-M1-H3
Method	BLASTX
NCBI GI	g2072966
BLAST score	314
E value	1.0e-47
Match length	133
% identity	72
NCBI Description	(U93570) p40 [Homo sapiens]

Seq. No.	228517
Seq. ID	LIB3196-008-P1-M1-H6
Method	BLASTX
NCBI GI	g119165
BLAST score	326
E value	3.0e-30
Match length	59
% identity	98
NCBI Description	ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) >gi_105918_pir__S22655 translation elongation factor eEF-1 gamma chain - human >gi_31102_emb_CAA45089_ (X63526) homologue to elongation factor 1-gamma from A.salina [Homo sapiens] >gi_31104_emb_CAA77630_ (Z11531) elongation factor-1-gamma [Homo sapiens] >gi_4503481_ref_NP_001395.1_pEEF1G_ eukaryotic translation elongation factor 1 gamma

Seq. No.	228518
Seq. ID	LIB3196-008-P1-M1-H7
Method	BLASTX

NCBI GI	g585241
BLAST score	151
E value	7.0e-10
Match length	85
% identity	47
NCBI Description	HISTONE H1 >gi_629668_pir__S45662 histone H1 - tomato >gi_424100 (U03391) histone H1 [Lycopersicon esculentum]

Seq. No.	228519
Seq. ID	LIB3196-008-P1-M1-H8
Method	BLASTX
NCBI GI	g2997745
BLAST score	301
E value	1.0e-27
Match length	65
% identity	92
NCBI Description	(AF054840) tetraspan TM4SF; Tspan-3 [Homo sapiens]

Seq. No.	228520
Seq. ID	LIB3196-009-P1-M1-A11
Method	BLASTX
NCBI GI	g137578
BLAST score	562
E value	4.0e-58
Match length	113
% identity	97
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228521
Seq. ID	LIB3196-009-P1-M1-A12
Method	BLASTX
NCBI GI	g3123349
BLAST score	206
E value	2.0e-16
Match length	85
% identity	48
NCBI Description	(AJ005788) hypothetical protein [Cicer arietinum]

Seq. No.	228522
Seq. ID	LIB3196-009-P1-M1-A2
Method	BLASTX
NCBI GI	g100488
BLAST score	266
E value	2.0e-23
Match length	88
% identity	57
NCBI Description	TNP2 protein - garden snapdragon

Seq. No.	228523
Seq. ID	LIB3196-009-P1-M1-A5
Method	BLASTX
NCBI GI	g2135748

BLAST score	300
E value	1.0e-27
Match length	84
% identity	35
NCBI Description	MLN 62 protein - human >gi_2135749_pir__S60681 MLN 62 protein - human >gi_951277_emb_CAA56491_ (X80200) cystein rich domain associated to RING and TRAF protein [Homo sapiens]

Seq. No.	228524
Seq. ID	LIB3196-009-P1-M1-B1
Method	BLASTX
NCBI GI	g1037127
BLAST score	666
E value	3.0e-70
Match length	133
% identity	95
NCBI Description	Mig-6=mitogen-inducible gene mig-6 product [human, WI-38 cells, Peptide, 462 aa]

Seq. No.	228525
Seq. ID	LIB3196-009-P1-M1-B4
Method	BLASTX
NCBI GI	g804996
BLAST score	252
E value	1.0e-21
Match length	64
% identity	77
NCBI Description	(Z49216) mitoxantrone-resistance associated gene [Homo sapiens]

Seq. No.	228526
Seq. ID	LIB3196-009-P1-M1-B7
Method	BLASTX
NCBI GI	g3043714
BLAST score	509
E value	6.0e-52
Match length	117
% identity	85
NCBI Description	(AB011167) KIAA0595 protein [Homo sapiens]

Seq. No.	228527
Seq. ID	LIB3196-009-P1-M1-B8
Method	BLASTX
NCBI GI	g547712
BLAST score	550
E value	1.0e-56
Match length	110
% identity	97
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	228528
Seq. ID	LIB3196-009-P1-M1-C1
Method	BLASTX

NCBI GI g181969
BLAST score 440
E value 8.0e-44
Match length 113
% identity 79
NCBI Description (M19997) elongation factor 2 [Homo sapiens]

Seq. No. 228529
Seq. ID LIB3196-009-P1-M1-C10
Method BLASTX
NCBI GI g2920535
BLAST score 146
E value 2.0e-09
Match length 76
% identity 49
NCBI Description (AF018081) type XVIII collagen [Homo sapiens]

Seq. No. 228530
Seq. ID LIB3196-009-P1-M1-C11
Method BLASTX
NCBI GI g113287
BLAST score 701
E value 2.0e-74
Match length 130
% identity 100
NCBI Description ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1)
>gi_71610_pir__ATHU actin, skeletal muscle - human
>gi_71612_pir__ATRT actin, skeletal muscle - rat
>gi_71613_pir__ATCH actin alpha, skeletal muscle - chicken
>gi_90264_pir__A24904 actin, skeletal muscle - mouse
>gi_55577_emb_CAA24529_ (V01218) actin [Rattus norvegicus]
>gi_63029_emb_CAA24753_ (V01507) a-actin [Gallus gallus]
>gi_178029 (J00068) alpha-actin [Homo sapiens] >gi_309088
(M12866) actin [Mus musculus] >gi_337746 (M20543)
alpha-skeletal actin precursor [Homo sapiens] >gi_387081
(M12347) alpha-actin [Mus musculus] >gi_790202 (U16368)
skeletal alpha actin [Sus scrofa] >gi_223503_prf__0809315A
actin [Rattus norvegicus]
>gi_4501881_ref_NP_001091.1_pACTA1_ actin, alpha 1,
skeletal muscle

Seq. No. 228531
Seq. ID LIB3196-009-P1-M1-C12
Method BLASTX
NCBI GI g4539005
BLAST score 194
E value 6.0e-15
Match length 122
% identity 36
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 228532
Seq. ID LIB3196-009-P1-M1-C2
Method BLASTX
NCBI GI g1945609
BLAST score 599
E value 2.0e-62

Match length	124
% identity	100
NCBI Description	(AB003102) 26S proteasome subunit p44.5 [Homo sapiens]

Seq. No.	228533
Seq. ID	LIB3196-009-P1-M1-C5
Method	BLASTX
NCBI GI	g3845568
BLAST score	199
E value	2.0e-15
Match length	77
% identity	52
NCBI Description	(AB012042) keratin 6 beta [Mus musculus]

Seq. No.	228534
Seq. ID	LIB3196-009-P1-M1-C6
Method	BLASTX
NCBI GI	g1170097
BLAST score	257
E value	3.0e-22
Match length	59
% identity	85
NCBI Description	GLUTATHIONE S-TRANSFERASE MU 5 (GSTM5-5) (CLASS-MU) >gi_423000_pir__A46048 glutathione transferase (EC 2.5.1.18) class mu, GSTM5 - human >gi_468260 (L02321) glutathione S-transferase GSTM5-5 [Homo sapiens] >gi_4504181_ref_NP_000842.1_pGSTM5_ glutathione S-transferase M5

Seq. No.	228535
Seq. ID	LIB3196-009-P1-M1-C7
Method	BLASTX
NCBI GI	g3738257
BLAST score	458
E value	7.0e-46
Match length	96
% identity	94
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	228536
Seq. ID	LIB3196-009-P1-M1-C9
Method	BLASTX
NCBI GI	g2119228
BLAST score	189
E value	3.0e-14
Match length	111
% identity	46
NCBI Description	keratin K4a - human (fragment) >gi_313159_emb_CAA47914_ (X67683) keratin K4a [Homo sapiens]

Seq. No.	228537
Seq. ID	LIB3196-009-P1-M1-D1
Method	BLASTX
NCBI GI	g730832
BLAST score	159
E value	7.0e-11

Match length	53
% identity	53
NCBI Description	8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN) (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi_18748_emb_CAA78359_ (Z13956) a protein similar to potato tuber protein p322 homolgous to Bowman-Birk Proteinase Inhibitor [Glycine max]

Seq. No.	228538
Seq. ID	LIB3196-009-P1-M1-D10
Method	BLASTX
NCBI GI	g3776559
BLAST score	251
E value	1.0e-21
Match length	56
% identity	79
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	228539
Seq. ID	LIB3196-009-P1-M1-D2
Method	BLASTX
NCBI GI	g2072425
BLAST score	281
E value	4.0e-25
Match length	54
% identity	98
NCBI Description	(U83115) non-lens beta gamma-crystallin like protein [Homo sapiens]

Seq. No.	228540
Seq. ID	LIB3196-009-P1-M1-D3
Method	BLASTX
NCBI GI	g2500354
BLAST score	499
E value	8.0e-51
Match length	101
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No.	228541
Seq. ID	LIB3196-009-P1-M1-D4
Method	BLASTX
NCBI GI	g1916613
BLAST score	192
E value	1.0e-14
Match length	94
% identity	50
NCBI Description	(U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]

Seq. No.	228542
Seq. ID	LIB3196-009-P1-M1-D5
Method	BLASTX

NCBI GI	g1082337
BLAST score	654
E value	8.0e-69
Match length	131
% identity	94
NCBI Description	DNA helicase Q1 - human >gi_531243_dbj_BAA07200_ (D37984) DNA helicase Q1 [Homo sapiens]

Seq. No.	228543
Seq. ID	LIB3196-009-P1-M1-D7
Method	BLASTX
NCBI GI	g3641280
BLAST score	170
E value	4.0e-12
Match length	33
% identity	100
NCBI Description	(AF074382) IkB kinase gamma subunit [Homo sapiens] >gi_4504631_ref_NP_003630.1_pIKBKG_ inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma

Seq. No.	228544
Seq. ID	LIB3196-009-P1-M1-D8
Method	BLASTX
NCBI GI	g2501439
BLAST score	464
E value	1.0e-46
Match length	99
% identity	87
NCBI Description	UBIQUITIN FUSION DEGRADATION PROTEIN 1 HOMOLOG (UB FUSION PROTEIN 1) >gi_1654348 (U64445) ubiquitin fusion-degradation 1 like protein; UFD1p [Mus musculus]

Seq. No.	228545
Seq. ID	LIB3196-009-P1-M1-D9
Method	BLASTX
NCBI GI	g2137308
BLAST score	530
E value	3.0e-54
Match length	102
% identity	40
NCBI Description	G protein beta subuit like - mouse >gi_475012_dbj_BAA06185_ (D29802) G protein beta subuit like [Mus musculus]

Seq. No.	228546
Seq. ID	LIB3196-009-P1-M1-E3
Method	BLASTX
NCBI GI	g120669
BLAST score	441
E value	7.0e-44
Match length	88
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	228547
Seq. ID	LIB3196-009-P1-M1-E4
Method	BLASTX
NCBI GI	g2196542
BLAST score	179
E value	3.0e-13
Match length	45
% identity	76
NCBI Description	(AF001894) glycine-rich protein [Oryza sativa]

Seq. No.	228548
Seq. ID	LIB3196-009-P1-M1-F1
Method	BLASTX
NCBI GI	g3319958
BLAST score	575
E value	2.0e-59
Match length	115
% identity	11
NCBI Description	(AJ228139) VAKTI precursor [Homo sapiens]

Seq. No.	228549
Seq. ID	LIB3196-009-P1-M1-F10
Method	BLASTX
NCBI GI	g1407625
BLAST score	174
E value	1.0e-12
Match length	32
% identity	56
NCBI Description	(U40317) PTPsigma [Homo sapiens]

Seq. No.	228550
Seq. ID	LIB3196-009-P1-M1-F11
Method	BLASTX
NCBI GI	g167367
BLAST score	374
E value	4.0e-36
Match length	102
% identity	72
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	228551
Seq. ID	LIB3196-009-P1-M1-F2
Method	BLASTX
NCBI GI	g2642435
BLAST score	447
E value	1.0e-44
Match length	104
% identity	79
NCBI Description	(AC002391) MYB-related protein [Arabidopsis thaliana]

Seq. No.	228552
Seq. ID	LIB3196-009-P1-M1-F9
Method	BLASTX
NCBI GI	g3915742
BLAST score	443
E value	3.0e-44
Match length	96

% identity	89
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228553
Seq. ID	LIB3196-009-P1-M1-G1
Method	BLASTX
NCBI GI	g220141
BLAST score	471
E value	2.0e-47
Match length	88
% identity	99
NCBI Description	(D01038) VLA-3 alpha subunit [Homo sapiens]

Seq. No.	228554
Seq. ID	LIB3196-009-P1-M1-G10
Method	BLASTX
NCBI GI	g4098244
BLAST score	314
E value	5.0e-29
Match length	94
% identity	66
NCBI Description	(U76409) homeobox 1 protein [Lycopersicon esculentum]

Seq. No.	228555
Seq. ID	LIB3196-009-P1-M1-G11
Method	BLASTX
NCBI GI	g2135121
BLAST score	387
E value	6.0e-38
Match length	79
% identity	95
NCBI Description	flightless-I homolog - human (fragment) >gi_440177 (U01184) flightless-I homolog [Homo sapiens]

Seq. No.	228556
Seq. ID	LIB3196-009-P1-M1-G3
Method	BLASTX
NCBI GI	g2459420
BLAST score	464
E value	1.0e-46
Match length	112
% identity	82
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	228557
Seq. ID	LIB3196-009-P1-M1-G5
Method	BLASTX
NCBI GI	g4455246
BLAST score	202
E value	3.0e-16
Match length	55
% identity	69
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	228558
Seq. ID	LIB3196-009-P1-M1-G8
Method	BLASTX
NCBI GI	g3980397
BLAST score	427
E value	3.0e-42
Match length	117
% identity	68
NCBI Description	(AC004561) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	228559
Seq. ID	LIB3196-009-P1-M1-G9
Method	BLASTX
NCBI GI	g137578
BLAST score	541
E value	1.0e-55
Match length	103
% identity	100
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228560
Seq. ID	LIB3196-009-P1-M1-H10
Method	BLASTX
NCBI GI	g1890152
BLAST score	259
E value	1.0e-22
Match length	69
% identity	68
NCBI Description	(X92510) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	228561
Seq. ID	LIB3196-009-P1-M1-H12
Method	BLASTX
NCBI GI	g683553
BLAST score	265
E value	3.0e-23
Match length	87
% identity	64
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	228562
Seq. ID	LIB3196-009-P1-M1-H2
Method	BLASTX
NCBI GI	g3122072
BLAST score	585
E value	9.0e-61
Match length	112
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION

	FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]
Seq. No.	228563
Seq. ID	LIB3196-009-P1-M1-H6
Method	BLASTX
NCBI GI	g82228
BLAST score	295
E value	1.0e-26
Match length	72
% identity	85
NCBI Description	hypothetical protein 77 - common tobacco chloroplast >gi_225199_prf__1211235AD ORF 77 [Nicotiana tabacum]
Seq. No.	228564
Seq. ID	LIB3196-009-P1-M1-H9
Method	BLASTX
NCBI GI	g226120
BLAST score	258
E value	9.0e-23
Match length	74
% identity	54
NCBI Description	vicilin gene B [Saguinus oedipus]
Seq. No.	228565
Seq. ID	LIB3196-010-P1-M1-A3
Method	BLASTX
NCBI GI	g3551523
BLAST score	201
E value	1.0e-15
Match length	119
% identity	34
NCBI Description	(AB017026) oxysterol-binding protein [Mus musculus]
Seq. No.	228566
Seq. ID	LIB3196-010-P1-M1-A4
Method	BLASTX
NCBI GI	g2738949
BLAST score	500
E value	9.0e-51
Match length	108
% identity	88
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]
Seq. No.	228567
Seq. ID	LIB3196-010-P1-M1-B1
Method	BLASTX
NCBI GI	g1352450
BLAST score	480
E value	1.0e-48
Match length	97
% identity	99
NCBI Description	INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA) (HEMATOPOIETIN-1) >gi_644806 (U19844) interleukin-1 alpha [Macaca mulatta]

Seq. No.	228568
Seq. ID	LIB3196-010-P1-M1-B10
Method	BLASTX
NCBI GI	g2119228
BLAST score	196
E value	3.0e-15
Match length	67
% identity	61
NCBI Description	keratin K4a - human (fragment) >gi_313159_emb_CAA47914_ (X67683) keratin K4a [Homo sapiens]

Seq. No.	228569
Seq. ID	LIB3196-010-P1-M1-B3
Method	BLASTX
NCBI GI	g2369766
BLAST score	449
E value	9.0e-45
Match length	127
% identity	70
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	228570
Seq. ID	LIB3196-010-P1-M1-B6
Method	BLASTX
NCBI GI	g3063647
BLAST score	491
E value	1.0e-49
Match length	132
% identity	74
NCBI Description	(AF057285) intersectin-EH binding protein Ibp1 [Mus musculus]

Seq. No.	228571
Seq. ID	LIB3196-010-P1-M1-B8
Method	BLASTX
NCBI GI	g2736153
BLAST score	178
E value	5.0e-13
Match length	77
% identity	49
NCBI Description	(AF021936) myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta [Rattus norvegicus]

Seq. No.	228572
Seq. ID	LIB3196-010-P1-M1-C1
Method	BLASTX
NCBI GI	g114127
BLAST score	664
E value	6.0e-70
Match length	130
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 5 >gi_105230_pir__A23741 ADP-ribosylation factor 5 - human >gi_2137130_pir__JC4949 ADP-ribosylation factor type 5 - mouse >gi_178987 (M57567) ADP-ribosylation factor [Homo sapiens] >gi_438870 (L12384) ADP-ribosylation factor 5 [Rattus norvegicus]

	>gi_1565215_dbj_BAA13494_ (D87902) ARF5 [Mus musculus] >gi_2088529 (U73002) ADP-ribosylation factor 5 [Homo sapiens] >gi_4502209_ref_NP_001653.1_pARF5_ ADP-ribosylation factor
Seq. No.	228573
Seq. ID	LIB3196-010-P1-M1-C10
Method	BLASTX
NCBI GI	g3327136
BLAST score	604
E value	5.0e-63
Match length	115
% identity	99
NCBI Description	(AB014561) KIAA0661 protein [Homo sapiens]
Seq. No.	228574
Seq. ID	LIB3196-010-P1-M1-C2
Method	BLASTX
NCBI GI	g2497543
BLAST score	274
E value	3.0e-24
Match length	115
% identity	46
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]
Seq. No.	228575
Seq. ID	LIB3196-010-P1-M1-C3
Method	BLASTX
NCBI GI	g137578
BLAST score	499
E value	1.0e-50
Match length	98
% identity	97
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	228576
Seq. ID	LIB3196-010-P1-M1-C4
Method	BLASTX
NCBI GI	g3947733
BLAST score	204
E value	4.0e-16
Match length	111
% identity	42
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]
Seq. No.	228577
Seq. ID	LIB3196-010-P1-M1-D4
Method	BLASTX
NCBI GI	g2078350
BLAST score	598

E value	3.0e-62
Match length	128
% identity	88
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	228578
Seq. ID	LIB3196-010-P1-M1-D8
Method	BLASTX
NCBI GI	g126156
BLAST score	290
E value	4.0e-26
Match length	96
% identity	61
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228579
Seq. ID	LIB3196-010-P1-M1-E1
Method	BLASTX
NCBI GI	g126047
BLAST score	715
E value	6.0e-76
Match length	134
% identity	100
NCBI Description	L-LACTATE DEHYDROGENASE M CHAIN (LDH-A) >gi_65922_pir__DEHULM L-lactate dehydrogenase (EC 1.1.1.27) chain M - human >gi_34313_emb_CAA26088_ (X02152) lactate dehydrogenase-A [Homo sapiens] >gi_780261_emb_CAA26879_ (X03077) lactate dehydrogenase-A [Homo sapiens]

Seq. No.	228580
Seq. ID	LIB3196-010-P1-M1-E10
Method	BLASTX
NCBI GI	g3876766
BLAST score	224
E value	2.0e-18
Match length	93
% identity	49
NCBI Description	(Z69637) predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]

Seq. No.	228581
Seq. ID	LIB3196-010-P1-M1-E11
Method	BLASTX
NCBI GI	g464444
BLAST score	171
E value	5.0e-23
Match length	90
% identity	63
NCBI Description	PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome - Arabidopsis thaliana >gi_166830 (M98495) proteasome

[Arabidopsis thaliana]

Seq. No.	228582
Seq. ID	LIB3196-010-P1-M1-E2
Method	BLASTX
NCBI GI	g126047
BLAST score	263
E value	4.0e-23
Match length	65
% identity	80
NCBI Description	L-LACTATE DEHYDROGENASE M CHAIN (LDH-A) >gi_65922_pir__DEHULM L-lactate dehydrogenase (EC 1.1.1.27) chain M - human >gi_34313_emb_CAA26088_ (X02152) lactate dehydrogenase-A [Homo sapiens] >gi_780261_emb_CAA26879_ (X03077) lactate dehydrogenase-A [Homo sapiens]

Seq. No.	228583
Seq. ID	LIB3196-010-P1-M1-E5
Method	BLASTX
NCBI GI	g464444
BLAST score	546
E value	4.0e-56
Match length	118
% identity	90
NCBI Description	PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome - Arabidopsis thaliana >gi_166830 (M98495) proteasome [Arabidopsis thaliana]

Seq. No.	228584
Seq. ID	LIB3196-010-P1-M1-E7
Method	BLASTX
NCBI GI	g115613
BLAST score	520
E value	4.0e-53
Match length	129
% identity	73
NCBI Description	CALCIUM-DEPENDENT PROTEASE, SMALL (REGULATORY) SUBUNIT (CALPAIN) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) >gi_67666_pir__CIPGL calpain (EC 3.4.22.17) light chain - pig >gi_164403 (M11778) calpain I light subunit (EC 3.4.22.17) [Sus scrofa] >gi_164405 (M11779) pig calpain I light subunit (EC 3.4.22.17) [Sus scrofa]

Seq. No.	228585
Seq. ID	LIB3196-010-P1-M1-E9
Method	BLASTX
NCBI GI	g137578
BLAST score	525
E value	1.0e-53
Match length	119
% identity	52
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A

[Saguinus oedipus]

Seq. No.	228586
Seq. ID	LIB3196-010-P1-M1-F11
Method	BLASTX
NCBI GI	g88044
BLAST score	627
E value	1.0e-65
Match length	133
% identity	96
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	228587
Seq. ID	LIB3196-010-P1-M1-F3
Method	BLASTX
NCBI GI	g542200
BLAST score	372
E value	9.0e-36
Match length	129
% identity	53
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	228588
Seq. ID	LIB3196-010-P1-M1-F4
Method	BLASTX
NCBI GI	g3738257
BLAST score	438
E value	2.0e-43
Match length	92
% identity	93
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	228589
Seq. ID	LIB3196-010-P1-M1-G11
Method	BLASTX
NCBI GI	g125077
BLAST score	190
E value	8.0e-17
Match length	58
% identity	73
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	228590
Seq. ID	LIB3196-010-P1-M1-G8
Method	BLASTX
NCBI GI	g2586071
BLAST score	317
E value	3.0e-29
Match length	126

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% identity	52
NCBI Description	(AF027728) kinesin-related protein [Xenopus laevis]
Seq. No.	228591
Seq. ID	LIB3196-010-P1-M1-G9
Method	BLASTX
NCBI GI	g728836
BLAST score	144
E value	4.0e-09
Match length	129
% identity	29
NCBI Description	ALU SUBFAMILY SP WARNING ENTRY !!!!
Seq. No.	228592
Seq. ID	LIB3196-010-P1-M1-H10
Method	BLASTX
NCBI GI	g2739008
BLAST score	363
E value	1.0e-34
Match length	102
% identity	74
NCBI Description	(AF022463) CYP78A3p [Glycine max]
Seq. No.	228593
Seq. ID	LIB3196-010-P1-M1-H12
Method	BLASTX
NCBI GI	g2662343
BLAST score	164
E value	8.0e-12
Match length	59
% identity	64
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]
Seq. No.	228594
Seq. ID	LIB3196-010-P1-M1-H3
Method	BLASTX
NCBI GI	g2995990
BLAST score	230
E value	4.0e-19
Match length	116
% identity	48
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]
Seq. No.	228595
Seq. ID	LIB3196-010-P1-M1-H4
Method	BLASTX
NCBI GI	g542184
BLAST score	166
E value	1.0e-11
Match length	94
% identity	37
NCBI Description	globulin-1S, GLB1S - maize
Seq. No.	228596
Seq. ID	LIB3196-010-P1-M1-H8

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Method	BLASTX
NCBI GI	g2833389
BLAST score	513
E value	3.0e-52
Match length	125
% identity	78
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III) >gi_1200154_emb_CAA65065_ (X95759) glycogen (starch) synthase [Solanum tuberosum]

Seq. No.	228597
Seq. ID	LIB3196-010-P1-M1-H9
Method	BLASTX
NCBI GI	g126156
BLAST score	431
E value	8.0e-43
Match length	109
% identity	82
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228598
Seq. ID	LIB3196-011-P1-M1-A10
Method	BLASTX
NCBI GI	g2136315
BLAST score	568
E value	9.0e-59
Match length	127
% identity	87
NCBI Description	translation elongation factor Tu precursor - human >gi_704416 (L38995) elongation factor Tu [Homo sapiens] >gi_4507733_ref_NP_003312.1_pTUFM_ Tu translation elongation factor, mitochondrial

Seq. No.	228599
Seq. ID	LIB3196-011-P1-M1-A11
Method	BLASTX
NCBI GI	g128378
BLAST score	187
E value	4.0e-14
Match length	58
% identity	59
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP) >gi_82031_pir__S07142 nonspecific lipid transfer protein - castor bean >gi_224909_prf__1204170A protein,nonspecific lipid transfer [Ricinus communis]

Seq. No.	228600
Seq. ID	LIB3196-011-P1-M1-A9
Method	BLASTX
NCBI GI	g3687234
BLAST score	247

E value 4.0e-21
Match length 92
% identity 51
NCBI Description (AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No. 228601
Seq. ID LIB3196-011-P1-M1-B1
Method BLASTX
NCBI GI g4559342
BLAST score 428
E value 2.0e-42
Match length 120
% identity 67
NCBI Description (AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No. 228602
Seq. ID LIB3196-011-P1-M1-B10
Method BLASTX
NCBI GI g2072361
BLAST score 656
E value 4.0e-69
Match length 127
% identity 99
NCBI Description (AF001008) p38Beta2 MAP Kinase [Homo sapiens] >gi_2232138 (AF001174) p38beta2 MAP kinase [Homo sapiens] >gi_2326554_emb_CAA74792_ (Y14440) stress activated protein kinase-2b [Homo sapiens] >gi_3025677 (AF031135) p38beta2 MAP kinase [Homo sapiens] >gi_4506083_ref_NP_002742.1_pPRKM11_ protein kinase mitogen- activated

Seq. No. 228603
Seq. ID LIB3196-011-P1-M1-B4
Method BLASTX
NCBI GI g2459421
BLAST score 368
E value 2.0e-35
Match length 102
% identity 67
NCBI Description (AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No. 228604
Seq. ID LIB3196-011-P1-M1-B5
Method BLASTX
NCBI GI g691752
BLAST score 321
E value 8.0e-30
Match length 121
% identity 51
NCBI Description (D29803) preproMP27-MP32 [Cucurbita sp.]

Seq. No. 228605
Seq. ID LIB3196-011-P1-M1-B6
Method BLASTX

NCBI GI	g3914435
BLAST score	400
E value	4.0e-39
Match length	84
% identity	87
NCBI Description	PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin [Glycine max]

Seq. No.	228606
Seq. ID	LIB3196-011-P1-M1-B7
Method	BLASTX
NCBI GI	g181912
BLAST score	366
E value	4.0e-35
Match length	71
% identity	97
NCBI Description	(M95586) E2A/HLF fusion protein [Homo sapiens]

Seq. No.	228607
Seq. ID	LIB3196-011-P1-M1-B9
Method	BLASTX
NCBI GI	g72287
BLAST score	382
E value	6.0e-37
Match length	109
% identity	71
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	228608
Seq. ID	LIB3196-011-P1-M1-C12
Method	BLASTX
NCBI GI	g3157943
BLAST score	313
E value	7.0e-29
Match length	110
% identity	57
NCBI Description	(AC002131) Contains similarity to BAP31 protein gb_X81816 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	228609
Seq. ID	LIB3196-011-P1-M1-C3
Method	BLASTX
NCBI GI	g4455192
BLAST score	459
E value	5.0e-46
Match length	124
% identity	66
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	228610
Seq. ID	LIB3196-011-P1-M1-C9
Method	BLASTX
NCBI GI	g2827699
BLAST score	301
E value	2.0e-27

Match length	106
% identity	63
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	228611
Seq. ID	LIB3196-011-P1-M1-D5
Method	BLASTX
NCBI GI	g207905
BLAST score	202
E value	6.0e-17
Match length	119
% identity	50
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	228612
Seq. ID	LIB3196-011-P1-M1-D7
Method	BLASTX
NCBI GI	g476850
BLAST score	637
E value	6.0e-67
Match length	128
% identity	99
NCBI Description	heat shock cognate protein 70 - mouse >gi_309319 (M19141) heat shock protein 70 cognate [Mus musculus] >gi_1661134_gb_AAB18391.1_ (U73744) heat shock 70 protein [Mus musculus]

Seq. No.	228613
Seq. ID	LIB3196-011-P1-M1-E2
Method	BLASTX
NCBI GI	g131392
BLAST score	363
E value	8.0e-47
Match length	119
% identity	82
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81479_pir__S00005 photosystem II oxygen-evolving complex protein 2 precursor - spinach >gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein [Spinacia oleracea] >gi_225596_prf__1307179A luminal protein 23kD [Spinacia oleracea]

Seq. No.	228614
Seq. ID	LIB3196-011-P1-M1-E3
Method	BLASTX
NCBI GI	g2642215
BLAST score	326
E value	2.0e-30
Match length	77
% identity	81
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]

Seq. No.	228615
Seq. ID	LIB3196-011-P1-M1-E4
Method	BLASTX
NCBI GI	g996057

BLAST score	584
E value	1.0e-60
Match length	121
% identity	92
NCBI Description	(X90872) associated to Golgi apparatus [Homo sapiens]

Seq. No.	228616
Seq. ID	LIB3196-011-P1-M1-E8
Method	BLASTX
NCBI GI	g2995405
BLAST score	453
E value	3.0e-45
Match length	115
% identity	70
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	228617
Seq. ID	LIB3196-011-P1-M1-E9
Method	BLASTX
NCBI GI	g2506379
BLAST score	230
E value	3.0e-19
Match length	114
% identity	41
NCBI Description	GTP-BINDING PROTEIN GUF1 (GTPASE GUF1) >gi_1077352_pir__S50374 GTP-binding protein GUF1 - yeast (Saccharomyces cerevisiae) >gi_596037 (U17243) Similar to GTP binding proteins [Saccharomyces cerevisiae]

Seq. No.	228618
Seq. ID	LIB3196-011-P1-M1-F1
Method	BLASTX
NCBI GI	g543794
BLAST score	514
E value	3.0e-52
Match length	128
% identity	74
NCBI Description	SERUM ALBUMIN PRECURSOR >gi_476379_pir__ABHOS serum albumin precursor - horse >gi_399672_emb_CAA52194_ (X74045) preproalbumin [Equus caballus]

Seq. No.	228619
Seq. ID	LIB3196-011-P1-M1-F10
Method	BLASTX
NCBI GI	g231536
BLAST score	565
E value	2.0e-58
Match length	121
% identity	88
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	228620
Seq. ID	LIB3196-011-P1-M1-F3
Method	BLASTX
NCBI GI	g4406656
BLAST score	439
E value	1.0e-43
Match length	109
% identity	81
NCBI Description	(AF131820) Unknown [Homo sapiens]

Seq. No.	228621
Seq. ID	LIB3196-011-P1-M1-F4
Method	BLASTX
NCBI GI	g3287489
BLAST score	632
E value	3.0e-66
Match length	125
% identity	100
NCBI Description	(AF028832) Hsp89-alpha-delta-N [Homo sapiens]

Seq. No.	228622
Seq. ID	LIB3196-011-P1-M1-F5
Method	BLASTX
NCBI GI	g1620018
BLAST score	595
E value	6.0e-62
Match length	125
% identity	95
NCBI Description	(D87666) heat shock protein 90 [Homo sapiens]

Seq. No.	228623
Seq. ID	LIB3196-011-P1-M1-F7
Method	BLASTX
NCBI GI	g3249065
BLAST score	142
E value	5.0e-09
Match length	54
% identity	57
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	228624
Seq. ID	LIB3196-011-P1-M1-F9
Method	BLASTX
NCBI GI	g1865677
BLAST score	267
E value	7.0e-24
Match length	72
% identity	71
NCBI Description	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	228625
Seq. ID	LIB3196-011-P1-M1-G1
Method	BLASTX
NCBI GI	g4204277

BLAST score	522
E value	2.0e-53
Match length	110
% identity	81
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	228626
Seq. ID	LIB3196-011-P1-M1-G2
Method	BLASTX
NCBI GI	g4204277
BLAST score	210
E value	3.0e-17
Match length	54
% identity	69
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	228627
Seq. ID	LIB3196-011-P1-M1-G6
Method	BLASTX
NCBI GI	g119165
BLAST score	422
E value	9.0e-42
Match length	110
% identity	76
NCBI Description	ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) >gi_105918_pir__S22655 translation elongation factor eEF-1 gamma chain - human >gi_31102_emb_CAA45089_ (X63526) homologue to elongation factor 1-gamma from A.salina [Homo sapiens] >gi_31104_emb_CAA77630_ (Z11531) elongation factor-1-gamma [Homo sapiens] >gi_4503481_ref_NP_001395.1_pEEF1G_ eukaryotic translation elongation factor 1 gamma

Seq. No.	228628
Seq. ID	LIB3196-011-P1-M1-H10
Method	BLASTX
NCBI GI	g1174592
BLAST score	484
E value	5.0e-49
Match length	112
% identity	85
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	228629
Seq. ID	LIB3196-011-P1-M1-H11
Method	BLASTX
NCBI GI	g2493130
BLAST score	627
E value	1.0e-65
Match length	122
% identity	100
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi_459200 (U07053) vacuolar H+-ATPase subunit B [Gossypium hirsutum]

Seq. No.	228630
Seq. ID	LIB3196-011-P1-M1-H12
Method	BLASTX
NCBI GI	g2995405
BLAST score	342
E value	7.0e-36
Match length	113
% identity	67
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	228631
Seq. ID	LIB3196-012-P1-M1-A4
Method	BLASTX
NCBI GI	g1923256
BLAST score	148
E value	9.0e-14
Match length	106
% identity	40
NCBI Description	(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]

Seq. No.	228632
Seq. ID	LIB3196-012-P1-M1-A9
Method	BLASTX
NCBI GI	g3158372
BLAST score	392
E value	2.0e-38
Match length	80
% identity	54
NCBI Description	(AF035383) polyubiquitin [Arabidopsis thaliana]

Seq. No.	228633
Seq. ID	LIB3196-012-P1-M1-B12
Method	BLASTX
NCBI GI	g4539292
BLAST score	306
E value	3.0e-28
Match length	68
% identity	82
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	228634
Seq. ID	LIB3196-012-P1-M1-B5
Method	BLASTX
NCBI GI	g434759
BLAST score	191
E value	2.0e-16
Match length	92
% identity	51
NCBI Description	(D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]

Seq. No.	228635
Seq. ID	LIB3196-012-P1-M1-B6
Method	BLASTX
NCBI GI	g3024122

BLAST score	419
E value	2.0e-41
Match length	96
% identity	85
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No.	228636
Seq. ID	LIB3196-012-P1-M1-B7
Method	BLASTX
NCBI GI	g3745821
BLAST score	455
E value	2.0e-45
Match length	89
% identity	94
NCBI Description	Chain A, Tubulin Alpha-Beta Dimer, Electron Diffraction

Seq. No.	228637
Seq. ID	LIB3196-012-P1-M1-B8
Method	BLASTX
NCBI GI	g167367
BLAST score	628
E value	1.0e-68
Match length	130
% identity	99
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	228638
Seq. ID	LIB3196-012-P1-M1-D1
Method	BLASTX
NCBI GI	g3790567
BLAST score	221
E value	4.0e-18
Match length	114
% identity	41
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	228639
Seq. ID	LIB3196-012-P1-M1-D10
Method	BLASTX
NCBI GI	g3688172
BLAST score	239
E value	2.0e-20
Match length	78
% identity	60
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	228640
Seq. ID	LIB3196-012-P1-M1-D7
Method	BLASTX
NCBI GI	g3850818
BLAST score	393
E value	2.0e-38
Match length	102
% identity	73

NCBI Description	(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza sativa]
Seq. No.	228641
Seq. ID	LIB3196-012-P1-M1-E12
Method	BLASTX
NCBI GI	g116486
BLAST score	420
E value	2.0e-41
Match length	83
% identity	98
NCBI Description	CALPACTIN I LIGHT CHAIN (P10 PROTEIN) (P11) (CELLULAR LIGAND OF ANNEXIN II) >gi_89438_pir__B28489 calpactin I light chain - bovine >gi_107251_pir__JC1139 calpactin I light chain - human >gi_162785 (M16464) calpactin I light chain [Bos taurus] >gi_179875 (M81457) calpactin I light chain [Homo sapiens] >gi_180596 (M38591) cellular ligand of annexin II [Homo sapiens] >gi_4506761_ref_NP_002957.1_pS100A10_ S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
Seq. No.	228642
Seq. ID	LIB3196-012-P1-M1-E2
Method	BLASTX
NCBI GI	g137578
BLAST score	367
E value	3.0e-35
Match length	101
% identity	76
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	228643
Seq. ID	LIB3196-012-P1-M1-E5
Method	BLASTX
NCBI GI	g2506477
BLAST score	558
E value	4.0e-62
Match length	129
% identity	96
NCBI Description	GRG PROTEIN (ESP1 PROTEIN) (AMINO ENHANCER OF SPLIT) (AES-1/AES-2) >gi_435425 (U04241) homologous to Swiss-Prot accession number P16371 [Homo sapiens] >gi_3850562 (AC005944) GRG_HUMAN; ESP1 PROTEIN; AMINO ENHANCER OF SPLIT; AES-1/AES-2; gp130 associated protein GAM [Homo sapiens]
Seq. No.	228644
Seq. ID	LIB3196-012-P1-M1-E6
Method	BLASTX
NCBI GI	g126156
BLAST score	444

E value	3.0e-44
Match length	86
% identity	99
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228645
Seq. ID	LIB3196-012-P1-M1-E7
Method	BLASTX
NCBI GI	g266691
BLAST score	319
E value	1.0e-29
Match length	62
% identity	100
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	228646
Seq. ID	LIB3196-012-P1-M1-E8
Method	BLASTX
NCBI GI	g1346342
BLAST score	426
E value	2.0e-48
Match length	115
% identity	89
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo sapiens]

Seq. No.	228647
Seq. ID	LIB3196-012-P1-M1-F1
Method	BLASTX
NCBI GI	g3395436
BLAST score	218
E value	9.0e-18
Match length	67
% identity	61
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	228648
Seq. ID	LIB3196-012-P1-M1-F10
Method	BLASTX
NCBI GI	g1703052
BLAST score	480
E value	2.0e-48
Match length	123
% identity	76
NCBI Description	ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT) (RF-C 37 KD SUBUNIT) (RFC37) >gi_1498256 (M87339) replication factor C, 37-kDa subunit [Homo sapiens] >gi_4506491_ref_NP_002907.1_pRFC4_ replication factor C (activator 1) 4 (37kD)

Seq. No.	228649
Seq. ID	LIB3196-012-P1-M1-F12
Method	BLASTX
NCBI GI	g125105
BLAST score	157
E value	1.0e-10
Match length	60
% identity	60
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	228650
Seq. ID	LIB3196-012-P1-M1-F5
Method	BLASTX
NCBI GI	g2270994
BLAST score	164
E value	6.0e-19
Match length	77
% identity	68
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	228651
Seq. ID	LIB3196-012-P1-M1-G2
Method	BLASTX
NCBI GI	g4530435
BLAST score	568
E value	1.0e-58
Match length	134
% identity	83
NCBI Description	(AF117657) thyroid hormone receptor-associated protein complex component TRAP80 [Homo sapiens]

Seq. No.	228652
Seq. ID	LIB3196-012-P1-M1-G7
Method	BLASTX
NCBI GI	g1922278
BLAST score	213
E value	1.0e-17
Match length	48
% identity	83
NCBI Description	(Z86091) TCTP protein [Fragaria x ananassa]

Seq. No.	228653
Seq. ID	LIB3196-012-P1-M1-G8
Method	BLASTX
NCBI GI	g2244763
BLAST score	440
E value	9.0e-44
Match length	114
% identity	72
NCBI Description	(Z97335) A6 anther-specific protein [Arabidopsis thaliana]

Seq. No.	228654
Seq. ID	LIB3196-012-P1-M1-H12

Method	BLASTX
NCBI GI	g131856
BLAST score	529
E value	3.0e-60
Match length	122
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAP-1B (GTP-BINDING PROTEIN SMG P21B) >gi_68951_pir__TVHUR1 transforming protein rap1b - human >gi_108713_pir__A34655 transforming protein rap1b - bovine >gi_163722 (M33141) GTP-binding protein (smg p21B) [Bos taurus]

Seq. No.	228655
Seq. ID	LIB3196-012-P1-M1-H6
Method	BLASTX
NCBI GI	g477138
BLAST score	326
E value	2.0e-30
Match length	110
% identity	52
NCBI Description	carcinoma-associated antigen GA733-1 precursor - human >gi_31591_emb_CAA31781_ (X13425) GA733-1 protein (AA 1-323) [Homo sapiens]

Seq. No.	228656
Seq. ID	LIB3196-012-P1-M1-H8
Method	BLASTX
NCBI GI	g2145023
BLAST score	216
E value	2.0e-17
Match length	112
% identity	42
NCBI Description	(U97700) 15.5 kDa oleosin [Sesamum indicum]

Seq. No.	228657
Seq. ID	LIB3196-013-P1-M1-A1
Method	BLASTX
NCBI GI	g2119106
BLAST score	632
E value	3.0e-66
Match length	125
% identity	98
NCBI Description	ribosomal protein L3 - human (fragment) >gi_337580 (M90054) ribosomal protein L3 [Homo sapiens]

Seq. No.	228658
Seq. ID	LIB3196-013-P1-M1-A10
Method	BLASTX
NCBI GI	g2340052
BLAST score	145
E value	3.0e-11
Match length	42
% identity	90
NCBI Description	(L48990) troponin T [Mus musculus]

Seq. No.	228659
Seq. ID	LIB3196-013-P1-M1-A4

Method	BLASTX
NCBI GI	g3702323
BLAST score	160
E value	5.0e-11
Match length	60
% identity	57
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	228660
Seq. ID	LIB3196-013-P1-M1-A6
Method	BLASTX
NCBI GI	g2244990
BLAST score	406
E value	8.0e-40
Match length	120
% identity	67
NCBI Description	(Z97340) similarity to LIM homeobox protein - Caenorhabditis [Arabidopsis thaliana]

Seq. No.	228661
Seq. ID	LIB3196-013-P1-M1-B1
Method	BLASTX
NCBI GI	g547753
BLAST score	270
E value	7.0e-24
Match length	102
% identity	65
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	228662
Seq. ID	LIB3196-013-P1-M1-B12
Method	BLASTX
NCBI GI	g2829918
BLAST score	190
E value	2.0e-14
Match length	56
% identity	71
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	228663
Seq. ID	LIB3196-013-P1-M1-B2
Method	BLASTX
NCBI GI	g126156
BLAST score	455
E value	1.0e-45
Match length	116
% identity	79
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228664
Seq. ID	LIB3196-013-P1-M1-B6

Method	BLASTX
NCBI GI	g2498882
BLAST score	168
E value	8.0e-14
Match length	68
% identity	69
NCBI Description	SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120) >gi_2146975_pir__S60735 splicing factor SF3a 120K chain - human >gi_899298_emb_CAA59494_ (X85237) human splicing factor [Homo sapiens] >gi_3212998 (AC004997) spliceosome associated protein 114 (SF3a) [Homo sapiens]

Seq. No.	228665
Seq. ID	LIB3196-013-P1-M1-C4
Method	BLASTX
NCBI GI	g4193388
BLAST score	313
E value	7.0e-29
Match length	81
% identity	75
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	228666
Seq. ID	LIB3196-013-P1-M1-D11
Method	BLASTX
NCBI GI	g1174448
BLAST score	197
E value	3.0e-15
Match length	56
% identity	66
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	228667
Seq. ID	LIB3196-013-P1-M1-D7
Method	BLASTX
NCBI GI	g2511594
BLAST score	410
E value	3.0e-40
Match length	84
% identity	93
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	228668
Seq. ID	LIB3196-013-P1-M1-D9
Method	BLASTX
NCBI GI	g2995384
BLAST score	170
E value	1.0e-12

Match length	44
% identity	75
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	228669
Seq. ID	LIB3196-013-P1-M1-E2
Method	BLASTX
NCBI GI	g133041
BLAST score	548
E value	2.0e-56
Match length	106
% identity	100
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi_71137_pir__R5HUP0 acidic ribosomal protein P0 - human >gi_190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041) [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_ ribosomal protein, large, P0

Seq. No.	228670
Seq. ID	LIB3196-013-P1-M1-E4
Method	BLASTX
NCBI GI	g125105
BLAST score	480
E value	2.0e-48
Match length	96
% identity	100
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	228671
Seq. ID	LIB3196-013-P1-M1-E6
Method	BLASTX
NCBI GI	g2146797
BLAST score	483
E value	8.0e-49
Match length	121
% identity	46
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	228672
Seq. ID	LIB3196-013-P1-M1-F1
Method	BLASTX
NCBI GI	g3721858
BLAST score	478
E value	3.0e-48
Match length	92
% identity	99
NCBI Description	(AB015234) uroplakin 1b [Homo sapiens]

Seq. No.	228673
Seq. ID	LIB3196-013-P1-M1-F10
Method	BLASTX
NCBI GI	g1346349
BLAST score	612
E value	6.0e-64
Match length	124
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II - human >gi_908805 (L42612) keratin type II [Homo sapiens]

Seq. No.	228674
Seq. ID	LIB3196-013-P1-M1-F12
Method	BLASTX
NCBI GI	g4567295
BLAST score	318
E value	2.0e-29
Match length	106
% identity	51
NCBI Description	(AC006918) putative pol polyprotein [Arabidopsis thaliana]

Seq. No.	228675
Seq. ID	LIB3196-013-P1-M1-F6
Method	BLASTX
NCBI GI	g2772564
BLAST score	378
E value	1.0e-36
Match length	79
% identity	57
NCBI Description	(AC004000) ADP/ATP carrier protein (adenine nucleotide translocator 2) [Homo sapiens]

Seq. No.	228676
Seq. ID	LIB3196-013-P1-M1-G1
Method	BLASTX
NCBI GI	g125080
BLAST score	487
E value	3.0e-49
Match length	99
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228677
Seq. ID	LIB3196-013-P1-M1-G10
Method	BLASTX
NCBI GI	g1596167
BLAST score	673
E value	4.0e-71
Match length	125
% identity	100
NCBI Description	(D87953) RTP [Homo sapiens] >gi_3046386 (AF004162) nickel-specific induction protein [Homo sapiens]

Seq. No.	228678
Seq. ID	LIB3196-013-P1-M1-G11
Method	BLASTX
NCBI GI	g3603456
BLAST score	610
E value	1.0e-63
Match length	121
% identity	34
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	228679
Seq. ID	LIB3196-013-P1-M1-G2
Method	BLASTX
NCBI GI	g1731412
BLAST score	467
E value	6.0e-47
Match length	123
% identity	6
NCBI Description	ZINC FINGER PROTEIN 136 >gi_2136405_pir__B57785 zinc finger protein ZNF136 - human >gi_487785 (U09367) zinc finger protein ZNF136 [Homo sapiens] >gi_1582216_prf__2118244B ZNF136 protein [Homo sapiens] >gi_4507987_ref_NP_003428.1_pZNF136_ zinc finger protein 136 (clone pHZ-20)

Seq. No.	228680
Seq. ID	LIB3196-013-P1-M1-G4
Method	BLASTX
NCBI GI	g423532
BLAST score	594
E value	8.0e-62
Match length	123
% identity	97
NCBI Description	plakoglobin - mouse (fragment)

Seq. No.	228681
Seq. ID	LIB3196-013-P1-M1-G5
Method	BLASTX
NCBI GI	g4580395
BLAST score	191
E value	1.0e-14
Match length	102
% identity	48
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	228682
Seq. ID	LIB3196-013-P1-M1-G7
Method	BLASTX
NCBI GI	g2194203
BLAST score	396
E value	1.0e-38
Match length	122
% identity	70
NCBI Description	(U78310) pescadillo [Homo sapiens]

Seq. No.	228683
Seq. ID	LIB3196-013-P1-M1-G8
Method	BLASTX
NCBI GI	g3334115
BLAST score	283
E value	2.0e-25
Match length	73
% identity	78
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	228684
Seq. ID	LIB3196-013-P1-M1-H10
Method	BLASTX
NCBI GI	g2245098
BLAST score	219
E value	2.0e-18
Match length	58
% identity	72
NCBI Description	(Z97343) ribosomal protein [Arabidopsis thaliana]

Seq. No.	228685
Seq. ID	LIB3196-013-P1-M1-H2
Method	BLASTX
NCBI GI	g121116
BLAST score	616
E value	2.0e-64
Match length	125
% identity	34
NCBI Description	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi_71649_pir__FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf__1211330A gelsolin [Homo sapiens] >gi_4504165_ref_NP_000168.1_pGSN_ gelsolin (amyloidosis, Finnish type)

Seq. No.	228686
Seq. ID	LIB3196-014-P1-M1-A10
Method	BLASTX
NCBI GI	g942596
BLAST score	581
E value	2.0e-60
Match length	119
% identity	96
NCBI Description	(U30467) alpha-tubulin [Urechis caupo]

Seq. No.	228687
Seq. ID	LIB3196-014-P1-M1-A11
Method	BLASTX
NCBI GI	g2995405
BLAST score	239
E value	2.0e-32
Match length	119
% identity	61
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	228688
Seq. ID	LIB3196-014-P1-M1-A2
Method	BLASTX
NCBI GI	g121116
BLAST score	218
E value	1.0e-17
Match length	44
% identity	95
NCBI Description	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi_71649_pir__FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf__1211330A gelsolin [Homo sapiens] >gi_4504165_ref_NP_000168.1_pGSN_ gelsolin (amyloidosis, Finnish type)

Seq. No.	228689
Seq. ID	LIB3196-014-P1-M1-A3
Method	BLASTX
NCBI GI	g3334115
BLAST score	378
E value	2.0e-36
Match length	94
% identity	81
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	228690
Seq. ID	LIB3196-014-P1-M1-A4
Method	BLASTX
NCBI GI	g125080
BLAST score	559
E value	9.0e-58
Match length	112
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228691
Seq. ID	LIB3196-014-P1-M1-A6
Method	BLASTX
NCBI GI	g2495365
BLAST score	597
E value	4.0e-62
Match length	126
% identity	93
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	228692
Seq. ID	LIB3196-014-P1-M1-A8
Method	BLASTX

NCBI GI	g1737218
BLAST score	269
E value	6.0e-24
Match length	94
% identity	60
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	228693
Seq. ID	LIB3196-014-P1-M1-B3
Method	BLASTX
NCBI GI	g207905
BLAST score	290
E value	4.0e-26
Match length	87
% identity	66
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	228694
Seq. ID	LIB3196-014-P1-M1-B4
Method	BLASTX
NCBI GI	g207905
BLAST score	184
E value	1.0e-19
Match length	81
% identity	67
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	228695
Seq. ID	LIB3196-014-P1-M1-C1
Method	BLASTX
NCBI GI	g3004948
BLAST score	450
E value	5.0e-45
Match length	89
% identity	93
NCBI Description	(AF037261) SH3-containing adaptor molecule-1 [Homo sapiens]

Seq. No.	228696
Seq. ID	LIB3196-014-P1-M1-C2
Method	BLASTX
NCBI GI	g430947
BLAST score	158
E value	6.0e-11
Match length	32
% identity	91
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	228697
Seq. ID	LIB3196-014-P1-M1-C3
Method	BLASTX
NCBI GI	g1806146
BLAST score	495
E value	3.0e-50
Match length	108
% identity	93

NCBI Description	(X97317) cdc2MsF [Medicago sativa]
Seq. No.	228698
Seq. ID	LIB3196-014-P1-M1-C4
Method	BLASTX
NCBI GI	g2351378
BLAST score	315
E value	2.0e-29
Match length	66
% identity	89
NCBI Description	(U54558) translation initiation factor eIF3 p66 subunit [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313) EIF3-P66 [Homo sapiens] >gi_4503523_ref_NP_003744.1_pEIF3S7_ UNKNOWN
Seq. No.	228699
Seq. ID	LIB3196-014-P1-M1-D1
Method	BLASTX
NCBI GI	g2244910
BLAST score	169
E value	6.0e-12
Match length	72
% identity	46
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]
Seq. No.	228700
Seq. ID	LIB3196-014-P1-M1-D3
Method	BLASTX
NCBI GI	g4204265
BLAST score	293
E value	2.0e-26
Match length	122
% identity	54
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]
Seq. No.	228701
Seq. ID	LIB3196-014-P1-M1-D6
Method	BLASTX
NCBI GI	g71881
BLAST score	566
E value	2.0e-58
Match length	127
% identity	87
NCBI Description	GTP-binding regulatory protein Gs alpha-S2 chain (adenylate cyclase-stimulating) - mouse >gi_51128_emb_CAA68695_ (Y00703) G-s-alpha protein (AA 1 - 394) [Mus musculus]
Seq. No.	228702
Seq. ID	LIB3196-014-P1-M1-E11
Method	BLASTX
NCBI GI	g1170508
BLAST score	209
E value	8.0e-17
Match length	43
% identity	91
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi_2119931_pir__S60244 translation initiation factor

	eIF-4A.8, anther-specific - common tobacco >gi_475219_emb_CAA55639_ (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi_475221_emb_CAA55640_ (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]
Seq. No.	228703
Seq. ID	LIB3196-014-P1-M1-E12
Method	BLASTX
NCBI GI	g1848212
BLAST score	487
E value	3.0e-49
Match length	95
% identity	47
NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]
Seq. No.	228704
Seq. ID	LIB3196-014-P1-M1-E6
Method	BLASTX
NCBI GI	g1848212
BLAST score	173
E value	4.0e-25
Match length	108
% identity	39
NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]
Seq. No.	228705
Seq. ID	LIB3196-014-P1-M1-E7
Method	BLASTX
NCBI GI	g2832906
BLAST score	499
E value	9.0e-51
Match length	99
% identity	94
NCBI Description	(D89340) dipeptidyl peptidase III [Rattus norvegicus]
Seq. No.	228706
Seq. ID	LIB3196-014-P1-M1-F12
Method	BLASTX
NCBI GI	g3882237
BLAST score	171
E value	4.0e-12
Match length	128
% identity	38
NCBI Description	(AB018301) KIAA0758 protein [Homo sapiens]
Seq. No.	228707
Seq. ID	LIB3196-014-P1-M1-F3
Method	BLASTX
NCBI GI	g4249649
BLAST score	221
E value	2.0e-20
Match length	106
% identity	52
NCBI Description	(AF082889) GPI-anchored metastasis-associated protein

homolog [Homo sapiens]

Seq. No.	228708
Seq. ID	LIB3196-014-P1-M1-F5
Method	BLASTX
NCBI GI	g728837
BLAST score	211
E value	4.0e-17
Match length	175
% identity	18
NCBI Description	ALU SUBFAMILY SQ WARNING ENTRY !!!!

Seq. No.	228709
Seq. ID	LIB3196-014-P1-M1-F6
Method	BLASTX
NCBI GI	g478811
BLAST score	236
E value	4.0e-20
Match length	60
% identity	20
NCBI Description	polyubiquitin - bovine >gi_645_emb_CAA79146_ (Z18245) polyubiquitin [Bos taurus]

Seq. No.	228710
Seq. ID	LIB3196-014-P1-M1-G10
Method	BLASTX
NCBI GI	g3242717
BLAST score	275
E value	2.0e-24
Match length	127
% identity	43
NCBI Description	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No.	228711
Seq. ID	LIB3196-014-P1-M1-G11
Method	BLASTX
NCBI GI	g418507
BLAST score	231
E value	3.0e-19
Match length	102
% identity	46
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	228712
Seq. ID	LIB3196-014-P1-M1-G2
Method	BLASTX
NCBI GI	g2129579
BLAST score	693
E value	2.0e-73
Match length	128
% identity	94

NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]
Seq. No.	228713
Seq. ID	LIB3196-014-P1-M1-G4
Method	BLASTX
NCBI GI	g207905
BLAST score	414
E value	1.0e-40
Match length	130
% identity	68
NCBI Description	(M18027) alpha globulin B [Artificial gene]
Seq. No.	228714
Seq. ID	LIB3196-014-P1-M1-G6
Method	BLASTX
NCBI GI	g2497464
BLAST score	164
E value	4.0e-14
Match length	93
% identity	56
NCBI Description	RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT (RAB GERANYL-GERANYLTRANSFERASE ALPHA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE)
Seq. No.	228715
Seq. ID	LIB3196-014-P1-M1-G8
Method	BLASTX
NCBI GI	g2497938
BLAST score	482
E value	1.0e-50
Match length	123
% identity	83
NCBI Description	AQUAPORIN 3 >gi_1854374_dbj_BAA19237_ (AB001325) aquaporin 3 [Homo sapiens]
Seq. No.	228716
Seq. ID	LIB3196-014-P1-M1-G9
Method	BLASTX
NCBI GI	g1362754
BLAST score	390
E value	2.0e-38
Match length	118
% identity	82
NCBI Description	aquaporin 3 - human
Seq. No.	228717
Seq. ID	LIB3196-014-P1-M1-H10
Method	BLASTX
NCBI GI	g401322
BLAST score	676
E value	2.0e-71
Match length	131
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	228718
Seq. ID	LIB3196-014-P1-M1-H12
Method	BLASTX
NCBI GI	g1688076
BLAST score	430
E value	2.0e-42
Match length	88
% identity	51
NCBI Description	(U46571) tetratricopeptide repeat protein [Homo sapiens] >gi_4507713_ref_NP_003306.1_pTTC2_ tetratricopeptide repeat domain

Seq. No.	228719
Seq. ID	LIB3196-014-P1-M1-H2
Method	BLASTX
NCBI GI	g3915742
BLAST score	581
E value	3.0e-60
Match length	122
% identity	90
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228720
Seq. ID	LIB3196-014-P1-M1-H3
Method	BLASTX
NCBI GI	g1762945
BLAST score	245
E value	7.0e-21
Match length	70
% identity	64
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	228721
Seq. ID	LIB3196-014-P1-M1-H4
Method	BLASTX
NCBI GI	g4493521
BLAST score	158
E value	6.0e-11
Match length	42
% identity	71
NCBI Description	(AL022476) dJ323M22.1 (human ortholog of chicken P52 and mouse H74) [Homo sapiens]

Seq. No.	228722
Seq. ID	LIB3196-014-P1-M1-H5
Method	BLASTX
NCBI GI	g386850
BLAST score	639
E value	5.0e-67
Match length	132
% identity	98
NCBI Description	(M19723) keratin K5 [Homo sapiens]

Seq. No.	228723
Seq. ID	LIB3196-014-P1-M1-H6
Method	BLASTX
NCBI GI	g2136102
BLAST score	175
E value	1.0e-12
Match length	76
% identity	51
NCBI Description	retinoblastoma 1 - human >gi_536845 (M26460) retinoblastoma 1 [Homo sapiens]

Seq. No.	228724
Seq. ID	LIB3196-014-P1-M1-H7
Method	BLASTX
NCBI GI	g2995405
BLAST score	263
E value	7.0e-26
Match length	113
% identity	59
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	228725
Seq. ID	LIB3196-015-P1-M1-A10
Method	BLASTX
NCBI GI	g1169534
BLAST score	519
E value	5.0e-53
Match length	112
% identity	89
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus communis]

Seq. No.	228726
Seq. ID	LIB3196-015-P1-M1-A11
Method	BLASTX
NCBI GI	g4512671
BLAST score	234
E value	1.0e-19
Match length	82
% identity	57
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	228727
Seq. ID	LIB3196-015-P1-M1-A6
Method	BLASTX
NCBI GI	g125105
BLAST score	633
E value	2.0e-66
Match length	127
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389)

	keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin
Seq. No.	228728
Seq. ID	LIB3196-015-P1-M1-A9
Method	BLASTX
NCBI GI	g226120
BLAST score	331
E value	5.0e-31
Match length	80
% identity	84
NCBI Description	vicilin gene B [Saguinus oedipus]
Seq. No.	228729
Seq. ID	LIB3196-015-P1-M1-B10
Method	BLASTX
NCBI GI	g1778145
BLAST score	439
E value	2.0e-46
Match length	108
% identity	92
NCBI Description	(U66402) phosphate/phosphoenolpyruvate translocator precursor [Nicotiana tabacum]
Seq. No.	228730
Seq. ID	LIB3196-015-P1-M1-B11
Method	BLASTX
NCBI GI	g115427
BLAST score	461
E value	2.0e-46
Match length	108
% identity	80
NCBI Description	PLACENTAL-CADHERIN PRECURSOR (P-CADHERIN) >gi_319934_pir__IJHUCP cadherin 3 precursor - human >gi_35323_emb_CAA45177_ (X63629) p-cadherin [Homo sapiens] >gi_226518_prf__1516312A Ca dependent cell adhesion protein [Homo sapiens] >gi_4502723_ref_NP_001784.1_pCDH3_ cadherin 3, P-cadherin (placental) (NOTE:redefinition of symbol)
Seq. No.	228731
Seq. ID	LIB3196-015-P1-M1-B3
Method	BLASTX
NCBI GI	g623590
BLAST score	187
E value	4.0e-14
Match length	40
% identity	85
NCBI Description	(L29275) putative [Nicotiana tabacum]
Seq. No.	228732
Seq. ID	LIB3196-015-P1-M1-B5
Method	BLASTX
NCBI GI	g3643595
BLAST score	298
E value	4.0e-27
Match length	106
% identity	55

NCBI Description	(AC005395) putative oleosin protein [Arabidopsis thaliana]

Seq. No.	228733
Seq. ID	LIB3196-015-P1-M1-B7
Method	BLASTX
NCBI GI	g2766165
BLAST score	435
E value	2.0e-43
Match length	82
% identity	96
NCBI Description	(AB008430) CDEP [Homo sapiens]

Seq. No.	228734
Seq. ID	LIB3196-015-P1-M1-C3
Method	BLASTX
NCBI GI	g3319958
BLAST score	166
E value	6.0e-12
Match length	82
% identity	8
NCBI Description	(AJ228139) VAKTI precursor [Homo sapiens]

Seq. No.	228735
Seq. ID	LIB3196-015-P1-M1-C5
Method	BLASTX
NCBI GI	g1304668
BLAST score	494
E value	4.0e-50
Match length	96
% identity	96
NCBI Description	(U42376) RIG-E precursor [Homo sapiens] >gi_1465747 (U56145) thymic shared antigen-1/stem cell antigen-2 [Homo sapiens] >gi_1519440 (U66711) 9804 [Homo sapiens] >gi_4454267_emb_CAA92321_ (Z68179) retinoic acid induced gene E [Homo sapiens] >gi_4505049_ref_NP_002337.1_pLY6E_ lymphocyte antigen 6 complex, locus E

Seq. No.	228736
Seq. ID	LIB3196-015-P1-M1-C6
Method	BLASTX
NCBI GI	g229506
BLAST score	156
E value	6.0e-11
Match length	36
% identity	83
NCBI Description	aldolase C [Oryctolagus cuniculus]

Seq. No.	228737
Seq. ID	LIB3196-015-P1-M1-D10
Method	BLASTX
NCBI GI	g3297816
BLAST score	450
E value	5.0e-45
Match length	108
% identity	79
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	228738
Seq. ID	LIB3196-015-P1-M1-D5
Method	BLASTX
NCBI GI	g1262890
BLAST score	507
E value	1.0e-51
Match length	117
% identity	81
NCBI Description	(U35627) MHC class I B [Papio hamadryas anubis]

Seq. No.	228739
Seq. ID	LIB3196-015-P1-M1-D7
Method	BLASTX
NCBI GI	g225581
BLAST score	142
E value	2.0e-09
Match length	52
% identity	60
NCBI Description	storage protein C94 [Saguinus oedipus]

Seq. No.	228740
Seq. ID	LIB3196-015-P1-M1-D8
Method	BLASTX
NCBI GI	g2583108
BLAST score	205
E value	3.0e-16
Match length	107
% identity	45
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	228741
Seq. ID	LIB3196-015-P1-M1-E2
Method	BLASTX
NCBI GI	g4417306
BLAST score	156
E value	2.0e-10
Match length	105
% identity	31
NCBI Description	(AC006446) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]

Seq. No.	228742
Seq. ID	LIB3196-015-P1-M1-E9
Method	BLASTX
NCBI GI	g1173444
BLAST score	454
E value	2.0e-45
Match length	126
% identity	70
NCBI Description	SKD1 PROTEIN >gi_1083520_pir__S48696 suppressor protein SKD1 - mouse >gi_557876 (U10119) SKD1 [Mus musculus]

Seq. No.	228743
Seq. ID	LIB3196-015-P1-M1-F1
Method	BLASTX
NCBI GI	g3687389
BLAST score	482

E value	1.0e-48
Match length	114
% identity	81
NCBI Description	(Y16124) putative cullin protein [Lycopersicon esculentum]

Seq. No.	228744
Seq. ID	LIB3196-015-P1-M1-F10
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	9.0e-20
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	228745
Seq. ID	LIB3196-015-P1-M1-F2
Method	BLASTX
NCBI GI	g2935291
BLAST score	535
E value	1.0e-54
Match length	108
% identity	97
NCBI Description	(AF035531) syntaxin 10 [Homo sapiens] >gi_4507285_ref_NP_003756.1_pSTX10_ UNKNOWN

Seq. No.	228746
Seq. ID	LIB3196-015-P1-M1-F3
Method	BLASTX
NCBI GI	g2842494
BLAST score	346
E value	9.0e-33
Match length	107
% identity	62
NCBI Description	(AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No.	228747
Seq. ID	LIB3196-015-P1-M1-F4
Method	BLASTX
NCBI GI	g167367
BLAST score	626
E value	1.0e-65
Match length	123
% identity	95
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	228748
Seq. ID	LIB3196-015-P1-M1-F7
Method	BLASTX
NCBI GI	g131786
BLAST score	534
E value	6.0e-55
Match length	103
% identity	100

NCBI Description	RAS-RELATED PROTEIN RAB-1A (YPT1-RELATED PROTEIN) >gi_68968_pir__TVMSYP GTP-binding protein ypt1 - mouse >gi_2144599_pir__TVHUYP GTP-binding protein Rab1 - human >gi_2144600_pir__TVDGYP GTP-binding protein Rab1 - dog >gi_55457_emb_CAA68284_ (Y00094) Ypt1 protein (AA 1-205) [Mus musculus] >gi_550060 (M28209) GTP-binding protein [Homo sapiens] >gi_763158_emb_CAA33760_ (X15744) GTP-binding protein [Mus musculus]
Seq. No.	228749
Seq. ID	LIB3196-015-P1-M1-G12
Method	BLASTX
NCBI GI	g730773
BLAST score	384
E value	3.0e-37
Match length	71
% identity	100
NCBI Description	SPLICING FACTOR, ARGININE/SERINE-RICH 1 (PRE-MRNA SPLICING FACTOR SF2, P33 SUBUNIT) (ALTERNATIVE SPLICING FACTOR ASF-1) >gi_105293_pir__A40040 alternative splicing factor ASF-1 - human >gi_179075 (M72709) alternative [Homo sapiens] >gi_338047 (M69040) SF2p33 [Homo sapiens]
Seq. No.	228750
Seq. ID	LIB3196-015-P1-M1-G7
Method	BLASTX
NCBI GI	g2582665
BLAST score	256
E value	2.0e-22
Match length	88
% identity	59
NCBI Description	(Z82983) thi [Citrus sinensis]
Seq. No.	228751
Seq. ID	LIB3196-015-P1-M1-G9
Method	BLASTX
NCBI GI	g133841
BLAST score	232
E value	2.0e-19
Match length	51
% identity	94
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi_71016_pir__R3NT18 ribosomal protein S18 - common tobacco chloroplast >gi_11851_emb_CAA77371_ (Z00044) ribosomal protein S18 [Nicotiana tabacum] >gi_225220_prf__1211235BB ribosomal protein S18 [Nicotiana tabacum]
Seq. No.	228752
Seq. ID	LIB3196-015-P1-M1-H1
Method	BLASTX
NCBI GI	g4512685
BLAST score	180
E value	3.0e-13
Match length	70
% identity	49
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)

hypothetical protein [Arabidopsis thaliana]

Seq. No.	228753
Seq. ID	LIB3196-015-P1-M1-H11
Method	BLASTX
NCBI GI	g417745
BLAST score	638
E value	6.0e-67
Match length	125
% identity	98
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No.	228754
Seq. ID	LIB3196-015-P1-M1-H12
Method	BLASTX
NCBI GI	g3236242
BLAST score	364
E value	7.0e-35
Match length	93
% identity	80
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	228755
Seq. ID	LIB3196-015-P1-M1-H4
Method	BLASTX
NCBI GI	g2143868
BLAST score	422
E value	1.0e-41
Match length	86
% identity	97
NCBI Description	NAB1 - rat >gi_915282 (U17253) NAB1 [Rattus norvegicus]

Seq. No.	228756
Seq. ID	LIB3196-015-P1-M1-H5
Method	BLASTX
NCBI GI	g2505876
BLAST score	258
E value	2.0e-22
Match length	99
% identity	55
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	228757
Seq. ID	LIB3196-016-P1-M1-A1
Method	BLASTX
NCBI GI	g218157
BLAST score	207
E value	6.0e-17
Match length	50
% identity	80
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	228758
Seq. ID	LIB3196-016-P1-M1-A10

Method	BLASTX
NCBI GI	g2119204
BLAST score	382
E value	6.0e-37
Match length	86
% identity	92
NCBI Description	vimentin - human >gi_37850_emb_CAA39600_ (X56134) vimentin [Homo sapiens]

Seq. No.	228759
Seq. ID	LIB3196-016-P1-M1-A11
Method	BLASTX
NCBI GI	g3746127
BLAST score	323
E value	4.0e-30
Match length	65
% identity	91
NCBI Description	(U76253) E25B protein [Mus musculus]

Seq. No.	228760
Seq. ID	LIB3196-016-P1-M1-A12
Method	BLASTX
NCBI GI	g3746127
BLAST score	130
E value	2.0e-17
Match length	60
% identity	83
NCBI Description	(U76253) E25B protein [Mus musculus]

Seq. No.	228761
Seq. ID	LIB3196-016-P1-M1-A2
Method	BLASTX
NCBI GI	g3041684
BLAST score	238
E value	4.0e-20
Match length	78
% identity	69
NCBI Description	EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED MEMBRANE PROTEIN) (CL-20) (B4B PROTEIN) >gi_1460068_emb_CAA90627_ (Z50751) B4B [Homo sapiens] >gi_1542883_emb_CAA69217_ (Y07909) progression associated protein [Homo sapiens] >gi_1932786 (U77085) epithelial membrane protein [Homo sapiens] >gi_2506160 (U43916) TMP [Homo sapiens] >gi_4503559_ref_NP_001414.1_pEMP1_ epithelial membrane protein

Seq. No.	228762
Seq. ID	LIB3196-016-P1-M1-A3
Method	BLASTX
NCBI GI	g3335359
BLAST score	210
E value	9.0e-17
Match length	125
% identity	43
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	228763

Seq. ID	LIB3196-016-P1-M1-A8
Method	BLASTX
NCBI GI	g179950
BLAST score	509
E value	5.0e-52
Match length	98
% identity	96
NCBI Description	(K02400) catalase [Homo sapiens]

Seq. No.	228764
Seq. ID	LIB3196-016-P1-M1-B11
Method	BLASTX
NCBI GI	g82426
BLAST score	537
E value	4.0e-55
Match length	112
% identity	45
NCBI Description	ubiquitin precursor - barley (fragment) >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare]

Seq. No.	228765
Seq. ID	LIB3196-016-P1-M1-B2
Method	BLASTX
NCBI GI	g388891
BLAST score	631
E value	4.0e-66
Match length	122
% identity	100
NCBI Description	(L12711) transketolase [Homo sapiens]

Seq. No.	228766
Seq. ID	LIB3196-016-P1-M1-B3
Method	BLASTX
NCBI GI	g107458
BLAST score	680
E value	8.0e-72
Match length	126
% identity	100
NCBI Description	protein kinase (EC 2.7.1.37) cdc2/cdc28-like - human

Seq. No.	228767
Seq. ID	LIB3196-016-P1-M1-B5
Method	BLASTX
NCBI GI	g3790102
BLAST score	389
E value	9.0e-38
Match length	85
% identity	82
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	228768
Seq. ID	LIB3196-016-P1-M1-B6
Method	BLASTX
NCBI GI	g3790102
BLAST score	366

E value	5.0e-35
Match length	87
% identity	77
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	228769
Seq. ID	LIB3196-016-P1-M1-B7
Method	BLASTX
NCBI GI	g3643595
BLAST score	396
E value	1.0e-38
Match length	111
% identity	68
NCBI Description	(AC005395) putative oleosin protein [Arabidopsis thaliana]

Seq. No.	228770
Seq. ID	LIB3196-016-P1-M1-B8
Method	BLASTX
NCBI GI	g3355311
BLAST score	189
E value	2.0e-18
Match length	59
% identity	90
NCBI Description	(AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No.	228771
Seq. ID	LIB3196-016-P1-M1-C10
Method	BLASTX
NCBI GI	g3176098
BLAST score	376
E value	3.0e-36
Match length	109
% identity	70
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	228772
Seq. ID	LIB3196-016-P1-M1-C11
Method	BLASTX
NCBI GI	g1001355
BLAST score	304
E value	8.0e-28
Match length	106
% identity	58
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	228773
Seq. ID	LIB3196-016-P1-M1-C12
Method	BLASTX
NCBI GI	g1001355
BLAST score	250
E value	2.0e-21
Match length	103
% identity	52
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	228774
Seq. ID	LIB3196-016-P1-M1-C6
Method	BLASTX
NCBI GI	g266690
BLAST score	169
E value	6.0e-12
Match length	78
% identity	47
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	228775
Seq. ID	LIB3196-016-P1-M1-C8
Method	BLASTX
NCBI GI	g3738257
BLAST score	327
E value	1.0e-30
Match length	72
% identity	90
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	228776
Seq. ID	LIB3196-016-P1-M1-D12
Method	BLASTX
NCBI GI	g3094014
BLAST score	153
E value	4.0e-10
Match length	41
% identity	73
NCBI Description	(AF060862) unknown [Homo sapiens]

Seq. No.	228777
Seq. ID	LIB3196-016-P1-M1-D2
Method	BLASTX
NCBI GI	g285957
BLAST score	174
E value	2.0e-12
Match length	133
% identity	31
NCBI Description	(D14689) KIAA0023 [Homo sapiens]

Seq. No.	228778
Seq. ID	LIB3196-016-P1-M1-D3
Method	BLASTX
NCBI GI	g3914480
BLAST score	389
E value	1.0e-37
Match length	77
% identity	94
NCBI Description	PROTEASE M PRECURSOR (NEUROSIN) (ZYME) (SP59) >gi_1518788 (U62801) protease M [Homo sapiens] >gi_1805493_dbj_BAA11306_ (D78203) neurosin [Homo sapiens] >gi_2318115 (AF013988) serine protease [Homo sapiens] >gi_4506155_ref_NP_002765.1_pPRSS9_ protease, serine, 9 (neurosin)

Seq. No.	228779
Seq. ID	LIB3196-016-P1-M1-D4
Method	BLASTX
NCBI GI	g2369714
BLAST score	497
E value	2.0e-50
Match length	107
% identity	88
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	228780
Seq. ID	LIB3196-016-P1-M1-D5
Method	BLASTX
NCBI GI	g3202042
BLAST score	355
E value	9.0e-34
Match length	104
% identity	67
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	228781
Seq. ID	LIB3196-016-P1-M1-D7
Method	BLASTX
NCBI GI	g2498490
BLAST score	649
E value	3.0e-68
Match length	129
% identity	97
NCBI Description	VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6_ murine mammary tumor integration site 6 (oncogene homolog)

Seq. No.	228782
Seq. ID	LIB3196-016-P1-M1-D8
Method	BLASTX
NCBI GI	g4544372
BLAST score	190
E value	2.0e-14
Match length	92
% identity	38
NCBI Description	(AC006920) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	228783
Seq. ID	LIB3196-016-P1-M1-E1
Method	BLASTX
NCBI GI	g81857
BLAST score	333
E value	3.0e-31
Match length	74
% identity	86

NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]
Seq. No.	228784
Seq. ID	LIB3196-016-P1-M1-E12
Method	BLASTX
NCBI GI	g2072977
BLAST score	183
E value	1.0e-13
Match length	117
% identity	45
NCBI Description	(U93574) putative p150 [Homo sapiens]
Seq. No.	228785
Seq. ID	LIB3196-016-P1-M1-E3
Method	BLASTX
NCBI GI	g3288675
BLAST score	363
E value	1.0e-34
Match length	100
% identity	74
NCBI Description	(D88575) TP55 [Homo sapiens] >gi_3769373 (AF027866) megsin [Homo sapiens] >gi_4505149_ref_NP_003775.1_pMEGSIN_ UNKNOWN
Seq. No.	228786
Seq. ID	LIB3196-016-P1-M1-E4
Method	BLASTX
NCBI GI	g3687237
BLAST score	203
E value	6.0e-16
Match length	100
% identity	50
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]
Seq. No.	228787
Seq. ID	LIB3196-016-P1-M1-E5
Method	BLASTX
NCBI GI	g127621
BLAST score	482
E value	1.0e-48
Match length	92
% identity	98
NCBI Description	MYC PROTO-ONCOGENE PROTEIN (C-MYC) >gi_86684_pir__JU0449 c-myc protein - chimpanzee >gi_176653 (M38057) [Chimpanzee c-myc proto-oncogene, complete cds.], gene products [Pan troglodytes]
Seq. No.	228788
Seq. ID	LIB3196-016-P1-M1-E6
Method	BLASTX
NCBI GI	g283985
BLAST score	492
E value	8.0e-50
Match length	129
% identity	77

NCBI Description	amphiglycan - human >gi_28680_emb_CAA47406_ (X67016) amphiglycan [Homo sapiens] >gi_4506861_ref_NP_002990.1_pSDC4_ syndecan 4 (amphiglycan, ryudocan)
Seq. No.	228789
Seq. ID	LIB3196-016-P1-M1-E7
Method	BLASTX
NCBI GI	g1350762
BLAST score	305
E value	6.0e-28
Match length	80
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT BINDING PROTEIN 107) (TAXREB107) (NEOPLASM-RELATED PROTEIN C140) >gi_2136251_pir__I51803 TAXREB107 - human >gi_433416_dbj_BAA04491_ (D17554) TAXREB107 [Homo sapiens]
Seq. No.	228790
Seq. ID	LIB3196-016-P1-M1-E8
Method	BLASTX
NCBI GI	g1620898
BLAST score	538
E value	2.0e-55
Match length	109
% identity	97
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]
Seq. No.	228791
Seq. ID	LIB3196-016-P1-M1-E9
Method	BLASTX
NCBI GI	g1666236
BLAST score	179
E value	4.0e-13
Match length	107
% identity	31
NCBI Description	(U76261) unknown [Hordeum vulgare]
Seq. No.	228792
Seq. ID	LIB3196-016-P1-M1-F1
Method	BLASTX
NCBI GI	g1488368
BLAST score	679
E value	1.0e-71
Match length	129
% identity	89
NCBI Description	(S80993) MG1=high molecular weight mucin {C-terminal} [human, sublingual gland, Peptide Partial, 196 aa] [Homo sapiens]
Seq. No.	228793
Seq. ID	LIB3196-016-P1-M1-F10
Method	BLASTX
NCBI GI	g1743354
BLAST score	536
E value	5.0e-55

Match length	130
% identity	75
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	228794
Seq. ID	LIB3196-016-P1-M1-F11
Method	BLASTX
NCBI GI	g82207
BLAST score	403
E value	2.0e-39
Match length	120
% identity	71
NCBI Description	hypothetical protein 1708 - common tobacco chloroplast

Seq. No.	228795
Seq. ID	LIB3196-016-P1-M1-F12
Method	BLASTX
NCBI GI	g1362804
BLAST score	572
E value	4.0e-59
Match length	124
% identity	91
NCBI Description	giantin - human >gi_405715_emb_CAA53052_ (X75304) giantin [Homo sapiens]

Seq. No.	228796
Seq. ID	LIB3196-016-P1-M1-F7
Method	BLASTX
NCBI GI	g266691
BLAST score	272
E value	4.0e-24
Match length	96
% identity	62
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	228797
Seq. ID	LIB3196-016-P1-M1-G4
Method	BLASTX
NCBI GI	g113116
BLAST score	160
E value	5.0e-11
Match length	82
% identity	43
NCBI Description	ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase [Rattus norvegicus]

Seq. No.	228798
Seq. ID	LIB3196-016-P1-M1-G5
Method	BLASTX
NCBI GI	g1350762
BLAST score	389
E value	1.0e-37
Match length	96
% identity	77

NCBI Description	60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT BINDING PROTEIN 107) (TAXREB107) (NEOPLASM-RELATED PROTEIN C140) >gi_2136251_pir__I51803 TAXREB107 - human >gi_433416_dbj_BAA04491_ (D17554) TAXREB107 [Homo sapiens]
Seq. No.	228799
Seq. ID	LIB3196-016-P1-M1-G9
Method	BLASTX
NCBI GI	g3668089
BLAST score	364
E value	6.0e-35
Match length	112
% identity	58
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	228800
Seq. ID	LIB3196-016-P1-M1-H10
Method	BLASTX
NCBI GI	g91300
BLAST score	207
E value	8.0e-23
Match length	110
% identity	57
NCBI Description	signal recognition particle 54K protein - mouse
Seq. No.	228801
Seq. ID	LIB3196-016-P1-M1-H9
Method	BLASTX
NCBI GI	g4335724
BLAST score	174
E value	1.0e-12
Match length	121
% identity	39
NCBI Description	(AC006248) putative RING-H2 finger protein [Arabidopsis thaliana]
Seq. No.	228802
Seq. ID	LIB3196-017-P1-M1-A1
Method	BLASTX
NCBI GI	g730832
BLAST score	169
E value	5.0e-12
Match length	53
% identity	57
NCBI Description	8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN) (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi_18748_emb_CAA78359_ (Z13956) a protein similar to potato tuber protein p322 homolgous to Bowman-Birk Proteinase Inhibitor [Glycine max]
Seq. No.	228803
Seq. ID	LIB3196-017-P1-M1-A11
Method	BLASTX
NCBI GI	g1703146
BLAST score	590
E value	2.0e-61

Match length	116
% identity	100
NCBI Description	ACTIN-LIKE PROTEIN 2 (ACTIN-LIKE PROTEIN ACTL) >gi_1079382_pir__JC4039 actin-like protein - chicken >gi_806554_emb_CAA52151_ (X73971) actin-like protein [Gallus gallus]

Seq. No.	228804
Seq. ID	LIB3196-017-P1-M1-A12
Method	BLASTX
NCBI GI	g1239957
BLAST score	276
E value	1.0e-24
Match length	109
% identity	59
NCBI Description	(L38487) estrogen receptor-related protein [Homo sapiens]

Seq. No.	228805
Seq. ID	LIB3196-017-P1-M1-A4
Method	BLASTX
NCBI GI	g2809244
BLAST score	192
E value	1.0e-14
Match length	87
% identity	47
NCBI Description	(AC002560) F21B7.13 [Arabidopsis thaliana]

Seq. No.	228806
Seq. ID	LIB3196-017-P1-M1-A6
Method	BLASTX
NCBI GI	g1703463
BLAST score	335
E value	1.0e-31
Match length	83
% identity	83
NCBI Description	POTASSIUM-TRANSPORTING ATPASE ALPHA-LIKE CHAIN (PROTON PUMP) (NON-GASTRIC H+/K+ ATPASE ALPHA SUBUNIT) >gi_404017 (U02076) ATP-driven ion pump [Homo sapiens] >gi_1237010 (L42563) non-gastric H+,K+-ATPase [Homo sapiens] >gi_1588308_prf__2208325A H/K-ATPase [Homo sapiens] >gi_4502275_ref_NP_001667.1_pATP1AL1_ ATPase, Na+/K+ transporting, alpha polypeptide-like

Seq. No.	228807
Seq. ID	LIB3196-017-P1-M1-A9
Method	BLASTX
NCBI GI	g3337356
BLAST score	514
E value	2.0e-52
Match length	116
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	228808
Seq. ID	LIB3196-017-P1-M1-B1
Method	BLASTX

NCBI GI	g3789925
BLAST score	232
E value	2.0e-19
Match length	90
% identity	51
NCBI Description	(AF086625) phosphoinositide-dependent protein kinase PDK1 [Mus musculus]

Seq. No.	228809
Seq. ID	LIB3196-017-P1-M1-B10
Method	BLASTX
NCBI GI	g3821280
BLAST score	415
E value	4.0e-41
Match length	86
% identity	88
NCBI Description	(AJ009952) asparagine synthetase type II [Phaseolus vulgaris]

Seq. No.	228810
Seq. ID	LIB3196-017-P1-M1-B11
Method	BLASTX
NCBI GI	g547299
BLAST score	550
E value	1.0e-56
Match length	99
% identity	100
NCBI Description	beta 2-microglobulin, beta 2-M [Papio hamadryas=baboons, 26CB-1, Peptide, 99 aa]

Seq. No.	228811
Seq. ID	LIB3196-017-P1-M1-B12
Method	BLASTX
NCBI GI	g3004502
BLAST score	631
E value	4.0e-66
Match length	121
% identity	97
NCBI Description	(U97276) quiescin [Homo sapiens] >gi_4506361_ref_NP_002817.1_pQSCN6_ quiescin Q6

Seq. No.	228812
Seq. ID	LIB3196-017-P1-M1-B2
Method	BLASTX
NCBI GI	g1346190
BLAST score	447
E value	2.0e-44
Match length	89
% identity	96
NCBI Description	GLUTAMATE--CYSTEINE LIGASE CATALYTIC SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS HEAVY CHAIN) >gi_87540_pir__JH0611 glutamate--cysteine ligase (EC 6.3.2.2) heavy chain - human >gi_183039 (M90656) gamma-glutamylcysteine synthetase [Homo sapiens] >gi_4557625_ref_NP_001489.1_pGLCLC_ glutamate-cysteine ligase

Seq. No.	228813
Seq. ID	LIB3196-017-P1-M1-B5
Method	BLASTX
NCBI GI	g2160166
BLAST score	246
E value	4.0e-21
Match length	108
% identity	48
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	228814
Seq. ID	LIB3196-017-P1-M1-B7
Method	BLASTX
NCBI GI	g2098705
BLAST score	178
E value	3.0e-13
Match length	91
% identity	43
NCBI Description	(U82973) pectinesterase [Citrus sinensis]

Seq. No.	228815
Seq. ID	LIB3196-017-P1-M1-C10
Method	BLASTX
NCBI GI	g207905
BLAST score	522
E value	2.0e-53
Match length	103
% identity	99
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	228816
Seq. ID	LIB3196-017-P1-M1-C12
Method	BLASTX
NCBI GI	g2589011
BLAST score	563
E value	3.0e-58
Match length	119
% identity	53
NCBI Description	(AB008549) type 1 procollagen C-proteinase enhancer protein [Homo sapiens] >gi_3135316 (AF053356) PCOLCE [Homo sapiens] >gi_4322387_gb_AAD16041_ (AF083655) procollagen C-proteinase enhancer protein [Homo sapiens]

Seq. No.	228817
Seq. ID	LIB3196-017-P1-M1-C3
Method	BLASTX
NCBI GI	g122007
BLAST score	416
E value	6.0e-41
Match length	106
% identity	78
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	228818
Seq. ID	LIB3196-017-P1-M1-C9

Method	BLASTX
NCBI GI	g137580
BLAST score	173
E value	7.0e-13
Match length	36
% identity	97
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No.	228819
Seq. ID	LIB3196-017-P1-M1-D1
Method	BLASTX
NCBI GI	g3901014
BLAST score	280
E value	5.0e-25
Match length	62
% identity	79
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	228820
Seq. ID	LIB3196-017-P1-M1-D12
Method	BLASTX
NCBI GI	g586120
BLAST score	231
E value	3.0e-19
Match length	102
% identity	49
NCBI Description	TRICHOHYALIN >gi_539701_pir__A45973 trichohyalin - human >gi_292836 (L09190) trichohyalin [Homo sapiens]

Seq. No.	228821
Seq. ID	LIB3196-017-P1-M1-D5
Method	BLASTX
NCBI GI	g126156
BLAST score	432
E value	7.0e-43
Match length	106
% identity	79
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228822
Seq. ID	LIB3196-017-P1-M1-D6
Method	BLASTX
NCBI GI	g3834307
BLAST score	322
E value	6.0e-30
Match length	121
% identity	50
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679

	putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]
Seq. No.	228823
Seq. ID	LIB3196-017-P1-M1-D8
Method	BLASTX
NCBI GI	g2262170
BLAST score	344
E value	2.0e-32
Match length	122
% identity	57
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]
Seq. No.	228824
Seq. ID	LIB3196-017-P1-M1-D9
Method	BLASTX
NCBI GI	g126156
BLAST score	215
E value	6.0e-19
Match length	65
% identity	78
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]
Seq. No.	228825
Seq. ID	LIB3196-017-P1-M1-E1
Method	BLASTX
NCBI GI	g130770
BLAST score	561
E value	6.0e-58
Match length	121
% identity	88
NCBI Description	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA) >gi_2135910_pir__I53775 phosphatidylinositol transfer protein - human >gi_189939 (M73704) phosphatidylinositol transfer protein [Homo sapiens]
Seq. No.	228826
Seq. ID	LIB3196-017-P1-M1-E11
Method	BLASTX
NCBI GI	g1174592
BLAST score	573
E value	2.0e-59
Match length	114
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]
Seq. No.	228827

Seq. ID	LIB3196-017-P1-M1-E2
Method	BLASTX
NCBI GI	g4063760
BLAST score	179
E value	4.0e-13
Match length	55
% identity	58
NCBI Description	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq. No.	228828
Seq. ID	LIB3196-017-P1-M1-E3
Method	BLASTX
NCBI GI	g2160517
BLAST score	325
E value	3.0e-30
Match length	89
% identity	79
NCBI Description	(U42408) ladinin [Homo sapiens]

Seq. No.	228829
Seq. ID	LIB3196-017-P1-M1-E4
Method	BLASTX
NCBI GI	g1946355
BLAST score	152
E value	5.0e-10
Match length	109
% identity	35
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	228830
Seq. ID	LIB3196-017-P1-M1-F1
Method	BLASTX
NCBI GI	g2833280
BLAST score	621
E value	6.0e-65
Match length	128
% identity	92
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (COMPLEX I-39KD) (CI-39KD)

Seq. No.	228831
Seq. ID	LIB3196-017-P1-M1-F10
Method	BLASTX
NCBI GI	g683553
BLAST score	179
E value	3.0e-13
Match length	44
% identity	77
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	228832
Seq. ID	LIB3196-017-P1-M1-F3
Method	BLASTX
NCBI GI	g3413706

BLAST score	460
E value	4.0e-46
Match length	117
% identity	68
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228833
Seq. ID	LIB3196-017-P1-M1-F5
Method	BLASTX
NCBI GI	g3335375
BLAST score	606
E value	3.0e-63
Match length	117
% identity	97
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	228834
Seq. ID	LIB3196-017-P1-M1-G1
Method	BLASTX
NCBI GI	g1362107
BLAST score	177
E value	5.0e-13
Match length	44
% identity	82
NCBI Description	GUT8-2a protein - common tobacco

Seq. No.	228835
Seq. ID	LIB3196-017-P1-M1-G10
Method	BLASTX
NCBI GI	g4191319
BLAST score	162
E value	3.0e-11
Match length	31
% identity	100
NCBI Description	(AF044670) 33 kDa Vamp-associated protein; VAP-33 [Homo sapiens] >gi_4240456 (AF086627) VAMP-associated protein A [Homo sapiens]

Seq. No.	228836
Seq. ID	LIB3196-017-P1-M1-G12
Method	BLASTX
NCBI GI	g2119228
BLAST score	188
E value	3.0e-14
Match length	67
% identity	60
NCBI Description	keratin K4a - human (fragment) >gi_313159_emb_CAA47914_ (X67683) keratin K4a [Homo sapiens]

Seq. No.	228837
Seq. ID	LIB3196-017-P1-M1-G6
Method	BLASTX
NCBI GI	g2583135
BLAST score	389
E value	9.0e-38
Match length	92
% identity	79

NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana] >gi_3822216 (AF074948) FIL [Arabidopsis thaliana] >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs protein [Arabidopsis thaliana]
Seq. No.	228838
Seq. ID	LIB3196-017-P1-M1-G9
Method	BLASTX
NCBI GI	g117501
BLAST score	285
E value	8.0e-26
Match length	54
% identity	96
NCBI Description	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A) >gi_87015_pir__A37047 calreticulin precursor - human >gi_179882 (M84739) calreticulin [Homo sapiens] >gi_337487 (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A) precursor [Homo sapiens] >gi_1905911 (AD000092) calreticulin [Homo sapiens]
Seq. No.	228839
Seq. ID	LIB3196-017-P1-M1-H1
Method	BLASTX
NCBI GI	g224293
BLAST score	375
E value	3.0e-36
Match length	76
% identity	100
NCBI Description	histone H4 [Triticum aestivum]
Seq. No.	228840
Seq. ID	LIB3196-017-P1-M1-H10
Method	BLASTX
NCBI GI	g2894607
BLAST score	359
E value	3.0e-34
Match length	101
% identity	65
NCBI Description	(AL021889) NAM (no apical meristem) - like protein [Arabidopsis thaliana]
Seq. No.	228841
Seq. ID	LIB3196-017-P1-M1-H11
Method	BLASTX
NCBI GI	g2384671
BLAST score	407
E value	4.0e-40
Match length	91
% identity	85
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]
Seq. No.	228842
Seq. ID	LIB3196-017-P1-M1-H5
Method	BLASTX
NCBI GI	g683553

BLAST score	272
E value	4.0e-24
Match length	104
% identity	57
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	228843
Seq. ID	LIB3196-017-P1-M1-H6
Method	BLASTX
NCBI GI	g4580472
BLAST score	545
E value	5.0e-56
Match length	114
% identity	86
NCBI Description	(AC006081) DNA binding protein;similar to CDC27 and nuclear scaffold proteins [Arabidopsis thaliana]

Seq. No.	228844
Seq. ID	LIB3196-017-P1-M1-H8
Method	BLASTX
NCBI GI	g113287
BLAST score	551
E value	9.0e-57
Match length	105
% identity	100
NCBI Description	ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1) >gi_71610_pir__ATHU actin, skeletal muscle - human >gi_71612_pir__ATRT actin, skeletal muscle - rat >gi_71613_pir__ATCH actin alpha, skeletal muscle - chicken >gi_90264_pir__A24904 actin, skeletal muscle - mouse >gi_55577_emb_CAA24529_ (V01218) actin [Rattus norvegicus] >gi_63029_emb_CAA24753_ (V01507) a-actin [Gallus gallus] >gi_178029 (J00068) alpha-actin [Homo sapiens] >gi_309088 (M12866) actin [Mus musculus] >gi_337746 (M20543) alpha-skeletal actin precursor [Homo sapiens] >gi_387081 (M12347) alpha-actin [Mus musculus] >gi_790202 (U16368) skeletal alpha actin [Sus scrofa] >gi_223503_prf__0809315A actin [Rattus norvegicus] >gi_4501881_ref_NP_001091.1_pACTA1_ actin, alpha 1, skeletal muscle

Seq. No.	228845
Seq. ID	LIB3196-018-P1-M1-A10
Method	BLASTX
NCBI GI	g1076510
BLAST score	446
E value	2.0e-44
Match length	107
% identity	79
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No.	228846
Seq. ID	LIB3196-018-P1-M1-A12
Method	BLASTX

NCBI GI	g3786007
BLAST score	276
E value	1.0e-24
Match length	104
% identity	59
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228847
Seq. ID	LIB3196-018-P1-M1-A2
Method	BLASTX
NCBI GI	g3688191
BLAST score	196
E value	3.0e-15
Match length	63
% identity	63
NCBI Description	(AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]

Seq. No.	228848
Seq. ID	LIB3196-018-P1-M1-A4
Method	BLASTX
NCBI GI	g137578
BLAST score	497
E value	2.0e-50
Match length	118
% identity	79
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228849
Seq. ID	LIB3196-018-P1-M1-A6
Method	BLASTX
NCBI GI	g2244754
BLAST score	465
E value	1.0e-46
Match length	97
% identity	84
NCBI Description	(Z97335) heat shock transcription factor homolog [Arabidopsis thaliana]

Seq. No.	228850
Seq. ID	LIB3196-018-P1-M1-B11
Method	BLASTX
NCBI GI	g2879792
BLAST score	129
E value	2.0e-16
Match length	88
% identity	60
NCBI Description	(AL021813) SPAC23A1.04c, possible glycosyl hydrolase, len:756aa, similar eg. to C. elegans Q18679, (586aa), fasta scores, opt:566, E():0, (48.0% identity in 452 aa overlap), also similar to YHR204W, YH04_YEAST, P38888, hypothet

Seq. No.	228851
Seq. ID	LIB3196-018-P1-M1-B2
Method	BLASTX
NCBI GI	g226407
BLAST score	290
E value	3.0e-26
Match length	121
% identity	46
NCBI Description	retrotransposon del1-46 [Lilium henryi]

Seq. No.	228852
Seq. ID	LIB3196-018-P1-M1-B4
Method	BLASTX
NCBI GI	g2224931
BLAST score	312
E value	9.0e-29
Match length	119
% identity	57
NCBI Description	(AF004215) ethylene-insensitive3-like3 [Arabidopsis thaliana]

Seq. No.	228853
Seq. ID	LIB3196-018-P1-M1-C4
Method	BLASTX
NCBI GI	g1375485
BLAST score	631
E value	4.0e-66
Match length	119
% identity	100
NCBI Description	(U43077) CDC37 homolog [Homo sapiens] >gi_1421821 (U63131) CDC37 homolog [Homo sapiens]

Seq. No.	228854
Seq. ID	LIB3196-018-P1-M1-C5
Method	BLASTX
NCBI GI	g280816
BLAST score	441
E value	7.0e-44
Match length	86
% identity	99
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin

Seq. No.	228855
Seq. ID	LIB3196-018-P1-M1-C7
Method	BLASTX
NCBI GI	g3445207
BLAST score	306
E value	3.0e-28
Match length	99
% identity	64
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	228856
Seq. ID	LIB3196-018-P1-M1-C8

Method	BLASTX
NCBI GI	g3096949
BLAST score	262
E value	2.0e-25
Match length	98
% identity	62
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	228857
Seq. ID	LIB3196-018-P1-M1-C9
Method	BLASTX
NCBI GI	g1070592
BLAST score	590
E value	2.0e-61
Match length	114
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - human >gi_37565_emb_CAA40313_ (X56998) ubiquitin-52 amino acid fusion protein [Homo sapiens] >gi_37567_emb_CAA40312_ (X56997) ubiquitin-52 amino acid fusion protein [Homo sapiens] >gi_37569_emb_CAA40314_ (X56999) ubiquitin-52 amino acid fusion protein [Homo sapiens] >gi_600538 (M24508) ubiquitin [Artificial sequence] >gi_1050758_emb_CAA57958_ (X82636) ubiquitin/ribosomal protein L40 [Rattus norvegicus] >gi_1628608 (U72496) ubiquitin/ribosomal fusion protein [Sus scrofa] >gi_3288887 (AC005253) ubiquitin-52 amino acid fusion protein [Homo sapiens] >gi_4139066 (AF081142) ubiquitin/ribosomal protein CEP52 fusion protein [Cricetulus sp.] >gi_4262555_gb_AAD14688_ (AF118402) ubiquitin/60S ribosomal fusion protein [Mus musculus] >gi_4507761_ref_NP_003324.1_pUBA52_ ubiquitin A-52 residue ribosomal protein fusion product

Seq. No.	228858
Seq. ID	LIB3196-018-P1-M1-D10
Method	BLASTX
NCBI GI	g125077
BLAST score	238
E value	4.0e-20
Match length	52
% identity	94
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	228859
Seq. ID	LIB3196-018-P1-M1-D2
Method	BLASTX
NCBI GI	g123101
BLAST score	316
E value	2.0e-29
Match length	80
% identity	81

NCBI Description	NONHISTONE CHROMOSOMAL PROTEIN HMG-14 >gi_107207_pir__A33310 nonhistone chromosomal protein HMG-14 - human >gi_306863 (J02621) high mobility group protein 14 [Homo sapiens] >gi_386779 (M21339) high mobility group protein 14 [Homo sapiens] >gi_3171155 (AF064861) HMG-14 [Homo sapiens]

Seq. No.	228860
Seq. ID	LIB3196-018-P1-M1-D4
Method	BLASTX
NCBI GI	g2392771
BLAST score	321
E value	6.0e-30
Match length	94
% identity	65
NCBI Description	(AC002534) putative kinesin-like protein [Arabidopsis thaliana]

Seq. No.	228861
Seq. ID	LIB3196-018-P1-M1-D5
Method	BLASTX
NCBI GI	g2088654
BLAST score	526
E value	7.0e-54
Match length	117
% identity	88
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	228862
Seq. ID	LIB3196-018-P1-M1-D7
Method	BLASTX
NCBI GI	g435480
BLAST score	313
E value	5.0e-29
Match length	78
% identity	78
NCBI Description	(X76679) MAL-b [Homo sapiens]

Seq. No.	228863
Seq. ID	LIB3196-018-P1-M1-E10
Method	BLASTX
NCBI GI	g3063396
BLAST score	432
E value	7.0e-43
Match length	99
% identity	82
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	228864
Seq. ID	LIB3196-018-P1-M1-E4
Method	BLASTX
NCBI GI	g115502
BLAST score	453
E value	3.0e-45
Match length	88
% identity	53

NCBI Description	CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) >gi_71690_pir__MCHUNB calmodulin-related protein NB-1 - human >gi_29650_emb_CAA31809_ (X13461) hGH6 calmodulin-like protein [Homo sapiens] >gi_189081 (M58026) NB-1 [Homo sapiens]

Seq. No.	228865
Seq. ID	LIB3196-018-P1-M1-E5
Method	BLASTX
NCBI GI	g2245020
BLAST score	526
E value	7.0e-54
Match length	120
% identity	81
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	228866
Seq. ID	LIB3196-018-P1-M1-F1
Method	BLASTX
NCBI GI	g3851636
BLAST score	471
E value	2.0e-47
Match length	107
% identity	82
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	228867
Seq. ID	LIB3196-018-P1-M1-F10
Method	BLASTX
NCBI GI	g2119180
BLAST score	519
E value	5.0e-53
Match length	118
% identity	94
NCBI Description	S-laminin - human (fragment) >gi_288401_emb_CAA51288_ (X72760) S-laminin [Homo sapiens]

Seq. No.	228868
Seq. ID	LIB3196-018-P1-M1-F11
Method	BLASTX
NCBI GI	g2137594
BLAST score	168
E value	7.0e-12
Match length	46
% identity	65
NCBI Description	neuropsin - mouse >gi_1020091_dbj_BAA06451_ (D30785) neuropsin [Mus musculus] >gi_1582323_prf__2118319A neuropsin [Mus musculus]

Seq. No.	228869
Seq. ID	LIB3196-018-P1-M1-F7
Method	BLASTX
NCBI GI	g114682
BLAST score	162
E value	2.0e-11
Match length	59

% identity	59
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No.	228870
Seq. ID	LIB3196-018-P1-M1-G10
Method	BLASTX
NCBI GI	g419482
BLAST score	185
E value	7.0e-14
Match length	111
% identity	43
NCBI Description	pol polyprotein - human endogenous virus S71

Seq. No.	228871
Seq. ID	LIB3196-018-P1-M1-G11
Method	BLASTX
NCBI GI	g2190550
BLAST score	456
E value	1.0e-45
Match length	122
% identity	75
NCBI Description	(AC001229) ESTs gb_T45673,gb_N37512 come from this gene. [Arabidopsis thaliana]

Seq. No.	228872
Seq. ID	LIB3196-018-P1-M1-G12
Method	BLASTX
NCBI GI	g2119204
BLAST score	194
E value	6.0e-15
Match length	62
% identity	66
NCBI Description	vimentin - human >gi_37850_emb_CAA39600_ (X56134) vimentin [Homo sapiens]

Seq. No.	228873
Seq. ID	LIB3196-018-P1-M1-G2
Method	BLASTX
NCBI GI	g3355465
BLAST score	382
E value	5.0e-37
Match length	114
% identity	62
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	228874
Seq. ID	LIB3196-018-P1-M1-G3
Method	BLASTX
NCBI GI	g2605714
BLAST score	243
E value	1.0e-20

Match length	63
% identity	79
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	228875
Seq. ID	LIB3196-018-P1-M1-G4
Method	BLASTX
NCBI GI	g2507389
BLAST score	617
E value	2.0e-64
Match length	124
% identity	94
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_1848137_emb_CAA62998_ (X91902) serine hydroxymethyltransferase [Oryctolagus cuniculus]

Seq. No.	228876
Seq. ID	LIB3196-018-P1-M1-G5
Method	BLASTX
NCBI GI	g2119340
BLAST score	666
E value	3.0e-70
Match length	127
% identity	98
NCBI Description	calponin - human >gi_1526432_dbj_BAA12090_ (D83735) neutral calponin [Homo sapiens]

Seq. No.	228877
Seq. ID	LIB3196-018-P1-M1-G7
Method	BLASTX
NCBI GI	g1174637
BLAST score	175
E value	1.0e-12
Match length	37
% identity	97
NCBI Description	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) >gi_1083817_pir__A55190 transitional endoplasmic reticulum ATPase - rat >gi_641973 (U11760) transitional endoplasmic reticulum ATPase [Rattus norvegicus] >gi_1093322_prf__2103265A transitional endoplasmic reticulum ATPase [Rattus norvegicus]

Seq. No.	228878
Seq. ID	LIB3196-018-P1-M1-H1
Method	BLASTX
NCBI GI	g477094
BLAST score	243
E value	1.0e-20
Match length	115
% identity	47
NCBI Description	STE11 protein kinase homolog NPK1 - common tobacco

Seq. No.	228879
Seq. ID	LIB3196-018-P1-M1-H4

Method	BLASTX
NCBI GI	g1906828
BLAST score	390
E value	7.0e-38
Match length	123
% identity	70
NCBI Description	(Y11828) heat shock protein [Arabidopsis thaliana]

Seq. No.	228880
Seq. ID	LIB3196-018-P1-M1-H7
Method	BLASTX
NCBI GI	g114181
BLAST score	183
E value	1.0e-13
Match length	84
% identity	49
NCBI Description	3-DEHYDROQUINATE SYNTHASE >gi_68385_pir__SYECQ 3-dehydroquinate synthase (EC 4.6.1.3) - Escherichia coli >gi_40968_emb_CAA27495_ (X03867) 3-dehydroquinate synthase (aa 1-362) [Escherichia coli] >gi_41225_emb_CAA79666_ (Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett. 200:11-17(1986) [Escherichia coli] >gi_606323 (U18997) 3-dehydroquinate synthase [Escherichia coli] >gi_1789791 (AE000414) 3-dehydroquinate synthase [Escherichia coli]

Seq. No.	228881
Seq. ID	LIB3196-019-P1-M1-A1
Method	BLASTX
NCBI GI	g4432854
BLAST score	146
E value	3.0e-09
Match length	57
% identity	47
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228882
Seq. ID	LIB3196-019-P1-M1-A10
Method	BLASTX
NCBI GI	g547753
BLAST score	576
E value	1.0e-59
Match length	120
% identity	96
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	228883
Seq. ID	LIB3196-019-P1-M1-A12
Method	BLASTX
NCBI GI	g81546
BLAST score	547
E value	2.0e-56
Match length	106
% identity	100
NCBI Description	alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No.	228884

Seq. ID LIB3196-019-P1-M1-A3
Method BLASTX
NCBI GI g1843527
BLAST score 330
E value 5.0e-31
Match length 91
% identity 76
NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 228885
Seq. ID LIB3196-019-P1-M1-B10
Method BLASTX
NCBI GI g3123271
BLAST score 446
E value 2.0e-44
Match length 104
% identity 81
NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No. 228886
Seq. ID LIB3196-019-P1-M1-B2
Method BLASTX
NCBI GI g88052
BLAST score 548
E value 1.0e-56
Match length 108
% identity 100
NCBI Description keratin K5, 58K type II, epidermal (version 2) - human (fragment)

Seq. No. 228887
Seq. ID LIB3196-019-P1-M1-B4
Method BLASTX
NCBI GI g3738302
BLAST score 494
E value 4.0e-50
Match length 115
% identity 81
NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No. 228888
Seq. ID LIB3196-019-P1-M1-B5
Method BLASTX
NCBI GI g3184186
BLAST score 332
E value 4.0e-31
Match length 115
% identity 61
NCBI Description (AB004788) BNIP3L [Homo sapiens] >gi_3342915 (AF079221) BCL2/adenovirus E1B 19kDa-interacting protein 3a [Homo sapiens] >gi_4138826 (AF067396) NIX [Homo sapiens]

Seq. No. 228889
Seq. ID LIB3196-019-P1-M1-B6

Method	BLASTX
NCBI GI	g280816
BLAST score	627
E value	1.0e-65
Match length	126
% identity	98
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin

Seq. No.	228890
Seq. ID	LIB3196-019-P1-M1-B7
Method	BLASTX
NCBI GI	g3876053
BLAST score	167
E value	9.0e-12
Match length	105
% identity	33
NCBI Description	(Z69789) cDNA EST EMBL:D66552 comes from this gene; cDNA EST EMBL:D70371 comes from this gene; cDNA EST EMBL:C11164 comes from this gene; cDNA EST EMBL:C13175 comes from this gene; cDNA EST yk270e3.3 comes from this gene; cDNA ... >gi_3878811_emb_CAA93682_ (Z69794) cDNA EST EMBL:D66552 comes from this gene; cDNA EST EMBL:D70371 comes from this gene; cDNA EST EMBL:C11164 comes from this gene; cDNA EST EMBL:C13175 comes from this gene; cDNA EST yk270e3.3 comes from this gene; cDNA

Seq. No.	228891
Seq. ID	LIB3196-019-P1-M1-C1
Method	BLASTX
NCBI GI	g547753
BLAST score	392
E value	3.0e-38
Match length	87
% identity	90
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	228892
Seq. ID	LIB3196-019-P1-M1-C10
Method	BLASTX
NCBI GI	g1778838
BLAST score	560
E value	7.0e-58
Match length	122
% identity	89
NCBI Description	(U83113) INS-1 winged-helix homolog [Homo sapiens]

Seq. No.	228893
Seq. ID	LIB3196-019-P1-M1-C12
Method	BLASTX
NCBI GI	g4263790
BLAST score	524
E value	1.0e-53
Match length	113
% identity	91

NCBI Description	(AC006068) putative ch-TOG protein [Arabidopsis thaliana]
Seq. No.	228894
Seq. ID	LIB3196-019-P1-M1-C3
Method	BLASTX
NCBI GI	g3901014
BLAST score	234
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	228895
Seq. ID	LIB3196-019-P1-M1-C4
Method	BLASTX
NCBI GI	g2605714
BLAST score	222
E value	3.0e-18
Match length	57
% identity	81
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]
Seq. No.	228896
Seq. ID	LIB3196-019-P1-M1-C8
Method	BLASTX
NCBI GI	g2245104
BLAST score	150
E value	8.0e-10
Match length	105
% identity	34
NCBI Description	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
Seq. No.	228897
Seq. ID	LIB3196-019-P1-M1-D1
Method	BLASTX
NCBI GI	g3947448
BLAST score	279
E value	6.0e-25
Match length	115
% identity	50
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi
Seq. No.	228898
Seq. ID	LIB3196-019-P1-M1-D10
Method	BLASTX
NCBI GI	g125080
BLAST score	148

E value	1.0e-09
Match length	58
% identity	57
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	228899
Seq. ID	LIB3196-019-P1-M1-D11
Method	BLASTX
NCBI GI	g3201554
BLAST score	232
E value	1.0e-19
Match length	88
% identity	56
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	228900
Seq. ID	LIB3196-019-P1-M1-D12
Method	BLASTX
NCBI GI	g464986
BLAST score	416
E value	5.0e-41
Match length	77
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	228901
Seq. ID	LIB3196-019-P1-M1-D2
Method	BLASTX
NCBI GI	g1710840
BLAST score	542
E value	9.0e-56
Match length	118
% identity	84
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57) >gi_441217_dbj_BAA03709_ (D16138) S-adenosyl-L-homocystein hydrolase [Nicotiana sylvestris] >gi_1857024_dbj_BAA08142_ (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum] >gi_2588781_dbj_BAA23164_ (D49804) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No.	228902
Seq. ID	LIB3196-019-P1-M1-D5

Method	BLASTX
NCBI GI	g124224
BLAST score	462
E value	2.0e-46
Match length	103
% identity	87
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	228903
Seq. ID	LIB3196-019-P1-M1-D7
Method	BLASTX
NCBI GI	g3868758
BLAST score	400
E value	4.0e-39
Match length	73
% identity	96
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	228904
Seq. ID	LIB3196-019-P1-M1-E1
Method	BLASTX
NCBI GI	g1363944
BLAST score	480
E value	2.0e-48
Match length	97
% identity	97
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	228905
Seq. ID	LIB3196-019-P1-M1-E10
Method	BLASTX
NCBI GI	g3915742
BLAST score	577
E value	7.0e-60
Match length	112
% identity	98
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228906
Seq. ID	LIB3196-019-P1-M1-E11
Method	BLASTX
NCBI GI	g49868
BLAST score	625
E value	2.0e-65
Match length	124
% identity	100
NCBI Description	(X03765) put. beta-actin (aa 27-375) [Mus musculus] >gi_387083 (M12481) cytoplasmic beta-actin [Mus musculus]

Seq. No.	228907
Seq. ID	LIB3196-019-P1-M1-E12
Method	BLASTX
NCBI GI	g3880433
BLAST score	259
E value	2.0e-22
Match length	95
% identity	28
NCBI Description	(Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]

Seq. No.	228908
Seq. ID	LIB3196-019-P1-M1-E3
Method	BLASTX
NCBI GI	g4056469
BLAST score	274
E value	2.0e-24
Match length	85
% identity	74
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	228909
Seq. ID	LIB3196-019-P1-M1-E5
Method	BLASTX
NCBI GI	g3859591
BLAST score	199
E value	2.0e-15
Match length	87
% identity	43
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

Seq. No.	228910
Seq. ID	LIB3196-019-P1-M1-E6
Method	BLASTX
NCBI GI	g3915742
BLAST score	554
E value	4.0e-57
Match length	117
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228911
Seq. ID	LIB3196-019-P1-M1-E9
Method	BLASTX
NCBI GI	g3915742
BLAST score	513
E value	2.0e-52
Match length	110
% identity	89

NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	228912
Seq. ID	LIB3196-019-P1-M1-F1
Method	BLASTX
NCBI GI	g2618721
BLAST score	168
E value	6.0e-12
Match length	102
% identity	50
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	228913
Seq. ID	LIB3196-019-P1-M1-F4
Method	BLASTX
NCBI GI	g1346347
BLAST score	594
E value	8.0e-62
Match length	124
% identity	97
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	228914
Seq. ID	LIB3196-019-P1-M1-F6
Method	BLASTX
NCBI GI	g2582665
BLAST score	216
E value	1.0e-17
Match length	76
% identity	58
NCBI Description	(Z82983) thi [Citrus sinensis]

Seq. No.	228915
Seq. ID	LIB3196-019-P1-M1-F8
Method	BLASTX
NCBI GI	g137578
BLAST score	224
E value	3.0e-25
Match length	93
% identity	64
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228916
Seq. ID	LIB3196-019-P1-M1-G1
Method	BLASTX
NCBI GI	g110630

BLAST score	632
E value	3.0e-66
Match length	126
% identity	100
NCBI Description	lamin B - mouse >gi_293689 (M35153) lamin B [Mus musculus]

Seq. No.	228917
Seq. ID	LIB3196-019-P1-M1-G11
Method	BLASTX
NCBI GI	g133500
BLAST score	283
E value	2.0e-25
Match length	52
% identity	100
NCBI Description	RETINOIC ACID RECEPTOR GAMMA-2 (RAR-GAMMA-2)

Seq. No.	228918
Seq. ID	LIB3196-019-P1-M1-G2
Method	BLASTX
NCBI GI	g3075398
BLAST score	170
E value	4.0e-12
Match length	71
% identity	51
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	228919
Seq. ID	LIB3196-019-P1-M1-G5
Method	BLASTX
NCBI GI	g72287
BLAST score	386
E value	2.0e-37
Match length	108
% identity	71
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	228920
Seq. ID	LIB3196-019-P1-M1-G6
Method	BLASTX
NCBI GI	g4008006
BLAST score	276
E value	2.0e-24
Match length	120
% identity	47
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	228921
Seq. ID	LIB3196-019-P1-M1-G9
Method	BLASTX
NCBI GI	g2224911
BLAST score	192
E value	8.0e-15
Match length	89
% identity	46

NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]
Seq. No.	228922
Seq. ID	LIB3196-019-P1-M1-H5
Method	BLASTX
NCBI GI	g1710008
BLAST score	402
E value	2.0e-39
Match length	117
% identity	73
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN1B >gi_1370205_emb_CAA98188_ (Z73960) RAN1B [Lotus japonicus]
Seq. No.	228923
Seq. ID	LIB3196-019-P1-M1-H6
Method	BLASTX
NCBI GI	g71532
BLAST score	511
E value	4.0e-52
Match length	111
% identity	93
NCBI Description	keratin, type II cytoskeletal - human (fragment) >gi_34069_emb_CAA24760_ (V01516) keratin [Homo sapiens] >gi_386847 (J00269) keratin [Homo sapiens]
Seq. No.	228924
Seq. ID	LIB3196-019-P1-M1-H7
Method	BLASTX
NCBI GI	g1703129
BLAST score	433
E value	5.0e-43
Match length	86
% identity	98
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]
Seq. No.	228925
Seq. ID	LIB3196-020-P1-M1-A2
Method	BLASTX
NCBI GI	g1346344
BLAST score	588
E value	5.0e-61
Match length	129
% identity	95
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II - human >gi_908779 (L42583) keratin type II [Homo sapiens]
Seq. No.	228926
Seq. ID	LIB3196-020-P1-M1-A5
Method	BLASTX
NCBI GI	g2982453
BLAST score	540
E value	2.0e-55
Match length	118

% identity	90
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	228927
Seq. ID	LIB3196-020-P1-M1-A6
Method	BLASTX
NCBI GI	g4176522
BLAST score	159
E value	8.0e-11
Match length	116
% identity	28
NCBI Description	(AL035263) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	228928
Seq. ID	LIB3196-020-P1-M1-A8
Method	BLASTX
NCBI GI	g4539307
BLAST score	183
E value	1.0e-13
Match length	62
% identity	58
NCBI Description	(AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	228929
Seq. ID	LIB3196-020-P1-M1-A9
Method	BLASTX
NCBI GI	g2134803
BLAST score	677
E value	2.0e-71
Match length	134
% identity	99
NCBI Description	band-6-protein - human >gi_535015_emb_CAA55881_ (X79293) band-6-protein [Homo sapiens]

Seq. No.	228930
Seq. ID	LIB3196-020-P1-M1-B1
Method	BLASTX
NCBI GI	g2995405
BLAST score	124
E value	9.0e-15
Match length	99
% identity	47
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	228931
Seq. ID	LIB3196-020-P1-M1-B11
Method	BLASTX
NCBI GI	g1732411
BLAST score	644
E value	1.0e-67
Match length	125
% identity	99
NCBI Description	(U47924) isopeptidase T [Homo sapiens]

Seq. No.	228932

Seq. ID	LIB3196-020-P1-M1-B12
Method	BLASTX
NCBI GI	g441457
BLAST score	520
E value	4.0e-53
Match length	96
% identity	99
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	228933
Seq. ID	LIB3196-020-P1-M1-B2
Method	BLASTX
NCBI GI	g116850
BLAST score	588
E value	5.0e-61
Match length	114
% identity	100
NCBI Description	COFILIN, NON-MUSCLE ISOFORM >gi_89176_pir__A29240 cofilin - pig >gi_164425 (M20866) cofilin [Sus scrofa]

Seq. No.	228934
Seq. ID	LIB3196-020-P1-M1-B3
Method	BLASTX
NCBI GI	g3970854
BLAST score	396
E value	1.0e-38
Match length	126
% identity	63
NCBI Description	(AB015332) HRIHFB2018 [Homo sapiens]

Seq. No.	228935
Seq. ID	LIB3196-020-P1-M1-B7
Method	BLASTX
NCBI GI	g3269284
BLAST score	347
E value	8.0e-33
Match length	109
% identity	67
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	228936
Seq. ID	LIB3196-020-P1-M1-B8
Method	BLASTX
NCBI GI	g125887
BLAST score	272
E value	5.0e-24
Match length	119
% identity	50
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	228937
Seq. ID	LIB3196-020-P1-M1-B9
Method	BLASTX

NCBI GI	g137578
BLAST score	442
E value	4.0e-44
Match length	83
% identity	100
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228938
Seq. ID	LIB3196-020-P1-M1-C1
Method	BLASTX
NCBI GI	g113944
BLAST score	586
E value	8.0e-61
Match length	118
% identity	44
NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi_71756_pir__LUHU annexin I - human >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I (lipocortin I)

Seq. No.	228939
Seq. ID	LIB3196-020-P1-M1-C3
Method	BLASTX
NCBI GI	g133841
BLAST score	351
E value	3.0e-33
Match length	78
% identity	91
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi_71016_pir__R3NT18 ribosomal protein S18 - common tobacco chloroplast >gi_11851_emb_CAA77371_ (Z00044) ribosomal protein S18 [Nicotiana tabacum] >gi_225220_prf__1211235BB ribosomal protein S18 [Nicotiana tabacum]

Seq. No.	228940
Seq. ID	LIB3196-020-P1-M1-C4
Method	BLASTX
NCBI GI	g4115933
BLAST score	281
E value	4.0e-25
Match length	87
% identity	70
NCBI Description	(AF118223) contains similarity to human RNA polymerase II complex component SRB7 (GB:U52960) [Arabidopsis thaliana]

Seq. No.	228941
Seq. ID	LIB3196-020-P1-M1-C5
Method	BLASTX
NCBI GI	g1408471

BLAST score	447
E value	1.0e-44
Match length	101
% identity	79
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	228942
Seq. ID	LIB3196-020-P1-M1-C8
Method	BLASTX
NCBI GI	g4415917
BLAST score	390
E value	7.0e-38
Match length	123
% identity	58
NCBI Description	(AC006282) putative protein containing zinc finger domain [Arabidopsis thaliana]

Seq. No.	228943
Seq. ID	LIB3196-020-P1-M1-D11
Method	BLASTX
NCBI GI	g2911047
BLAST score	402
E value	2.0e-39
Match length	100
% identity	73
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	228944
Seq. ID	LIB3196-020-P1-M1-D12
Method	BLASTX
NCBI GI	g4455787
BLAST score	148
E value	5.0e-10
Match length	51
% identity	47
NCBI Description	(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe]

Seq. No.	228945
Seq. ID	LIB3196-020-P1-M1-D2
Method	BLASTX
NCBI GI	g399132
BLAST score	451
E value	5.0e-45
Match length	89
% identity	97
NCBI Description	BTG1 PROTEIN (B-CELL TRANSLOCATION GENE 1 PROTEIN) >gi_86982_pir__S20947 BTG1 protein - human >gi_2137175_pir__I48272 btg1 protein - mouse >gi_29509_emb_CAA43435_ (X61123) BTG1 [Homo sapiens] >gi_50188_emb_CAA78902_ (Z16410) btg1 [Mus musculus] >gi_293306 (L16846) BTG1 [Mus musculus] >gi_4502473_ref_NP_001722.1_pBTG1_ B-cell translocation protein

Seq. No.	228946
Seq. ID	LIB3196-020-P1-M1-D5
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	228947
Seq. ID	LIB3196-020-P1-M1-D8
Method	BLASTX
NCBI GI	g1000207
BLAST score	624
E value	2.0e-65
Match length	120
% identity	99
NCBI Description	(U33920) semaphorin [Homo sapiens]

Seq. No.	228948
Seq. ID	LIB3196-020-P1-M1-D9
Method	BLASTX
NCBI GI	g125105
BLAST score	625
E value	2.0e-65
Match length	130
% identity	95
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	228949
Seq. ID	LIB3196-020-P1-M1-E10
Method	BLASTX
NCBI GI	g1351111
BLAST score	431
E value	9.0e-43
Match length	86
% identity	97
NCBI Description	SIGNAL RECOGNITION PARTICLE 9 KD PROTEIN (SRP9) >gi_1362938_pir__A57292 signal recognition particle protein SRP9 - human >gi_897851 (U20998) signal recognition particle subunit 9 [Homo sapiens] >gi_4507217_ref_NP_003124.1_pSRP9_ signal recognition particle 9kD

Seq. No.	228950
Seq. ID	LIB3196-020-P1-M1-E11
Method	BLASTX
NCBI GI	g4454706
BLAST score	378
E value	2.0e-36
Match length	91

% identity	85
NCBI Description	(AF070665) HSPC009 [Homo sapiens]
Seq. No.	228951
Seq. ID	LIB3196-020-P1-M1-E2
Method	BLASTX
NCBI GI	g100196
BLAST score	498
E value	1.0e-50
Match length	110
% identity	84
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato
Seq. No.	228952
Seq. ID	LIB3196-020-P1-M1-E3
Method	BLASTX
NCBI GI	g1711507
BLAST score	227
E value	7.0e-19
Match length	68
% identity	60
NCBI Description	SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) >gi_624221 (U19030) signal recognition particle 19 kDa protein subunit SRP19 [Oryza sativa]
Seq. No.	228953
Seq. ID	LIB3196-020-P1-M1-E4
Method	BLASTX
NCBI GI	g2760345
BLAST score	381
E value	4.0e-37
Match length	88
% identity	22
NCBI Description	(U84967) ubiquitin [Arabidopsis thaliana]
Seq. No.	228954
Seq. ID	LIB3196-020-P1-M1-E6
Method	BLASTX
NCBI GI	g137578
BLAST score	463
E value	2.0e-46
Match length	103
% identity	50
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	228955
Seq. ID	LIB3196-020-P1-M1-E8
Method	BLASTX
NCBI GI	g541849
BLAST score	212
E value	5.0e-17
Match length	100

% identity	47
NCBI Description	anthranilate synthase (EC 4.1.3.27) beta chain - Arabidopsis thaliana >gi_403434 (L22585) anthranilate synthase beta subunit [Arabidopsis thaliana]

Seq. No.	228956
Seq. ID	LIB3196-020-P1-M1-F1
Method	BLASTX
NCBI GI	g4263710
BLAST score	517
E value	8.0e-53
Match length	106
% identity	67
NCBI Description	(AC006223) putative pur-alpha transcriptional activator protein [Arabidopsis thaliana]

Seq. No.	228957
Seq. ID	LIB3196-020-P1-M1-F11
Method	BLASTX
NCBI GI	g3015538
BLAST score	375
E value	3.0e-36
Match length	111
% identity	69
NCBI Description	(U93181) nuclear dual-specificity phosphatase [Homo sapiens]

Seq. No.	228958
Seq. ID	LIB3196-020-P1-M1-F2
Method	BLASTX
NCBI GI	g3420900
BLAST score	188
E value	3.0e-14
Match length	98
% identity	40
NCBI Description	(AF081125) ER lumen protein retaining receptor [Caenorhabditis elegans]

Seq. No.	228959
Seq. ID	LIB3196-020-P1-M1-F3
Method	BLASTX
NCBI GI	g130582
BLAST score	186
E value	6.0e-14
Match length	74
% identity	50
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi_100342_pir__S04273 hypothetical protein - common tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana tabacum]

Seq. No.	228960
Seq. ID	LIB3196-020-P1-M1-F4
Method	BLASTX
NCBI GI	g118926
BLAST score	206

E value	2.0e-16
Match length	110
% identity	43
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]
Seq. No.	228961
Seq. ID	LIB3196-020-P1-M1-F5
Method	BLASTX
NCBI GI	g135005
BLAST score	173
E value	2.0e-12
Match length	76
% identity	39
NCBI Description	STRICTOSIDINE SYNTHASE PRECURSOR >gi_82067_pir__S01325 strictosidine synthase (EC 4.3.3.2) - serpentwood >gi_21127_emb_CAA44208_ (X62334) strictosidine synthase [Rauvolfia serpentina] >gi_21129_emb_CAA68725_ (Y00756) strictosidine synthase [Rauvolfia serpentina] >gi_226162_prf__1413232A strictosidine synthase [Rauvolfia serpentina]
Seq. No.	228962
Seq. ID	LIB3196-020-P1-M1-F6
Method	BLASTX
NCBI GI	g122007
BLAST score	419
E value	3.0e-41
Match length	111
% identity	76
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]
Seq. No.	228963
Seq. ID	LIB3196-020-P1-M1-F9
Method	BLASTX
NCBI GI	g3913414
BLAST score	457
E value	9.0e-46
Match length	122
% identity	75
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2) (SAMDC 2) (SAMDC16) >gi_1155242 (U38527) S-adenosylmethionine decarboxylase 2 [Dianthus caryophyllus]
Seq. No.	228964
Seq. ID	LIB3196-020-P1-M1-G1
Method	BLASTX
NCBI GI	g88044
BLAST score	580
E value	3.0e-60

Match length	121
% identity	96
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	228965
Seq. ID	LIB3196-020-P1-M1-G5
Method	BLASTX
NCBI GI	g126156
BLAST score	584
E value	1.0e-60
Match length	117
% identity	99
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228966
Seq. ID	LIB3196-020-P1-M1-G6
Method	BLASTX
NCBI GI	g547713
BLAST score	283
E value	2.0e-25
Match length	78
% identity	62
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_322866_pir__B44452 translation initiation factor eIF-4F isozyme form subunit p28 - wheat >gi_170751 (M95818) initiation factor (iso)4F p28 subunit [Triticum aestivum]

Seq. No.	228967
Seq. ID	LIB3196-020-P1-M1-G9
Method	BLASTX
NCBI GI	g547751
BLAST score	650
E value	2.0e-68
Match length	132
% identity	99
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (39.1) (VERSION 1) >gi_422802_pir__S30433 keratin 17, cytoskeletal - human >gi_30379_emb_CAA79626_ (Z19574) cytokeratin 17 [Homo sapiens] >gi_34075_emb_CAA44451_ (X62571) keratin related product [Homo sapiens] >gi_4557701_ref_NP_000413.1_pKRT17_ keratin

Seq. No.	228968
Seq. ID	LIB3196-020-P1-M1-H10
Method	BLASTX
NCBI GI	g3694872
BLAST score	297
E value	4.0e-27

Match length	64
% identity	83
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	228969
Seq. ID	LIB3196-020-P1-M1-H11
Method	BLASTX
NCBI GI	g3334157
BLAST score	199
E value	1.0e-20
Match length	63
% identity	78
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1220142_emb_CAA59468_ (X85185) cyclophilin [Catharanthus roseus]

Seq. No.	228970
Seq. ID	LIB3196-020-P1-M1-H3
Method	BLASTX
NCBI GI	g126156
BLAST score	195
E value	5.0e-15
Match length	95
% identity	53
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	228971
Seq. ID	LIB3196-020-P1-M1-H4
Method	BLASTX
NCBI GI	g416662
BLAST score	316
E value	3.0e-29
Match length	127
% identity	53
NCBI Description	21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin inhibitor homolog - soybean >gi_21909_emb_CAA39860_ (X56509) 21 kDa seed protein [Theobroma cacao]

Seq. No.	228972
Seq. ID	LIB3196-020-P1-M1-H9
Method	BLASTX
NCBI GI	g2465540
BLAST score	248
E value	3.0e-21
Match length	55
% identity	85
NCBI Description	(AF005632) phosphodiesterase I/nucleotide pyrophosphatase beta [Homo sapiens]

Seq. No.	228973
Seq. ID	LIB3196-021-P1-M1-A1

Method	BLASTX
NCBI GI	g4539459
BLAST score	245
E value	7.0e-21
Match length	53
% identity	72
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	228974
Seq. ID	LIB3196-021-P1-M1-A10
Method	BLASTX
NCBI GI	g2914703
BLAST score	312
E value	9.0e-29
Match length	122
% identity	52
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	228975
Seq. ID	LIB3196-021-P1-M1-A3
Method	BLASTX
NCBI GI	g4263522
BLAST score	322
E value	6.0e-30
Match length	126
% identity	45
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228976
Seq. ID	LIB3196-021-P1-M1-A4
Method	BLASTX
NCBI GI	g4510364
BLAST score	170
E value	4.0e-12
Match length	100
% identity	46
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	228977
Seq. ID	LIB3196-021-P1-M1-A5
Method	BLASTX
NCBI GI	g232190
BLAST score	347
E value	8.0e-33
Match length	78
% identity	85
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG 6P229 >gi_100291_pir__S20501 glutathione peroxidase homolog - wood tobacco >gi_19739_emb_CAA42780_ (X60219) homologous to animal glutathione peroxidases [Nicotiana sylvestris]

Seq. No.	228978
Seq. ID	LIB3196-021-P1-M1-A6
Method	BLASTX
NCBI GI	g266690
BLAST score	401
E value	4.0e-39

Match length	109
% identity	75
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	228979
Seq. ID	LIB3196-021-P1-M1-A8
Method	BLASTX
NCBI GI	g4415931
BLAST score	176
E value	4.0e-13
Match length	53
% identity	64
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	228980
Seq. ID	LIB3196-021-P1-M1-B10
Method	BLASTX
NCBI GI	g88052
BLAST score	553
E value	3.0e-57
Match length	110
% identity	100
NCBI Description	keratin K5, 58K type II, epidermal (version 2) - human (fragment)

Seq. No.	228981
Seq. ID	LIB3196-021-P1-M1-B2
Method	BLASTX
NCBI GI	g3220164
BLAST score	155
E value	3.0e-10
Match length	53
% identity	91
NCBI Description	(AF029777) hGCN5 [Homo sapiens]

Seq. No.	228982
Seq. ID	LIB3196-021-P1-M1-B3
Method	BLASTX
NCBI GI	g4539660
BLAST score	445
E value	3.0e-44
Match length	127
% identity	65
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	228983
Seq. ID	LIB3196-021-P1-M1-B4
Method	BLASTX
NCBI GI	g1169475
BLAST score	697
E value	7.0e-74
Match length	132
% identity	100

NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_556301 (M22432) elongation factor Tu [Mus musculus]
Seq. No.	228984
Seq. ID	LIB3196-021-P1-M1-B6
Method	BLASTX
NCBI GI	g4204308
BLAST score	217
E value	1.0e-17
Match length	39
% identity	92
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	228985
Seq. ID	LIB3196-021-P1-M1-B8
Method	BLASTX
NCBI GI	g3915742
BLAST score	468
E value	3.0e-47
Match length	95
% identity	94
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]
Seq. No.	228986
Seq. ID	LIB3196-021-P1-M1-C1
Method	BLASTX
NCBI GI	g119172
BLAST score	349
E value	4.0e-33
Match length	84
% identity	87
NCBI Description	ELONGATION FACTOR 2 (EF-2) >gi_2144947_pir__EFHU2 translation elongation factor eEF-2 - human >gi_31106_emb_CAA35829_ (X51466) elongation factor 2 [Homo sapiens] >gi_31108_emb_CAA77750_ (Z11692) human elongation factor 2 [Homo sapiens] >gi_4503483_ref_NP_001952.1_pEEF2_ eukaryotic translation elongation factor
Seq. No.	228987
Seq. ID	LIB3196-021-P1-M1-C10
Method	BLASTX
NCBI GI	g131770
BLAST score	333
E value	3.0e-31
Match length	91
% identity	66
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	228988
Seq. ID	LIB3196-021-P1-M1-C2
Method	BLASTX
NCBI GI	g226120
BLAST score	683
E value	3.0e-72
Match length	130
% identity	100
NCBI Description	vicilin gene B [Saguinus oedipus]

Seq. No.	228989
Seq. ID	LIB3196-021-P1-M1-C3
Method	BLASTX
NCBI GI	g3643609
BLAST score	238
E value	4.0e-20
Match length	103
% identity	56
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	228990
Seq. ID	LIB3196-021-P1-M1-C4
Method	BLASTX
NCBI GI	g207384
BLAST score	286
E value	1.0e-25
Match length	87
% identity	69
NCBI Description	(M15202) tropomyosin T class IIa beta-1 [Rattus norvegicus]

Seq. No.	228991
Seq. ID	LIB3196-021-P1-M1-C5
Method	BLASTX
NCBI GI	g2224907
BLAST score	382
E value	6.0e-37
Match length	129
% identity	58
NCBI Description	(U78294) 15S-lipoxygenase [Homo sapiens] >gi_4557309_ref_NP_001132.1_pALOX15B_ arachidonate 15-lipoxygenase, second type

Seq. No.	228992
Seq. ID	LIB3196-021-P1-M1-D11
Method	BLASTX
NCBI GI	g2160166
BLAST score	386
E value	1.0e-37
Match length	93
% identity	77
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	228993
Seq. ID	LIB3196-021-P1-M1-D12
Method	BLASTX
NCBI GI	g3327392

BLAST score	144
E value	5.0e-09
Match length	79
% identity	44
NCBI Description	(AC004483) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq. No.	228994
Seq. ID	LIB3196-021-P1-M1-D5
Method	BLASTX
NCBI GI	g2135344
BLAST score	695
E value	1.0e-73
Match length	133
% identity	50
NCBI Description	HER3 protein precursor - human >gi_306841 (M34309) HER3 protein precursor [Homo sapiens] >gi_4503597_ref_NP_001973.1_pERBB3_ v-erb-b2 avian erythroblastic leukemia viral oncogene homolog

Seq. No.	228995
Seq. ID	LIB3196-021-P1-M1-D6
Method	BLASTX
NCBI GI	g3877645
BLAST score	142
E value	8.0e-09
Match length	68
% identity	43
NCBI Description	(Z83230) cDNA EST yk355g3.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	228996
Seq. ID	LIB3196-021-P1-M1-D8
Method	BLASTX
NCBI GI	g1706571
BLAST score	373
E value	7.0e-36
Match length	127
% identity	56
NCBI Description	EPITHELIAL CHLORIDE CHANNEL PROTEIN (CALCIUM-ACTIVATED CHLORIDE CHANNEL) >gi_1184066 (U36445) calcium-activated chloride channel [Bos taurus]

Seq. No.	228997
Seq. ID	LIB3196-021-P1-M1-E11
Method	BLASTX
NCBI GI	g2499488
BLAST score	569
E value	6.0e-59
Match length	112
% identity	91
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	228998
Seq. ID	LIB3196-021-P1-M1-E2
Method	BLASTX
NCBI GI	g137578
BLAST score	511
E value	4.0e-52
Match length	124
% identity	84
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	228999
Seq. ID	LIB3196-021-P1-M1-E5
Method	BLASTX
NCBI GI	g121283
BLAST score	613
E value	5.0e-64
Match length	125
% identity	90
NCBI Description	GLUCOSYLCERAMIDASE PRECURSOR (BETA-GLUCOCEREBROSIDASE) (ACID BETA-GLUCOSIDASE) (D-GLUCOSYL-N-ACYLSPHINGOSINE GLUCOHYDROLASE) >gi_183028 (M19285) glucocerebrosidase [Homo sapiens] >gi_4503935_ref_NP_000148.1_pGBA_ glucosidase, beta; acid (includes glucosylceramidase)

Seq. No.	229000
Seq. ID	LIB3196-021-P1-M1-E6
Method	BLASTX
NCBI GI	g125080
BLAST score	624
E value	3.0e-65
Match length	126
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	229001
Seq. ID	LIB3196-021-P1-M1-E7
Method	BLASTX
NCBI GI	g3915742
BLAST score	348
E value	5.0e-33
Match length	85
% identity	80
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229002
Seq. ID	LIB3196-021-P1-M1-E8
Method	BLASTX
NCBI GI	g4098124
BLAST score	389
E value	7.0e-38
Match length	106
% identity	62
NCBI Description	(U73522) AMSH [Homo sapiens]

Seq. No.	229003
Seq. ID	LIB3196-021-P1-M1-E9
Method	BLASTX
NCBI GI	g3608171
BLAST score	531
E value	2.0e-54
Match length	126
% identity	83
NCBI Description	(D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Seq. No.	229004
Seq. ID	LIB3196-021-P1-M1-F1
Method	BLASTX
NCBI GI	g2498017
BLAST score	512
E value	4.0e-52
Match length	133
% identity	77
NCBI Description	HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA) >gi_2135434_pir__I38972 hypoxia-inducible factor 1 alpha - human >gi_881346 (U22431) hypoxia-inducible factor 1 alpha [Homo sapiens] >gi_1144013 (U29165) ARNT interacting protein [Homo sapiens] >gi_1097959_prf__2114407A hypoxia-inducible factor 1 [Homo sapiens] >gi_4504385_ref_NP_001521.1_pHIF1A_ hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)

Seq. No.	229005
Seq. ID	LIB3196-021-P1-M1-F10
Method	BLASTX
NCBI GI	g4415947
BLAST score	267
E value	1.0e-23
Match length	99
% identity	53
NCBI Description	(AC006418) putative laccase [Arabidopsis thaliana]

Seq. No.	229006
Seq. ID	LIB3196-021-P1-M1-F3
Method	BLASTX
NCBI GI	g3421134
BLAST score	398
E value	7.0e-39
Match length	112

% identity	77
NCBI Description	(AF045666) arginine decarboxylase [Theobroma cacao]

Seq. No.	229007
Seq. ID	LIB3196-021-P1-M1-F6
Method	BLASTX
NCBI GI	g2224569
BLAST score	229
E value	6.0e-19
Match length	71
% identity	55
NCBI Description	(AB002312) KIAA0314 [Homo sapiens]

Seq. No.	229008
Seq. ID	LIB3196-021-P1-M1-F7
Method	BLASTX
NCBI GI	g3150035
BLAST score	191
E value	9.0e-15
Match length	61
% identity	64
NCBI Description	(U37100) aldose reductase-like peptide [Homo sapiens]

Seq. No.	229009
Seq. ID	LIB3196-021-P1-M1-F8
Method	BLASTX
NCBI GI	g2505870
BLAST score	303
E value	1.0e-27
Match length	125
% identity	57
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229010
Seq. ID	LIB3196-021-P1-M1-F9
Method	BLASTX
NCBI GI	g137578
BLAST score	395
E value	1.0e-38
Match length	98
% identity	44
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229011
Seq. ID	LIB3196-021-P1-M1-G1
Method	BLASTX
NCBI GI	g2499488
BLAST score	550
E value	1.0e-56
Match length	109
% identity	91
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE

09568450.060704

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	229012
Seq. ID	LIB3196-021-P1-M1-G11
Method	BLASTX
NCBI GI	g3986758
BLAST score	374
E value	5.0e-36
Match length	71
% identity	100
NCBI Description	(AF109905) CLCP [Mus musculus]

Seq. No.	229013
Seq. ID	LIB3196-021-P1-M1-G12
Method	BLASTX
NCBI GI	g3193316
BLAST score	573
E value	2.0e-59
Match length	125
% identity	85
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	229014
Seq. ID	LIB3196-021-P1-M1-G5
Method	BLASTX
NCBI GI	g4406703
BLAST score	368
E value	3.0e-35
Match length	71
% identity	97
NCBI Description	(AF131856) Unknown [Homo sapiens]

Seq. No.	229015
Seq. ID	LIB3196-021-P1-M1-G7
Method	BLASTX
NCBI GI	g2578033
BLAST score	175
E value	1.0e-12
Match length	39
% identity	87
NCBI Description	(X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No.	229016
Seq. ID	LIB3196-021-P1-M1-G8
Method	BLASTX
NCBI GI	g3775993
BLAST score	545
E value	5.0e-56
Match length	123
% identity	86
NCBI Description	(AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No.	229017
Seq. ID	LIB3196-021-P1-M1-G9
Method	BLASTX
NCBI GI	g1723614
BLAST score	152
E value	3.0e-10
Match length	84
% identity	45
NCBI Description	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE D (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) >gi_2121009_pir__S60168 hypothetical protein X - Zymomonas mobilis >gi_1143378_dbj_BAA09443_ (D50832) homologue of E. coli ClpB5' ORF [Zymomonas mobilis]

Seq. No.	229018
Seq. ID	LIB3196-021-P1-M1-H11
Method	BLASTX
NCBI GI	g2745974
BLAST score	558
E value	1.0e-57
Match length	131
% identity	83
NCBI Description	(U84004) putative tumor suppressor [Homo sapiens]

Seq. No.	229019
Seq. ID	LIB3196-021-P1-M1-H12
Method	BLASTX
NCBI GI	g2431771
BLAST score	212
E value	5.0e-17
Match length	104
% identity	44
NCBI Description	(U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No.	229020
Seq. ID	LIB3196-021-P1-M1-H5
Method	BLASTX
NCBI GI	g136452
BLAST score	341
E value	4.0e-32
Match length	105
% identity	62
NCBI Description	STEM-SPECIFIC PROTEIN TSJT1 >gi_100383_pir__S13551 stem-specific protein - common tobacco >gi_20037_emb_CAA36525_ (X52283) stem specific, weakly expressed in other organs [Nicotiana tabacum]

Seq. No.	229021
Seq. ID	LIB3196-021-P1-M1-H7
Method	BLASTX
NCBI GI	g126041
BLAST score	419
E value	2.0e-41
Match length	87
% identity	99
NCBI Description	L-LACTATE DEHYDROGENASE H CHAIN (LDH-B) >gi_1070432_pir__DEHULH L-lactate dehydrogenase (EC

	1.1.1.27) chain H - human >gi_34329_emb_CAA68701_ (Y00711) lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >gi_1200083_emb_CAA32033_ (X13794) lactate dehydrogenase B [Homo sapiens] >gi_4557032_ref_NP_002291.1_pLDHB_ lactate dehydrogenase B
Seq. No.	229022
Seq. ID	LIB3196-021-P1-M1-H8
Method	BLASTX
NCBI GI	g280816
BLAST score	342
E value	2.0e-32
Match length	66
% identity	98
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin
Seq. No.	229023
Seq. ID	LIB3196-021-P1-M1-H9
Method	BLASTX
NCBI GI	g1707032
BLAST score	143
E value	5.0e-09
Match length	81
% identity	41
NCBI Description	(U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8
Seq. No.	229024
Seq. ID	LIB3196-022-P1-M1-A1
Method	BLASTX
NCBI GI	g346219
BLAST score	240
E value	3.0e-20
Match length	127
% identity	50
NCBI Description	keratin K4a - human (fragment)
Seq. No.	229025
Seq. ID	LIB3196-022-P1-M1-A11
Method	BLASTX
NCBI GI	g226120
BLAST score	484
E value	6.0e-49
Match length	93
% identity	100
NCBI Description	vicilin gene B [Saguinus oedipus]
Seq. No.	229026
Seq. ID	LIB3196-022-P1-M1-A2
Method	BLASTX
NCBI GI	g2467274

BLAST score 202
E value 7.0e-16
Match length 65
% identity 63
NCBI Description (Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 229027
Seq. ID LIB3196-022-P1-M1-A6
Method BLASTX
NCBI GI g2369714
BLAST score 625
E value 2.0e-65
Match length 121
% identity 98
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 229028
Seq. ID LIB3196-022-P1-M1-A8
Method BLASTX
NCBI GI g4467804
BLAST score 445
E value 3.0e-44
Match length 117
% identity 76
NCBI Description (AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No. 229029
Seq. ID LIB3196-022-P1-M1-B10
Method BLASTX
NCBI GI g115833
BLAST score 374
E value 5.0e-36
Match length 100
% identity 74
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No. 229030
Seq. ID LIB3196-022-P1-M1-B12
Method BLASTX
NCBI GI g3367523
BLAST score 371
E value 1.0e-35
Match length 105
% identity 66
NCBI Description (AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No. 229031
Seq. ID LIB3196-022-P1-M1-B3
Method BLASTX
NCBI GI g4490741
BLAST score 170

E value	3.0e-22
Match length	102
% identity	58
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229032
Seq. ID	LIB3196-022-P1-M1-B4
Method	BLASTX
NCBI GI	g4539327
BLAST score	400
E value	3.0e-39
Match length	111
% identity	72
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	229033
Seq. ID	LIB3196-022-P1-M1-B7
Method	BLASTX
NCBI GI	g2352906
BLAST score	342
E value	3.0e-32
Match length	82
% identity	83
NCBI Description	(AF011794) cell cycle progression restoration 8 protein [Homo sapiens]

Seq. No.	229034
Seq. ID	LIB3196-022-P1-M1-B8
Method	BLASTX
NCBI GI	g3702342
BLAST score	243
E value	1.0e-20
Match length	109
% identity	48
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229035
Seq. ID	LIB3196-022-P1-M1-C10
Method	BLASTX
NCBI GI	g1208427
BLAST score	329
E value	9.0e-31
Match length	88
% identity	44
NCBI Description	(D83485) ER-60 protease [Homo sapiens]

Seq. No.	229036
Seq. ID	LIB3196-022-P1-M1-C3
Method	BLASTX
NCBI GI	g1710017
BLAST score	562
E value	5.0e-58
Match length	112
% identity	97
NCBI Description	RAS-RELATED PROTEIN RAB-18 >gi_478319_pir__JN0874 ras-related GTP-binding protein Rab18 - mouse >gi_388325 (L04966) Rab18 [Mus musculus] >gi_515041_emb_CAA56583_

(X80333) rab18 [Mus musculus]

Seq. No.	229037
Seq. ID	LIB3196-022-P1-M1-C4
Method	BLASTX
NCBI GI	g125105
BLAST score	529
E value	7.0e-59
Match length	127
% identity	95
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	229038
Seq. ID	LIB3196-022-P1-M1-C5
Method	BLASTX
NCBI GI	g2498864
BLAST score	255
E value	4.0e-22
Match length	72
% identity	33
NCBI Description	RRP5 PROTEIN HOMOLOG (KIAA0185) >gi_1136430_dbj_BAA11502_ (D80007) similar to hypothetical protein YM9959.11C of S.cerevisiae. [Homo sapiens]

Seq. No.	229039
Seq. ID	LIB3196-022-P1-M1-C8
Method	BLASTX
NCBI GI	g3297823
BLAST score	213
E value	4.0e-17
Match length	75
% identity	63
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	229040
Seq. ID	LIB3196-022-P1-M1-C9
Method	BLASTX
NCBI GI	g3915742
BLAST score	488
E value	2.0e-54
Match length	120
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229041
Seq. ID	LIB3196-022-P1-M1-D11
Method	BLASTX
NCBI GI	g225580
BLAST score	519
E value	5.0e-53

Match length	121
% identity	85
NCBI Description	storage protein C72 [Saguinus oedipus]

Seq. No.	229042
Seq. ID	LIB3196-022-P1-M1-D4
Method	BLASTX
NCBI GI	g1173187
BLAST score	530
E value	2.0e-54
Match length	105
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	229043
Seq. ID	LIB3196-022-P1-M1-D6
Method	BLASTX
NCBI GI	g1695719
BLAST score	629
E value	6.0e-66
Match length	123
% identity	99
NCBI Description	(D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No.	229044
Seq. ID	LIB3196-022-P1-M1-D7
Method	BLASTX
NCBI GI	g1737218
BLAST score	460
E value	4.0e-46
Match length	101
% identity	76
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	229045
Seq. ID	LIB3196-022-P1-M1-D9
Method	BLASTX
NCBI GI	g2500380
BLAST score	514
E value	2.0e-52
Match length	94
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	229046
Seq. ID	LIB3196-022-P1-M1-E1
Method	BLASTX
NCBI GI	g3319958
BLAST score	567

E value	1.0e-58
Match length	112
% identity	10
NCBI Description	(AJ228139) VAKTI precursor [Homo sapiens]

Seq. No.	229047
Seq. ID	LIB3196-022-P1-M1-E10
Method	BLASTX
NCBI GI	g88052
BLAST score	337
E value	1.0e-31
Match length	122
% identity	55
NCBI Description	keratin K5, 58K type II, epidermal (version 2) - human (fragment)

Seq. No.	229048
Seq. ID	LIB3196-022-P1-M1-E3
Method	BLASTX
NCBI GI	g3510264
BLAST score	218
E value	9.0e-18
Match length	115
% identity	41
NCBI Description	(AC005310) hypothetical protein, 5' partial [Arabidopsis thaliana]

Seq. No.	229049
Seq. ID	LIB3196-022-P1-M1-E6
Method	BLASTX
NCBI GI	g2982453
BLAST score	512
E value	3.0e-52
Match length	116
% identity	86
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	229050
Seq. ID	LIB3196-022-P1-M1-E8
Method	BLASTX
NCBI GI	g178052
BLAST score	654
E value	8.0e-69
Match length	125
% identity	100
NCBI Description	(M95178) alpha-actinin [Homo sapiens] >gi_4501891_ref_NP_001093.1_pACTN1_ actinin, alpha

Seq. No.	229051
Seq. ID	LIB3196-022-P1-M1-F1
Method	BLASTX
NCBI GI	g3882211
BLAST score	628
E value	9.0e-66
Match length	127
% identity	97

NCBI Description	(AB018288) KIAA0745 protein [Homo sapiens]
Seq. No.	229052
Seq. ID	LIB3196-022-P1-M1-F11
Method	BLASTX
NCBI GI	g1707855
BLAST score	499
E value	1.0e-50
Match length	113
% identity	79
NCBI Description	(Y09292) obtusifoliol 14-alpha-demethylase [Triticum aestivum]
Seq. No.	229053
Seq. ID	LIB3196-022-P1-M1-F12
Method	BLASTX
NCBI GI	g1363944
BLAST score	592
E value	1.0e-61
Match length	119
% identity	99
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]
Seq. No.	229054
Seq. ID	LIB3196-022-P1-M1-F3
Method	BLASTX
NCBI GI	g2135234
BLAST score	224
E value	8.0e-27
Match length	126
% identity	44
NCBI Description	gene PP2A protein - human >gi_1000888 (L42373) protein phosphatase 2A B56-alpha [Homo sapiens] >gi_1585671_prf__2201437A phospholipase 2A:SUBUNIT=regulatory:ISOTYPE=alpha [Homo sapiens]
Seq. No.	229055
Seq. ID	LIB3196-022-P1-M1-F5
Method	BLASTX
NCBI GI	g2559012
BLAST score	548
E value	2.0e-56
Match length	114
% identity	100
NCBI Description	(AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapiens] >gi_4090929 (AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens]
Seq. No.	229056
Seq. ID	LIB3196-022-P1-M1-F8
Method	BLASTX
NCBI GI	g2586125
BLAST score	444
E value	3.0e-44

Match length	113
% identity	74
NCBI Description	(U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No.	229057
Seq. ID	LIB3196-022-P1-M1-F9
Method	BLASTX
NCBI GI	g1346349
BLAST score	316
E value	9.0e-30
Match length	72
% identity	89
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II - human >gi_908805 (L42612) keratin type II [Homo sapiens]

Seq. No.	229058
Seq. ID	LIB3196-022-P1-M1-G1
Method	BLASTX
NCBI GI	g3879146
BLAST score	175
E value	1.0e-12
Match length	100
% identity	43
NCBI Description	(Z93386) Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes

Seq. No.	229059
Seq. ID	LIB3196-022-P1-M1-G6
Method	BLASTX
NCBI GI	g2662343
BLAST score	481
E value	1.0e-48
Match length	93
% identity	99
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	229060
Seq. ID	LIB3196-022-P1-M1-G7
Method	BLASTX
NCBI GI	g4249382
BLAST score	329
E value	7.0e-31
Match length	105
% identity	59
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	229061
Seq. ID	LIB3196-022-P1-M1-G9
Method	BLASTX
NCBI GI	g137578
BLAST score	527

E value	5.0e-54
Match length	121
% identity	88
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	229062
Seq. ID	LIB3196-022-P1-M1-H11
Method	BLASTX
NCBI GI	g585165
BLAST score	333
E value	3.0e-31
Match length	119
% identity	62
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]
Seq. No.	229063
Seq. ID	LIB3196-022-P1-M1-H2
Method	BLASTX
NCBI GI	g2388575
BLAST score	220
E value	5.0e-18
Match length	110
% identity	38
NCBI Description	(AC000098) YUP8H12.18 [Arabidopsis thaliana]
Seq. No.	229064
Seq. ID	LIB3196-022-P1-M1-H5
Method	BLASTX
NCBI GI	g280816
BLAST score	413
E value	1.0e-40
Match length	82
% identity	98
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin
Seq. No.	229065
Seq. ID	LIB3196-022-P1-M1-H7
Method	BLASTX
NCBI GI	g124427
BLAST score	605
E value	4.0e-63
Match length	116
% identity	100
NCBI Description	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (IMP DEHYDROGENASE 2) (IMPDH-II) (IMPD 2) >gi_110569_pir__JT0565 IMP

	dehydrogenase (EC 1.1.1.205) - mouse >gi_309413 (M33934) IMP dehydrogenase (EC 1.2.1.14) [Mus musculus]
Seq. No.	229066
Seq. ID	LIB3196-023-P1-M1-A4
Method	BLASTX
NCBI GI	g2119228
BLAST score	196
E value	3.0e-15
Match length	67
% identity	61
NCBI Description	keratin K4a - human (fragment) >gi_313159_emb_CAA47914_ (X67683) keratin K4a [Homo sapiens]
Seq. No.	229067
Seq. ID	LIB3196-023-P1-M1-A6
Method	BLASTX
NCBI GI	g1223922
BLAST score	441
E value	6.0e-44
Match length	100
% identity	76
NCBI Description	(U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata]
Seq. No.	229068
Seq. ID	LIB3196-023-P1-M1-B3
Method	BLASTX
NCBI GI	g549090
BLAST score	392
E value	4.0e-38
Match length	76
% identity	95
NCBI Description	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR) >gi_2136332_pir__I54182 tumor necrosis factor receptor 2-related protein - human >gi_339762 (L04270) tumor necrosis factor receptor 2 related protein [Homo sapiens] >gi_4505039_ref_NP_002333.1_pLTBR_ lymphotoxin B receptor
Seq. No.	229069
Seq. ID	LIB3196-023-P1-M1-B5
Method	BLASTX
NCBI GI	g3478700
BLAST score	322
E value	4.0e-30
Match length	96
% identity	62
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]
Seq. No.	229070
Seq. ID	LIB3196-023-P1-M1-C1
Method	BLASTX
NCBI GI	g125080
BLAST score	599
E value	2.0e-62

09504604.1000

Match length	124
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	229071
Seq. ID	LIB3196-023-P1-M1-C10
Method	BLASTX
NCBI GI	g167311
BLAST score	465
E value	9.0e-47
Match length	103
% identity	84
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	229072
Seq. ID	LIB3196-023-P1-M1-C12
Method	BLASTX
NCBI GI	g729985
BLAST score	261
E value	7.0e-23
Match length	106
% identity	50
NCBI Description	PROCESSING ALPHA-1,2-MANNOSIDASE (ALPHA-1,2-MANNOSIDASE 1B) >gi_474278 (U03458) alpha-mannosidase [Mus musculus] >gi_3335696 (AF078095) alpha 1,2-mannosidase IB [Mus musculus]

Seq. No.	229073
Seq. ID	LIB3196-023-P1-M1-C2
Method	BLASTX
NCBI GI	g266691
BLAST score	368
E value	3.0e-35
Match length	113
% identity	70
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	229074
Seq. ID	LIB3196-023-P1-M1-C4
Method	BLASTX
NCBI GI	g2498323
BLAST score	590
E value	2.0e-61
Match length	107
% identity	62
NCBI Description	EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) >gi_1488324 (U65932) extracellular matrix protein 1 [Homo sapiens] >gi_1488332 (U65938) extracellular matrix protein 1 [Homo sapiens] >gi_2654433 (U68186) extracellular matrix protein 1 [Homo sapiens]

Seq. No.	229075

Seq. ID	LIB3196-023-P1-M1-C7
Method	BLASTX
NCBI GI	g1619602
BLAST score	391
E value	5.0e-38
Match length	122
% identity	63
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	229076
Seq. ID	LIB3196-023-P1-M1-C8
Method	BLASTX
NCBI GI	g1654244
BLAST score	564
E value	2.0e-58
Match length	114
% identity	96
NCBI Description	(U55339) Gossypium barbadense NADH dehydrogenase [Gossypium barbadense]

Seq. No.	229077
Seq. ID	LIB3196-023-P1-M1-D1
Method	BLASTX
NCBI GI	g549063
BLAST score	408
E value	5.0e-40
Match length	92
% identity	84
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	229078
Seq. ID	LIB3196-023-P1-M1-D10
Method	BLASTX
NCBI GI	g4176446
BLAST score	599
E value	2.0e-62
Match length	125
% identity	97
NCBI Description	(AL022238) dJ1042K10.2.1 (novel protein with probable rabGAP domains and Src homology domain 3) (isoform 1) [Homo sapiens]

Seq. No.	229079
Seq. ID	LIB3196-023-P1-M1-D3
Method	BLASTX
NCBI GI	g3176668
BLAST score	544
E value	6.0e-56
Match length	117
% identity	89
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	229080
Seq. ID	LIB3196-023-P1-M1-D5
Method	BLASTX
NCBI GI	g1363944
BLAST score	653
E value	1.0e-68
Match length	131
% identity	99
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	229081
Seq. ID	LIB3196-023-P1-M1-D8
Method	BLASTX
NCBI GI	g4006893
BLAST score	148
E value	1.0e-09
Match length	55
% identity	85
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	229082
Seq. ID	LIB3196-023-P1-M1-E1
Method	BLASTX
NCBI GI	g3915742
BLAST score	559
E value	1.0e-57
Match length	118
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229083
Seq. ID	LIB3196-023-P1-M1-E12
Method	BLASTX
NCBI GI	g2065531
BLAST score	552
E value	7.0e-57
Match length	126
% identity	77
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	229084
Seq. ID	LIB3196-023-P1-M1-E2
Method	BLASTX
NCBI GI	g115492
BLAST score	505
E value	2.0e-51
Match length	98
% identity	50
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No. 229085

Seq. ID	LIB3196-023-P1-M1-E3
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	229086
Seq. ID	LIB3196-023-P1-M1-E4
Method	BLASTX
NCBI GI	g266344
BLAST score	640
E value	4.0e-67
Match length	132
% identity	95
NCBI Description	LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) >gi_284073_pir__S27383 elastase inhibitor - human >gi_2997692 (AF053630) monocyte/neutrophil elastase inhibitor [Homo sapiens]

Seq. No.	229087
Seq. ID	LIB3196-023-P1-M1-E6
Method	BLASTX
NCBI GI	g2098581
BLAST score	285
E value	1.0e-25
Match length	79
% identity	70
NCBI Description	(U53830) interferon regulatory factor 7A [Homo sapiens]

Seq. No.	229088
Seq. ID	LIB3196-023-P1-M1-F11
Method	BLASTX
NCBI GI	g4240261
BLAST score	157
E value	1.0e-10
Match length	30
% identity	100
NCBI Description	(AB020693) KIAA0886 protein [Homo sapiens]

Seq. No.	229089
Seq. ID	LIB3196-023-P1-M1-F12
Method	BLASTX
NCBI GI	g35053
BLAST score	590
E value	3.0e-61
Match length	115
% identity	97
NCBI Description	(X53778) uracil DNA glycosylase [Homo sapiens]

Seq. No.	229090
Seq. ID	LIB3196-023-P1-M1-F3
Method	BLASTX
NCBI GI	g88044

BLAST score	623
E value	3.0e-65
Match length	130
% identity	96
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	229091
Seq. ID	LIB3196-023-P1-M1-F4
Method	BLASTX
NCBI GI	g1350548
BLAST score	241
E value	2.0e-20
Match length	71
% identity	59
NCBI Description	(L47609) heat shock-like protein [Picea glauca]

Seq. No.	229092
Seq. ID	LIB3196-023-P1-M1-F7
Method	BLASTX
NCBI GI	g547752
BLAST score	150
E value	1.0e-09
Match length	30
% identity	97
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 2 ORAL (CYTOKERATIN 2P) (K2P) (CK 2P) >gi_2119218_pir__I53169 cytokeratin 2 - human >gi_181390 (M99063) cytokeratin 2 [Homo sapiens]

Seq. No.	229093
Seq. ID	LIB3196-023-P1-M1-F9
Method	BLASTX
NCBI GI	g2462077
BLAST score	157
E value	1.0e-10
Match length	41
% identity	66
NCBI Description	(Y11871) Oxa1 protein [Arabidopsis thaliana]

Seq. No.	229094
Seq. ID	LIB3196-023-P1-M1-G1
Method	BLASTX
NCBI GI	g2146926
BLAST score	161
E value	1.0e-23
Match length	82
% identity	68
NCBI Description	[phosphorylase] phosphatase (EC 3.1.3.17) 55K chain - African clawed frog (fragment) >gi_963087_emb_CAA56714_ (X80697) phosphorylase phosphatase [Xenopus laevis]

Seq. No.	229095
Seq. ID	LIB3196-023-P1-M1-G10
Method	BLASTX
NCBI GI	g1346347
BLAST score	594

E value	8.0e-62
Match length	122
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	229096
Seq. ID	LIB3196-023-P1-M1-G11
Method	BLASTX
NCBI GI	g3790610
BLAST score	501
E value	7.0e-51
Match length	98
% identity	89
NCBI Description	(AF093673) layilin [Cricetulus griseus]

Seq. No.	229097
Seq. ID	LIB3196-023-P1-M1-G2
Method	BLASTX
NCBI GI	g66179
BLAST score	361
E value	2.0e-34
Match length	93
% identity	77
NCBI Description	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - common tobacco chloroplast >gi_225255_prf__1211235CP NADH dehydrogenase 4-like ORF 509B [Nicotiana tabacum]

Seq. No.	229098
Seq. ID	LIB3196-023-P1-M1-G4
Method	BLASTX
NCBI GI	g189049
BLAST score	661
E value	1.0e-69
Match length	133
% identity	92
NCBI Description	(L04490) NADH dehydrogenase (ubiquinone) [Homo sapiens]

Seq. No.	229099
Seq. ID	LIB3196-023-P1-M1-G5
Method	BLASTX
NCBI GI	g908917
BLAST score	577
E value	9.0e-60
Match length	119
% identity	98
NCBI Description	(L24544) DNA helicase [Homo sapiens]

Seq. No.	229100
Seq. ID	LIB3196-023-P1-M1-G6
Method	BLASTX
NCBI GI	g2833388
BLAST score	496
E value	3.0e-50
Match length	123

% identity	79
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]
Seq. No.	229101
Seq. ID	LIB3196-023-P1-M1-G7
Method	BLASTX
NCBI GI	g485514
BLAST score	397
E value	9.0e-39
Match length	82
% identity	90
NCBI Description	ADR11-2 protein - soybean (fragment) >gi_296443_emb_CAA49341_ (X69640) auxin down regulated [Glycine max]
Seq. No.	229102
Seq. ID	LIB3196-023-P1-M1-G9
Method	BLASTX
NCBI GI	g2144118
BLAST score	191
E value	1.0e-15
Match length	100
% identity	44
NCBI Description	alpha-macroglobulin - guinea pig >gi_1304084_dbj_BAA12316_ (D84338) alpha-macroglobulin [Cavia porcellus]
Seq. No.	229103
Seq. ID	LIB3196-023-P1-M1-H1
Method	BLASTX
NCBI GI	g2950478
BLAST score	180
E value	2.0e-15
Match length	98
% identity	48
NCBI Description	(AL022070) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	229104
Seq. ID	LIB3196-023-P1-M1-H11
Method	BLASTX
NCBI GI	g137578
BLAST score	449
E value	6.0e-45
Match length	110
% identity	84
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	229105
Seq. ID	LIB3196-023-P1-M1-H2

Method	BLASTX
NCBI GI	g4263646
BLAST score	198
E value	1.0e-15
Match length	97
% identity	43
NCBI Description	(AC006136) putative TA1-like reverse transcriptase [Arabidopsis thaliana]

Seq. No.	229106
Seq. ID	LIB3196-023-P1-M1-H8
Method	BLASTX
NCBI GI	g126156
BLAST score	400
E value	4.0e-39
Match length	103
% identity	77
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229107
Seq. ID	LIB3196-024-P1-M1-A1
Method	BLASTX
NCBI GI	g1171978
BLAST score	457
E value	9.0e-46
Match length	124
% identity	23
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	229108
Seq. ID	LIB3196-024-P1-M1-A12
Method	BLASTX
NCBI GI	g950111
BLAST score	460
E value	4.0e-46
Match length	116
% identity	78
NCBI Description	(U22230) ribosomal protein S17 [Felis catus]

Seq. No.	229109
Seq. ID	LIB3196-024-P1-M1-A3
Method	BLASTX
NCBI GI	g4510339
BLAST score	272
E value	3.0e-24
Match length	58
% identity	83
NCBI Description	(AC006921) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No.	229110
Seq. ID	LIB3196-024-P1-M1-A4
Method	BLASTX
NCBI GI	g125077
BLAST score	646
E value	6.0e-68
Match length	132
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	229111
Seq. ID	LIB3196-024-P1-M1-A6
Method	BLASTX
NCBI GI	g4455367
BLAST score	392
E value	4.0e-38
Match length	126
% identity	62
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	229112
Seq. ID	LIB3196-024-P1-M1-B1
Method	BLASTX
NCBI GI	g3068713
BLAST score	240
E value	2.0e-20
Match length	78
% identity	71
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	229113
Seq. ID	LIB3196-024-P1-M1-B10
Method	BLASTX
NCBI GI	g3935151
BLAST score	438
E value	1.0e-43
Match length	101
% identity	74
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	229114
Seq. ID	LIB3196-024-P1-M1-B2
Method	BLASTX
NCBI GI	g3182976
BLAST score	510
E value	6.0e-52
Match length	117
% identity	82
NCBI Description	C-TERMINAL BINDING PROTEIN 2 >gi_2909777 (AF016507) C-terminal binding protein 2 [Homo sapiens] >gi_4557499_ref_NP_001320.1_pCTBP2_ C-terminal binding protein

Seq. No.	229115
Seq. ID	LIB3196-024-P1-M1-B3
Method	BLASTX
NCBI GI	g3915742
BLAST score	455
E value	1.0e-45
Match length	95
% identity	92
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229116
Seq. ID	LIB3196-024-P1-M1-B4
Method	BLASTX
NCBI GI	g2208944
BLAST score	350
E value	3.0e-33
Match length	118
% identity	58
NCBI Description	(Y11120) nodulin-35 homologue [Arabidopsis thaliana]

Seq. No.	229117
Seq. ID	LIB3196-024-P1-M1-B6
Method	BLASTX
NCBI GI	g1173256
BLAST score	419
E value	2.0e-41
Match length	81
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	229118
Seq. ID	LIB3196-024-P1-M1-B9
Method	BLASTX
NCBI GI	g2497442
BLAST score	272
E value	5.0e-24
Match length	51
% identity	96
NCBI Description	INTERFERON REGULATORY FACTOR 3 (IRF-3) >gi_1107689_emb_CAA91227_ (Z56281) interferon regulatory factor 3 [Homo sapiens] >gi_4504725_ref_NP_001562.1_pIRF3_ interferon regulatory factor

Seq. No.	229119
Seq. ID	LIB3196-024-P1-M1-C1
Method	BLASTX
NCBI GI	g4490741
BLAST score	178
E value	5.0e-13
Match length	94
% identity	39

NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229120
Seq. ID	LIB3196-024-P1-M1-C12
Method	BLASTX
NCBI GI	g4406780
BLAST score	516
E value	1.0e-52
Match length	122
% identity	82
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	229121
Seq. ID	LIB3196-024-P1-M1-C2
Method	BLASTX
NCBI GI	g1362047
BLAST score	219
E value	8.0e-18
Match length	52
% identity	77
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - soybean >gi_479060_emb_CAA83673_ (Z32795) cysteine proteinase [Glycine max] >gi_1096153_prf__2111244A Cys protease [Glycine max]

Seq. No.	229122
Seq. ID	LIB3196-024-P1-M1-C3
Method	BLASTX
NCBI GI	g2618686
BLAST score	183
E value	1.0e-13
Match length	88
% identity	53
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229123
Seq. ID	LIB3196-024-P1-M1-C4
Method	BLASTX
NCBI GI	g2146797
BLAST score	518
E value	7.0e-53
Match length	128
% identity	59
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	229124
Seq. ID	LIB3196-024-P1-M1-C5
Method	BLASTX
NCBI GI	g1552169
BLAST score	198
E value	2.0e-15
Match length	103
% identity	43

NCBI Description	(D42138) PIG-B [Homo sapiens]
Seq. No.	229125
Seq. ID	LIB3196-024-P1-M1-C6
Method	BLASTX
NCBI GI	g137580
BLAST score	554
E value	4.0e-57
Match length	107
% identity	100
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]
Seq. No.	229126
Seq. ID	LIB3196-024-P1-M1-C9
Method	BLASTX
NCBI GI	g125077
BLAST score	620
E value	7.0e-65
Match length	129
% identity	96
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]
Seq. No.	229127
Seq. ID	LIB3196-024-P1-M1-D1
Method	BLASTX
NCBI GI	g4056502
BLAST score	415
E value	8.0e-41
Match length	89
% identity	89
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.	229128
Seq. ID	LIB3196-024-P1-M1-D11
Method	BLASTX
NCBI GI	g2135074
BLAST score	141
E value	5.0e-09
Match length	31
% identity	87
NCBI Description	epidermal growth factor receptor-related protein - human (fragment) >gi_178252 (M99624) epidermal growth factor receptor-related protein [Homo sapiens]
Seq. No.	229129
Seq. ID	LIB3196-024-P1-M1-D2
Method	BLASTX
NCBI GI	g82426
BLAST score	525
E value	8.0e-54
Match length	110

% identity	43
NCBI Description	ubiquitin precursor - barley (fragment) >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare]

Seq. No.	229130
Seq. ID	LIB3196-024-P1-M1-D4
Method	BLASTX
NCBI GI	g4091879
BLAST score	157
E value	1.0e-10
Match length	53
% identity	64
NCBI Description	(AF061812) keratin 16 [Homo sapiens] >gi_4321795_gb_AAD15829_ (AF061809) keratin 16 [Homo sapiens]

Seq. No.	229131
Seq. ID	LIB3196-024-P1-M1-D6
Method	BLASTX
NCBI GI	g1397319
BLAST score	195
E value	5.0e-15
Match length	90
% identity	44
NCBI Description	(U61953) No definition line found [Caenorhabditis elegans]

Seq. No.	229132
Seq. ID	LIB3196-024-P1-M1-D8
Method	BLASTX
NCBI GI	g1053047
BLAST score	487
E value	2.0e-49
Match length	100
% identity	97
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	229133
Seq. ID	LIB3196-024-P1-M1-D9
Method	BLASTX
NCBI GI	g4539408
BLAST score	186
E value	5.0e-14
Match length	44
% identity	82
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	229134
Seq. ID	LIB3196-024-P1-M1-E1
Method	BLASTX
NCBI GI	g72287
BLAST score	663
E value	6.0e-70
Match length	124
% identity	100

NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]
Seq. No.	229135
Seq. ID	LIB3196-024-P1-M1-E11
Method	BLASTX
NCBI GI	g207905
BLAST score	277
E value	1.0e-24
Match length	83
% identity	64
NCBI Description	(M18027) alpha globulin B [Artificial gene]
Seq. No.	229136
Seq. ID	LIB3196-024-P1-M1-E12
Method	BLASTX
NCBI GI	g113271
BLAST score	305
E value	2.0e-53
Match length	131
% identity	85
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA ACTIN) >gi_85691_pir__S01077 actin beta, cytoskeletal - Kenyan clawed frog >gi_1334642_emb_CAA30390_ (X07507) actin [Xenopus borealis]
Seq. No.	229137
Seq. ID	LIB3196-024-P1-M1-E2
Method	BLASTX
NCBI GI	g72287
BLAST score	566
E value	2.0e-58
Match length	126
% identity	90
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]
Seq. No.	229138
Seq. ID	LIB3196-024-P1-M1-E5
Method	BLASTX
NCBI GI	g1479983
BLAST score	557
E value	2.0e-57
Match length	121
% identity	84
NCBI Description	(L78465) alpha-N-acetylglucosaminidase [Homo sapiens]
Seq. No.	229139
Seq. ID	LIB3196-024-P1-M1-F1
Method	BLASTX
NCBI GI	g1710401
BLAST score	599
E value	2.0e-62
Match length	123
% identity	89
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	229140
Seq. ID	LIB3196-024-P1-M1-F10
Method	BLASTX
NCBI GI	g2293575
BLAST score	694
E value	2.0e-73
Match length	131
% identity	100
NCBI Description	(AF013213) elongation factor 1 alpha [Bos taurus]

Seq. No.	229141
Seq. ID	LIB3196-024-P1-M1-F11
Method	BLASTX
NCBI GI	g586000
BLAST score	476
E value	6.0e-48
Match length	90
% identity	100
NCBI Description	SM22-ALPHA HOMOLOG (HA1756) (KIAA0120) >gi_434763_dbj_BAA04802_ (D21261) similar to human 22kDa, SM22 mRNA (HUM22SM). [Homo sapiens] >gi_4507357_ref_NP_003555.1_pTAGLN2_ transgelin

Seq. No.	229142
Seq. ID	LIB3196-024-P1-M1-F2
Method	BLASTX
NCBI GI	g629693
BLAST score	155
E value	4.0e-11
Match length	72
% identity	53
NCBI Description	probable integrase - common tobacco (fragment) >gi_530742_emb_CAA56791_ (X80830) integrase [Nicotiana tabacum]

Seq. No.	229143
Seq. ID	LIB3196-024-P1-M1-F3
Method	BLASTX
NCBI GI	g179212
BLAST score	523
E value	1.0e-53
Match length	104
% identity	99
NCBI Description	(J03007) Na+ K+ ATPase alpha subunit [Homo sapiens]

Seq. No.	229144
Seq. ID	LIB3196-024-P1-M1-F4
Method	BLASTX
NCBI GI	g88044
BLAST score	566
E value	1.0e-58
Match length	120
% identity	97

NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]
Seq. No.	229145
Seq. ID	LIB3196-024-P1-M1-F6
Method	BLASTX
NCBI GI	g1082798
BLAST score	258
E value	2.0e-22
Match length	126
% identity	45
NCBI Description	spliceosome-associated protein SAP 61 - human >gi_508723 (U08815) SAP 61 [Homo sapiens]
Seq. No.	229146
Seq. ID	LIB3196-024-P1-M1-G12
Method	BLASTX
NCBI GI	g1170567
BLAST score	573
E value	2.0e-59
Match length	121
% identity	90
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.	229147
Seq. ID	LIB3196-024-P1-M1-G2
Method	BLASTX
NCBI GI	g231723
BLAST score	478
E value	3.0e-48
Match length	90
% identity	100
NCBI Description	CD9 ANTIGEN (27 KD DIPHTHERIA TOXIN RECEPTOR-ASSOCIATED PROTEIN) (DRAP27) >gi_104994_pir__A42929 CD9 antigen - green monkey >gi_218566_dbj_BAA01569_ (D10726) diphtheria toxin receptor associated protein [Chlorocebus aethiops]
Seq. No.	229148
Seq. ID	LIB3196-024-P1-M1-G5
Method	BLASTX
NCBI GI	g1351173
BLAST score	587
E value	6.0e-61
Match length	118
% identity	97
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_1050527_emb_CAA62635_ (X91257) seryl-tRNA synthetase [Homo sapiens]
Seq. No.	229149
Seq. ID	LIB3196-024-P1-M1-G6
Method	BLASTX
NCBI GI	g2117159
BLAST score	146

E value	3.0e-09
Match length	98
% identity	28
NCBI Description	(Y13247) FB19 protein [Homo sapiens] >gi_4506009_ref_NP_002705.1_pPPP1R10_ protein phosphatase 1, regulatory subunit

Seq. No.	229150
Seq. ID	LIB3196-024-P1-M1-H1
Method	BLASTX
NCBI GI	g1350680
BLAST score	454
E value	2.0e-45
Match length	123
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	229151
Seq. ID	LIB3196-024-P1-M1-H3
Method	BLASTX
NCBI GI	g386850
BLAST score	655
E value	5.0e-69
Match length	130
% identity	100
NCBI Description	(M19723) keratin K5 [Homo sapiens]

Seq. No.	229152
Seq. ID	LIB3196-024-P1-M1-H8
Method	BLASTX
NCBI GI	g118607
BLAST score	461
E value	3.0e-46
Match length	98
% identity	94
NCBI Description	NAD(P)H DEHYDROGENASE (QUINONE) 1 (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) >gi_88226_pir__A30879 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 1 - human >gi_189246 (J03934) NAD(P)H:menadione oxidoreductase [Homo sapiens] >gi_189292 (M81600) NAD(P)H:quinone oxireductase [Homo sapiens] >gi_4505415_ref_NP_000894.1_pNMOR1_ NAD(P)H menadione oxidoreductase 1, dioxin-inducible

Seq. No.	229153
Seq. ID	LIB3196-024-P1-M1-H9
Method	BLASTX
NCBI GI	g4128133
BLAST score	195
E value	5.0e-15
Match length	81
% identity	44
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	229154
Seq. ID	LIB3196-025-P1-M1-A3
Method	BLASTX

NCBI GI	g2813965
BLAST score	423
E value	7.0e-42
Match length	85
% identity	96
NCBI Description	(Z97053) adenosine deaminase (ADA) [Homo sapiens]

Seq. No.	229155
Seq. ID	LIB3196-025-P1-M1-A4
Method	BLASTX
NCBI GI	g440945
BLAST score	419
E value	2.0e-41
Match length	92
% identity	86
NCBI Description	(S66773) adenosine deaminase, ADA {exon 10, exon 11} [human, ADA deficient patient AlNe, peripheral blood T cells, Peptide PartialMutant, 143 aa] [Homo sapiens]

Seq. No.	229156
Seq. ID	LIB3196-025-P1-M1-A5
Method	BLASTX
NCBI GI	g2459421
BLAST score	434
E value	5.0e-43
Match length	116
% identity	68
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	229157
Seq. ID	LIB3196-025-P1-M1-A6
Method	BLASTX
NCBI GI	g72287
BLAST score	582
E value	2.0e-60
Match length	126
% identity	88
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	229158
Seq. ID	LIB3196-025-P1-M1-A8
Method	BLASTX
NCBI GI	g633890
BLAST score	434
E value	4.0e-43
Match length	115
% identity	74
NCBI Description	(S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No.	229159
Seq. ID	LIB3196-025-P1-M1-B3
Method	BLASTX
NCBI GI	g2578033

BLAST score 429
E value 2.0e-42
Match length 83
% identity 96
NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 229160
Seq. ID LIB3196-025-P1-M1-B9
Method BLASTX
NCBI GI g120669
BLAST score 435
E value 4.0e-43
Match length 87
% identity 92
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 229161
Seq. ID LIB3196-025-P1-M1-C5
Method BLASTX
NCBI GI g478021
BLAST score 402
E value 3.0e-39
Match length 76
% identity 99
NCBI Description tumor surface antigen OA3-305 - human >gi_396705_emb_CAA80977_ (Z25521) integrin associated protein [Homo sapiens]

Seq. No. 229162
Seq. ID LIB3196-025-P1-M1-C8
Method BLASTX
NCBI GI g1531539
BLAST score 339
E value 7.0e-32
Match length 89
% identity 66
NCBI Description (D79989) KIAA0167 protein [Homo sapiens]

Seq. No. 229163
Seq. ID LIB3196-025-P1-M1-D1
Method BLASTX
NCBI GI g4091879
BLAST score 183
E value 7.0e-14
Match length 42
% identity 93
NCBI Description (AF061812) keratin 16 [Homo sapiens] >gi_4321795_gb_AAD15829_ (AF061809) keratin 16 [Homo sapiens]

Seq. No. 229164
Seq. ID LIB3196-025-P1-M1-E3
Method BLASTX

NCBI GI	g3413167
BLAST score	161
E value	4.0e-11
Match length	34
% identity	94
NCBI Description	(AJ010225) elongation factor 1-alpha [Cicer arietinum]

Seq. No.	229165
Seq. ID	LIB3196-025-P1-M1-E6
Method	BLASTX
NCBI GI	g3152583
BLAST score	315
E value	5.0e-29
Match length	122
% identity	55
NCBI Description	(AC002986) Contains similarity to inhibitor of apoptosis protein gb_U45881 from D. melanogaster. [Arabidopsis thaliana]

Seq. No.	229166
Seq. ID	LIB3196-025-P1-M1-E8
Method	BLASTX
NCBI GI	g3821055
BLAST score	583
E value	2.0e-60
Match length	127
% identity	87
NCBI Description	(AJ223603) hypothetical protein [Homo sapiens]

Seq. No.	229167
Seq. ID	LIB3196-025-P1-M1-E9
Method	BLASTX
NCBI GI	g137578
BLAST score	394
E value	2.0e-38
Match length	109
% identity	68
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229168
Seq. ID	LIB3196-025-P1-M1-F3
Method	BLASTX
NCBI GI	g3122659
BLAST score	460
E value	4.0e-46
Match length	106
% identity	75
NCBI Description	PEROXIREDOXIN (REHYDRIN HOMOLOG) >gi_1926269_emb_CAA72804_ (Y12089) peroxiredoxin [Arabidopsis thaliana]

Seq. No.	229169
Seq. ID	LIB3196-025-P1-M1-F4

Method	BLASTX
NCBI GI	g4097583
BLAST score	188
E value	3.0e-14
Match length	54
% identity	72
NCBI Description	(U64924) NTGP3 [Nicotiana tabacum]

Seq. No.	229170
Seq. ID	LIB3196-025-P1-M1-F9
Method	BLASTX
NCBI GI	g113271
BLAST score	478
E value	4.0e-49
Match length	104
% identity	100
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA ACTIN) >gi_85691_pir__S01077 actin beta, cytoskeletal - Kenyan clawed frog >gi_1334642_emb_CAA30390_ (X07507) actin [Xenopus borealis]

Seq. No.	229171
Seq. ID	LIB3196-025-P1-M1-G1
Method	BLASTX
NCBI GI	g4455235
BLAST score	255
E value	4.0e-22
Match length	68
% identity	75
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]

Seq. No.	229172
Seq. ID	LIB3196-025-P1-M1-G3
Method	BLASTX
NCBI GI	g1480220
BLAST score	503
E value	4.0e-51
Match length	118
% identity	78
NCBI Description	(D31816) HLA-B4007 [Homo sapiens]

Seq. No.	229173
Seq. ID	LIB3196-025-P1-M1-G8
Method	BLASTX
NCBI GI	g730565
BLAST score	692
E value	3.0e-73
Match length	130
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_423069_pir__S34195 ribosomal protein L3 - human >gi_313659_emb_CAA51839_ (X73460) ribosomal protein L3 [Homo sapiens] >gi_3850177_emb_CAA18450_ (AL022326) dJ333H23.1.1 (60S Ribosomal Protein L3) [Homo sapiens] >gi_4506649_ref_NP_000958.1_pRPL3_ ribosomal protein L3

Seq. No.	229174

Seq. ID	LIB3196-025-P1-M1-G9
Method	BLASTX
NCBI GI	g135655
BLAST score	524
E value	8.0e-54
Match length	105
% identity	99
NCBI Description	TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) >gi_105865_pir__A34734 transcription factor 3 - human >gi_339478 (M31523) transcription factor E2A [Homo sapiens]

Seq. No.	229175
Seq. ID	LIB3196-025-P1-M1-H1
Method	BLASTX
NCBI GI	g266945
BLAST score	502
E value	5.0e-51
Match length	116
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi_100065_pir__S19978 ribosomal protein L9 - garden pea >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum] >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9 [Pisum sativum]

Seq. No.	229176
Seq. ID	LIB3196-025-P1-M1-H2
Method	BLASTX
NCBI GI	g1944193
BLAST score	496
E value	3.0e-50
Match length	127
% identity	75
NCBI Description	(AB002810) nodulin 35 [Glycine max]

Seq. No.	229177
Seq. ID	LIB3196-025-P1-M1-H3
Method	BLASTX
NCBI GI	g3182898
BLAST score	421
E value	1.0e-41
Match length	99
% identity	85
NCBI Description	ACTIN 2 >gi_2653414_emb_CAA74016_ (Y13665) actin [Saccoglossus kowalevskii]

Seq. No.	229178
Seq. ID	LIB3196-025-P1-M1-H5
Method	BLASTX
NCBI GI	g1703129
BLAST score	568
E value	1.0e-58
Match length	105
% identity	99
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis

	thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]
Seq. No.	229179
Seq. ID	LIB3196-025-P1-M1-H8
Method	BLASTX
NCBI GI	g120222
BLAST score	470
E value	2.0e-47
Match length	88
% identity	100
NCBI Description	FK506-BINDING PROTEIN (FKBP-12) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) (IMMUNOPHILIN FKBP12) >gi_107276_pir__A35780 peptidylprolyl isomerase (EC 5.2.1.8) FKBP1 - human >gi_539777_pir__A42657 FK506-binding protein - rabbit >gi_165023 (M89928) binding protein [Oryctolagus cuniculus] >gi_182628 (M34539) FK506-binding protein (FKBP) [Homo sapiens] >gi_182633 (M80199) FKBP-12 protein [Homo sapiens] >gi_182649 (M93060) FK506-binding protein 12 [Homo sapiens] >gi_288196_emb_CAA39272_ (X55741) FKBP [Homo sapiens] >gi_665650_emb_CAA36462_ (X52220) FK-506 binding protein [Homo sapiens] >gi_227077_prf__1613455A FK506 binding protein FKBP [Homo sapiens] >gi_4503725_ref_NP_000792.1_pFKBP1A_ FK506-binding protein 1 (12kD)
Seq. No.	229180
Seq. ID	LIB3196-025-P1-M1-H9
Method	BLASTX
NCBI GI	g2497538
BLAST score	517
E value	7.0e-53
Match length	107
% identity	93
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]
Seq. No.	229181
Seq. ID	LIB3196-027-P1-M1-A11
Method	BLASTX
NCBI GI	g549732
BLAST score	215
E value	2.0e-17
Match length	67
% identity	55
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast (Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_ (Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF [Saccharomyces cerevisiae]
Seq. No.	229182
Seq. ID	LIB3196-027-P1-M1-A12
Method	BLASTX
NCBI GI	g49868

BLAST score 572
E value 3.0e-59
Match length 109
% identity 100
NCBI Description (X03765) put. beta-actin (aa 27-375) [Mus musculus]
>gi_387083 (M12481) cytoplasmic beta-actin [Mus musculus]

Seq. No. 229183
Seq. ID LIB3196-027-P1-M1-A4
Method BLASTX
NCBI GI g547299
BLAST score 550
E value 1.0e-56
Match length 99
% identity 100
NCBI Description beta 2-microglobulin, beta 2-M [Papio hamadryas=baboons, 26CB-1, Peptide, 99 aa]

Seq. No. 229184
Seq. ID LIB3196-027-P1-M1-A9
Method BLASTX
NCBI GI g2253411
BLAST score 258
E value 2.0e-22
Match length 89
% identity 46
NCBI Description (AF007219) PP2A inhibitor [Tetraodon fluviatilis]

Seq. No. 229185
Seq. ID LIB3196-027-P1-M1-B11
Method BLASTX
NCBI GI g3334756
BLAST score 442
E value 2.0e-50
Match length 105
% identity 87
NCBI Description (Y16672) putative arginine/serine-rich splicing factor [Medicago sativa]

Seq. No. 229186
Seq. ID LIB3196-027-P1-M1-B4
Method BLASTX
NCBI GI g4558462
BLAST score 174
E value 4.0e-26
Match length 111
% identity 57
NCBI Description (AF079404) cell cycle switch protein [Medicago sativa subsp. X varia]

Seq. No. 229187
Seq. ID LIB3196-027-P1-M1-B7
Method BLASTX
NCBI GI g1173218
BLAST score 337
E value 9.0e-32
Match length 64

% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	229188
Seq. ID	LIB3196-027-P1-M1-B9
Method	BLASTX
NCBI GI	g1743388
BLAST score	146
E value	3.0e-09
Match length	60
% identity	55
NCBI Description	(Y09874) pSbaNS5 protein [Sorghum bicolor]

Seq. No.	229189
Seq. ID	LIB3196-027-P1-M1-C10
Method	BLASTX
NCBI GI	g2117356
BLAST score	624
E value	2.0e-65
Match length	123
% identity	96
NCBI Description	core I protein - human >gi_468935_dbj_BAA05495_ (D26485) core I protein [Homo sapiens]

Seq. No.	229190
Seq. ID	LIB3196-027-P1-M1-C11
Method	BLASTX
NCBI GI	g2828280
BLAST score	584
E value	1.0e-60
Match length	113
% identity	95
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi_2832633_emb_CAA16762_ (AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	229191
Seq. ID	LIB3196-027-P1-M1-C12
Method	BLASTX
NCBI GI	g2583108
BLAST score	349
E value	4.0e-33
Match length	106
% identity	70
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	229192
Seq. ID	LIB3196-027-P1-M1-C2
Method	BLASTX
NCBI GI	g1346180
BLAST score	313
E value	7.0e-29
Match length	79
% identity	73
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374)

homology with RNA-binding proteins in meristematic tissue [Sinapis alba]

Seq. No.	229193
Seq. ID	LIB3196-027-P1-M1-C4
Method	BLASTX
NCBI GI	g3687234
BLAST score	252
E value	1.0e-28
Match length	118
% identity	54
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	229194
Seq. ID	LIB3196-027-P1-M1-C6
Method	BLASTX
NCBI GI	g2280476
BLAST score	646
E value	6.0e-68
Match length	125
% identity	100
NCBI Description	(AB002313) KIAA0315 [Homo sapiens]

Seq. No.	229195
Seq. ID	LIB3196-027-P1-M1-C8
Method	BLASTX
NCBI GI	g631839
BLAST score	222
E value	3.0e-18
Match length	93
% identity	56
NCBI Description	growth factor-responsive protein, vascular smooth muscle - rat >gi_469478 (U06713) SM-20 [Rattus norvegicus]

Seq. No.	229196
Seq. ID	LIB3196-027-P1-M1-C9
Method	BLASTX
NCBI GI	g3242177
BLAST score	549
E value	2.0e-56
Match length	124
% identity	88
NCBI Description	(AL022325) fF27C3.2.1 (unknown protein) (isoform 1) [Homo sapiens]

Seq. No.	229197
Seq. ID	LIB3196-027-P1-M1-D11
Method	BLASTX
NCBI GI	g2996096
BLAST score	619
E value	8.0e-65
Match length	117
% identity	100
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	229198
Seq. ID	LIB3196-027-P1-M1-D12
Method	BLASTX
NCBI GI	g124219
BLAST score	167
E value	9.0e-12
Match length	100
% identity	40
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4B (EIF-4B) >gi_106728_pir__S12566 translation initiation factor eIF-4B - human >gi_288100_emb_CAA39265_ (X55733) initation factor 4B [Homo sapiens] >gi_4503533_ref_NP_001408.1_pEIF4B_ eukaryotic translation initiation factor 4B

Seq. No.	229199
Seq. ID	LIB3196-027-P1-M1-D5
Method	BLASTX
NCBI GI	g1708967
BLAST score	515
E value	1.0e-52
Match length	105
% identity	99
NCBI Description	MALATE DEHYDROGENASE, CYTOPLASMIC >gi_1255604_dbj_BAA09513_ (D55654) cytosolic malate dehydrogenase [Homo sapiens] >gi_3133269 (U20352) malate dehydrogenase [Homo sapiens]

Seq. No.	229200
Seq. ID	LIB3196-027-P1-M1-D7
Method	BLASTX
NCBI GI	g137578
BLAST score	344
E value	2.0e-32
Match length	120
% identity	62
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229201
Seq. ID	LIB3196-027-P1-M1-D8
Method	BLASTX
NCBI GI	g88044
BLAST score	589
E value	3.0e-61
Match length	125
% identity	97
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	229202
Seq. ID	LIB3196-027-P1-M1-D9
Method	BLASTX
NCBI GI	g3913518

BLAST score	201
E value	3.0e-24
Match length	86
% identity	76
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	229203
Seq. ID	LIB3196-027-P1-M1-E10
Method	BLASTX
NCBI GI	g4322822
BLAST score	509
E value	8.0e-52
Match length	124
% identity	78
NCBI Description	(AF095193) BAG-family molecular chaperone regulator-3; BAG-3 [Homo sapiens]

Seq. No.	229204
Seq. ID	LIB3196-027-P1-M1-E11
Method	BLASTX
NCBI GI	g2583108
BLAST score	321
E value	8.0e-30
Match length	88
% identity	73
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	229205
Seq. ID	LIB3196-027-P1-M1-E7
Method	BLASTX
NCBI GI	g1170519
BLAST score	345
E value	1.0e-32
Match length	69
% identity	99
NCBI Description	INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUP I-5111) >gi_627550_pir__A54859 multicatalytic proteinase activator - human >gi_186513 (L07633) interferon-gamma [Homo sapiens] >gi_551491 (U10360) interferon-gamma [Homo sapiens]

Seq. No.	229206
Seq. ID	LIB3196-027-P1-M1-E9
Method	BLASTX
NCBI GI	g2880033
BLAST score	119
E value	1.0e-09
Match length	39
% identity	100
NCBI Description	(U73167) interferon-related putative protein [Homo sapiens]

Seq. No.	229207
Seq. ID	LIB3196-027-P1-M1-F1
Method	BLASTX

NCBI GI	g2306917
BLAST score	469
E value	3.0e-47
Match length	102
% identity	89
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	229208
Seq. ID	LIB3196-027-P1-M1-F11
Method	BLASTX
NCBI GI	g88044
BLAST score	606
E value	3.0e-63
Match length	125
% identity	99
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	229209
Seq. ID	LIB3196-027-P1-M1-F12
Method	BLASTX
NCBI GI	g547753
BLAST score	523
E value	2.0e-53
Match length	121
% identity	90
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	229210
Seq. ID	LIB3196-027-P1-M1-F3
Method	BLASTX
NCBI GI	g1055130
BLAST score	183
E value	1.0e-13
Match length	103
% identity	37
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	229211
Seq. ID	LIB3196-027-P1-M1-F5
Method	BLASTX
NCBI GI	g1857161
BLAST score	164
E value	2.0e-11
Match length	26
% identity	100
NCBI Description	(U70663) hEZF [Homo sapiens]

Seq. No.	229212
Seq. ID	LIB3196-027-P1-M1-F6
Method	BLASTX

NCBI GI g1223922
BLAST score 464
E value 1.0e-46
Match length 108
% identity 74
NCBI Description (U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata]

Seq. No. 229213
Seq. ID LIB3196-027-P1-M1-F9
Method BLASTX
NCBI GI g2401257
BLAST score 257
E value 2.0e-22
Match length 106
% identity 48
NCBI Description (D63951) TBZ17 [Nicotiana tabacum]

Seq. No. 229214
Seq. ID LIB3196-027-P1-M1-G12
Method BLASTX
NCBI GI g119339
BLAST score 427
E value 3.0e-42
Match length 86
% identity 99
NCBI Description ALPHA ENOLASE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE) >gi_87368_pir__A29170 phosphopyruvate hydratase (EC 4.2.1.11) alpha - human >gi_182114 (M14328) alpha enolase (EC 4.2.1.11) [Homo sapiens] >gi_1167843_emb_CAA34360_ (X16288) alpha-enolase [Homo sapiens] >gi_4503571_ref_NP_001419.1_pENO1_ enolase 1, (alpha)

Seq. No. 229215
Seq. ID LIB3196-027-P1-M1-G2
Method BLASTX
NCBI GI g3192909
BLAST score 261
E value 9.0e-23
Match length 101
% identity 47
NCBI Description (AF068836) cytohesin binding protein HE [Homo sapiens]

Seq. No. 229216
Seq. ID LIB3196-027-P1-M1-G4
Method BLASTX
NCBI GI g1644427
BLAST score 264
E value 4.0e-23
Match length 59
% identity 86
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 229217
Seq. ID LIB3196-027-P1-M1-G7
Method BLASTX

NCBI GI	g72287
BLAST score	618
E value	1.0e-64
Match length	119
% identity	100
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	229218
Seq. ID	LIB3196-027-P1-M1-G9
Method	BLASTX
NCBI GI	g2924509
BLAST score	201
E value	9.0e-16
Match length	91
% identity	45
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No.	229219
Seq. ID	LIB3196-027-P1-M1-H1
Method	BLASTX
NCBI GI	g495866
BLAST score	326
E value	2.0e-30
Match length	90
% identity	1
NCBI Description	(L23982) collagen type VII [Homo sapiens]

Seq. No.	229220
Seq. ID	LIB3196-027-P1-M1-H10
Method	BLASTX
NCBI GI	g82264
BLAST score	140
E value	1.0e-08
Match length	29
% identity	90
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)8I) - potato (fragment) >gi_498789_emb_CAA56109_ (X79597) cytochrome c1 [Solanum tuberosum]

Seq. No.	229221
Seq. ID	LIB3196-027-P1-M1-H12
Method	BLASTX
NCBI GI	g3859849
BLAST score	566
E value	2.0e-58
Match length	97
% identity	35
NCBI Description	(AF063002) LIM protein SLIMMER [Homo sapiens]

Seq. No.	229222
Seq. ID	LIB3196-027-P1-M1-H3
Method	BLASTX
NCBI GI	g1710151

BLAST score	574
E value	2.0e-59
Match length	120
% identity	88
NCBI Description	(U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No.	229223
Seq. ID	LIB3196-027-P1-M1-H4
Method	BLASTX
NCBI GI	g832876
BLAST score	535
E value	6.0e-55
Match length	114
% identity	92
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	229224
Seq. ID	LIB3196-027-P1-M1-H6
Method	BLASTX
NCBI GI	g730583
BLAST score	245
E value	6.0e-21
Match length	62
% identity	79
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	229225
Seq. ID	LIB3196-027-P1-M1-H7
Method	BLASTX
NCBI GI	g4388731
BLAST score	142
E value	5.0e-09
Match length	55
% identity	62
NCBI Description	(AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229226
Seq. ID	LIB3196-027-P1-M1-H8
Method	BLASTX
NCBI GI	g2996650
BLAST score	634
E value	2.0e-66
Match length	124
% identity	34
NCBI Description	(AC004493) KIAA0324 [Homo sapiens]

Seq. No.	229227
Seq. ID	LIB3196-027-P1-M1-H9
Method	BLASTX
NCBI GI	g126366
BLAST score	643
E value	1.0e-67
Match length	122

% identity	98
NCBI Description	LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN) >gi_71422_pir__MMHUB1 laminin chain B1 precursor - human >gi_186837 (M61916) laminin B1 [Homo sapiens] >gi_186876 (M55370) laminin B1 [Homo sapiens] >gi_186913 (M61951). laminin B1 [Homo sapiens] >gi_4504951_ref_NP_002282.1_pLAMB1_ laminin, beta

Seq. No.	229228
Seq. ID	LIB3196-028-P1-M1-A10
Method	BLASTX
NCBI GI	g4159888
BLAST score	267
E value	2.0e-23
Match length	113
% identity	6
NCBI Description	(AC004908) zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens]

Seq. No.	229229
Seq. ID	LIB3196-028-P1-M1-A11
Method	BLASTX
NCBI GI	g3063392
BLAST score	276
E value	1.0e-24
Match length	113
% identity	57
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	229230
Seq. ID	LIB3196-028-P1-M1-A12
Method	BLASTX
NCBI GI	g726034
BLAST score	427
E value	2.0e-42
Match length	102
% identity	83
NCBI Description	(U19177) Hin-2 [Homo sapiens]

Seq. No.	229231
Seq. ID	LIB3196-028-P1-M1-A5
Method	BLASTX
NCBI GI	g3063392
BLAST score	292
E value	2.0e-26
Match length	114
% identity	57
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	229232
Seq. ID	LIB3196-028-P1-M1-A8
Method	BLASTX
NCBI GI	g3023897
BLAST score	150
E value	3.0e-10
Match length	51
% identity	57

NCBI Description	GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS (RALGEF) >gi_2135317_pir__I38853 guanine nucleotide dissociation stimulator ralGDS - human (fragment) >gi_538200 (U14417) Ral guanine nucleotide dissociation stimulator [Homo sapiens]
Seq. No.	229233
Seq. ID	LIB3196-028-P1-M1-A9
Method	BLASTX
NCBI GI	g1619602
BLAST score	360
E value	2.0e-34
Match length	86
% identity	80
NCBI Description	(Y08726) MtN3 [Medicago truncatula]
Seq. No.	229234
Seq. ID	LIB3196-028-P1-M1-B1
Method	BLASTX
NCBI GI	g126156
BLAST score	444
E value	3.0e-44
Match length	94
% identity	95
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]
Seq. No.	229235
Seq. ID	LIB3196-028-P1-M1-B10
Method	BLASTX
NCBI GI	g3894189
BLAST score	149
E value	6.0e-10
Match length	50
% identity	60
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.	229236
Seq. ID	LIB3196-028-P1-M1-B12
Method	BLASTX
NCBI GI	g225581
BLAST score	393
E value	3.0e-38
Match length	111
% identity	71
NCBI Description	storage protein C94 [Saguinus oedipus]
Seq. No.	229237
Seq. ID	LIB3196-028-P1-M1-B5
Method	BLASTX
NCBI GI	g1381179
BLAST score	328
E value	1.0e-30

Match length	81
% identity	79
NCBI Description	(U58766) FX [Homo sapiens] >gi_4507709_ref_NP_003304.1_pTSTA3_ tissue specific transplantation antigen P35B

Seq. No.	229238
Seq. ID	LIB3196-028-P1-M1-B7
Method	BLASTX
NCBI GI	g3080420
BLAST score	359
E value	2.0e-34
Match length	82
% identity	83
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	229239
Seq. ID	LIB3196-028-P1-M1-C10
Method	BLASTX
NCBI GI	g2605714
BLAST score	261
E value	8.0e-23
Match length	67
% identity	81
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	229240
Seq. ID	LIB3196-028-P1-M1-C12
Method	BLASTX
NCBI GI	g3879684
BLAST score	278
E value	6.0e-25
Match length	97
% identity	55
NCBI Description	(Z74042) predicted using Genefinder; Similarity to Haemophilus 3-oxoacyl-(acyl-carrier protein) reductase (SW:FABG_HAEIN); cDNA EST yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	229241
Seq. ID	LIB3196-028-P1-M1-C3
Method	BLASTX
NCBI GI	g3243079
BLAST score	628
E value	9.0e-66
Match length	129
% identity	37
NCBI Description	(AF071771) SPH-binding factor [Homo sapiens]

Seq. No.	229242
Seq. ID	LIB3196-028-P1-M1-C9
Method	BLASTX
NCBI GI	g1220196
BLAST score	500

E value	8.0e-51
Match length	97
% identity	98
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	229243
Seq. ID	LIB3196-028-P1-M1-D2
Method	BLASTX
NCBI GI	g730832
BLAST score	174
E value	1.0e-12
Match length	53
% identity	58
NCBI Description	8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN) (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi_18748_emb_CAA78359_ (Z13956) a protein similar to potato tuber protein p322 homolgous to Bowman-Birk Proteinase Inhibitor [Glycine max]

Seq. No.	229244
Seq. ID	LIB3196-028-P1-M1-D3
Method	BLASTX
NCBI GI	g1944407
BLAST score	205
E value	3.0e-16
Match length	45
% identity	82
NCBI Description	(D86988) KIAA0221 [Homo sapiens]

Seq. No.	229245
Seq. ID	LIB3196-028-P1-M1-D5
Method	BLASTX
NCBI GI	g3122072
BLAST score	559
E value	1.0e-57
Match length	106
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]

Seq. No.	229246
Seq. ID	LIB3196-028-P1-M1-D6
Method	BLASTX
NCBI GI	g683653
BLAST score	202
E value	7.0e-16
Match length	102
% identity	47
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	229247
Seq. ID	LIB3196-028-P1-M1-D7
Method	BLASTX

NCBI GI	g3355468
BLAST score	452
E value	3.0e-45
Match length	109
% identity	87
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	229248
Seq. ID	LIB3196-028-P1-M1-D8
Method	BLASTX
NCBI GI	g1703470
BLAST score	656
E value	4.0e-69
Match length	126
% identity	97
NCBI Description	SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) >gi_1256802 (U51478) sodium/potassium-transporting ATPase beta-3 subunit [Homo sapiens] >gi_2224939 (AF005896) Na K-ATPase beta-3 subunit [Homo sapiens] >gi_4502281_ref_NP_001670.1_pATP1B3_ ATPase, Na+/K+ transporting, beta 3 polypeptide

Seq. No.	229249
Seq. ID	LIB3196-028-P1-M1-D9
Method	BLASTX
NCBI GI	g88052
BLAST score	171
E value	3.0e-12
Match length	67
% identity	58
NCBI Description	keratin K5, 58K type II, epidermal (version 2) - human (fragment)

Seq. No.	229250
Seq. ID	LIB3196-028-P1-M1-E1
Method	BLASTX
NCBI GI	g4539292
BLAST score	389
E value	8.0e-38
Match length	80
% identity	88
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	229251
Seq. ID	LIB3196-028-P1-M1-E10
Method	BLASTX
NCBI GI	g2501572
BLAST score	375
E value	4.0e-36
Match length	113
% identity	65
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No.	229252
Seq. ID	LIB3196-028-P1-M1-E12
Method	BLASTX
NCBI GI	g683553
BLAST score	230
E value	4.0e-19
Match length	109
% identity	49
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	229253
Seq. ID	LIB3196-028-P1-M1-E2
Method	BLASTX
NCBI GI	g4249403
BLAST score	498
E value	1.0e-50
Match length	118
% identity	78
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	229254
Seq. ID	LIB3196-028-P1-M1-E5
Method	BLASTX
NCBI GI	g1841870
BLAST score	265
E value	3.0e-23
Match length	93
% identity	60
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	229255
Seq. ID	LIB3196-028-P1-M1-E7
Method	BLASTX
NCBI GI	g1906828
BLAST score	529
E value	3.0e-54
Match length	105
% identity	97
NCBI Description	(Y11828) heat shock protein [Arabidopsis thaliana]

Seq. No.	229256
Seq. ID	LIB3196-028-P1-M1-E9
Method	BLASTX
NCBI GI	g2924601
BLAST score	461
E value	2.0e-46
Match length	85
% identity	51
NCBI Description	(AB000095) hepatocyte growth factor activator inhibitor [Homo sapiens] >gi_4504329_ref_NP_003701.1_pHAI_ hepatocyte growth factor activator inhibitor

Seq. No.	229257
Seq. ID	LIB3196-028-P1-M1-F1
Method	BLASTX
NCBI GI	g113621

BLAST score	470
E value	3.0e-47
Match length	106
% identity	88
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays]

Seq. No.	229258
Seq. ID	LIB3196-028-P1-M1-F11
Method	BLASTX
NCBI GI	g2274859
BLAST score	311
E value	1.0e-28
Match length	71
% identity	79
NCBI Description	(AJ000016) Cks1 protein [Arabidopsis thaliana] >gi_4510420_gb_AAD21506.1_ (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No.	229259
Seq. ID	LIB3196-028-P1-M1-F6
Method	BLASTX
NCBI GI	g3894183
BLAST score	146
E value	3.0e-09
Match length	104
% identity	40
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	229260
Seq. ID	LIB3196-028-P1-M1-F9
Method	BLASTX
NCBI GI	g81546
BLAST score	341
E value	2.0e-32
Match length	76
% identity	87
NCBI Description	alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No.	229261
Seq. ID	LIB3196-028-P1-M1-G10
Method	BLASTX
NCBI GI	g2961542
BLAST score	387
E value	9.0e-38
Match length	86
% identity	76
NCBI Description	(AF050463) zinc finger transcription factor [Arabidopsis thaliana]

Seq. No.	229262

Seq. ID	LIB3196-028-P1-M1-G11
Method	BLASTX
NCBI GI	g3892059
BLAST score	182
E value	2.0e-13
Match length	113
% identity	43
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	229263
Seq. ID	LIB3196-028-P1-M1-G12
Method	BLASTX
NCBI GI	g3776005
BLAST score	339
E value	6.0e-32
Match length	93
% identity	75
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	229264
Seq. ID	LIB3196-028-P1-M1-G2
Method	BLASTX
NCBI GI	g1053047
BLAST score	565
E value	2.0e-58
Match length	113
% identity	100
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	229265
Seq. ID	LIB3196-028-P1-M1-G3
Method	BLASTX
NCBI GI	g1731151
BLAST score	564
E value	3.0e-58
Match length	106
% identity	98
NCBI Description	HYPOTHETICAL PROTEIN S171 >gi_887362 (L40393) ORF; putative [Homo sapiens] >gi_4505479_ref_NP_003735.1_pNUMB_ homolog of Drosophila numb

Seq. No.	229266
Seq. ID	LIB3196-028-P1-M1-G4
Method	BLASTX
NCBI GI	g1706551
BLAST score	226
E value	1.0e-18
Match length	87
% identity	48
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta 1,3-glucanase [Triticum aestivum]

Seq. No.	229267
Seq. ID	LIB3196-028-P1-M1-G5
Method	BLASTX
NCBI GI	g3327142
BLAST score	531
E value	2.0e-54
Match length	129
% identity	85
NCBI Description	(AB014564) KIAA0664 protein [Homo sapiens]

Seq. No.	229268
Seq. ID	LIB3196-028-P1-M1-G6
Method	BLASTX
NCBI GI	g3327142
BLAST score	185
E value	5.0e-14
Match length	96
% identity	52
NCBI Description	(AB014564) KIAA0664 protein [Homo sapiens]

Seq. No.	229269
Seq. ID	LIB3196-028-P1-M1-G7
Method	BLASTX
NCBI GI	g547753
BLAST score	240
E value	2.0e-42
Match length	106
% identity	92
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	229270
Seq. ID	LIB3196-028-P1-M1-G9
Method	BLASTX
NCBI GI	g4406775
BLAST score	239
E value	3.0e-20
Match length	116
% identity	41
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	229271
Seq. ID	LIB3196-028-P1-M1-H1
Method	BLASTX
NCBI GI	g3450889
BLAST score	315
E value	4.0e-29
Match length	92
% identity	73
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	229272
Seq. ID	LIB3196-028-P1-M1-H12
Method	BLASTX
NCBI GI	g4512671
BLAST score	211
E value	5.0e-17
Match length	59

% identity	66
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	229273
Seq. ID	LIB3196-028-P1-M1-H2
Method	BLASTX
NCBI GI	g4062934
BLAST score	457
E value	8.0e-46
Match length	110
% identity	79
NCBI Description	(D88272) formate dehydrogenase [Hordeum vulgare]

Seq. No.	229274
Seq. ID	LIB3196-028-P1-M1-H6
Method	BLASTX
NCBI GI	g3252792
BLAST score	501
E value	6.0e-51
Match length	122
% identity	80
NCBI Description	(AB015609) S-adenosylmethionine decarboxylase [Nicotiana sylvestris]

Seq. No.	229275
Seq. ID	LIB3196-028-P1-M1-H9
Method	BLASTX
NCBI GI	g72287
BLAST score	540
E value	1.0e-55
Match length	103
% identity	100
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	229276
Seq. ID	LIB3196-029-P1-M1-A1
Method	BLASTX
NCBI GI	g4467804
BLAST score	461
E value	3.0e-46
Match length	114
% identity	80
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No.	229277
Seq. ID	LIB3196-029-P1-M1-A10
Method	BLASTX
NCBI GI	g2217972
BLAST score	401
E value	4.0e-39
Match length	126
% identity	66
NCBI Description	(Y12338) unnamed protein product [Homo sapiens]

Seq. No.	229278
Seq. ID	LIB3196-029-P1-M1-A12
Method	BLASTX
NCBI GI	g2970051
BLAST score	177
E value	4.0e-13
Match length	52
% identity	63
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	229279
Seq. ID	LIB3196-029-P1-M1-A2
Method	BLASTX
NCBI GI	g1053047
BLAST score	506
E value	1.0e-51
Match length	104
% identity	97
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	229280
Seq. ID	LIB3196-029-P1-M1-A4
Method	BLASTX
NCBI GI	g2338292
BLAST score	184
E value	1.0e-13
Match length	97
% identity	41
NCBI Description	(AF009243) proline-rich Gla protein 2 [Homo sapiens] >gi_4506137_ref_NP_000942.1_pPRRG2_ proline-rich Gla (G-carboxglutamic acid) polypeptide

Seq. No.	229281
Seq. ID	LIB3196-029-P1-M1-A5
Method	BLASTX
NCBI GI	g87645
BLAST score	306
E value	5.0e-28
Match length	61
% identity	97
NCBI Description	heparin-binding growth factor-binding protein precursor - human >gi_183951 (M60047) heparin binding protein [Homo sapiens]

Seq. No.	229282
Seq. ID	LIB3196-029-P1-M1-A7
Method	BLASTX
NCBI GI	g4467804
BLAST score	495
E value	3.0e-50
Match length	114
% identity	85
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).)

[Homo sapiens]

Seq. No.	229283
Seq. ID	LIB3196-029-P1-M1-A8
Method	BLASTX
NCBI GI	g1346342
BLAST score	298
E value	3.0e-27
Match length	58
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo sapiens]

Seq. No.	229284
Seq. ID	LIB3196-029-P1-M1-B1
Method	BLASTX
NCBI GI	g1346347
BLAST score	636
E value	8.0e-67
Match length	128
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	229285
Seq. ID	LIB3196-029-P1-M1-B10
Method	BLASTX
NCBI GI	g3845409
BLAST score	667
E value	2.0e-70
Match length	125
% identity	98
NCBI Description	(AC004976) glycyl tRNA synthetase [Homo sapiens]

Seq. No.	229286
Seq. ID	LIB3196-029-P1-M1-B11
Method	BLASTX
NCBI GI	g71611
BLAST score	634
E value	1.0e-66
Match length	118
% identity	100
NCBI Description	actin, skeletal muscle - rabbit

Seq. No.	229287
Seq. ID	LIB3196-029-P1-M1-B2
Method	BLASTX
NCBI GI	g72287
BLAST score	174
E value	8.0e-13
Match length	74
% identity	55
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium

hirsutum]

Seq. No.	229288
Seq. ID	LIB3196-029-P1-M1-B3
Method	BLASTX
NCBI GI	g1890182
BLAST score	426
E value	4.0e-42
Match length	86
% identity	90
NCBI Description	(Y11731) DNA glycosylase/AP lyase [Homo sapiens] >gi_1903206_emb_CAA72536_ (Y11838) 8-oxoguanine DNA glycosylase homolog 1 [Homo sapiens] >gi_1906757_dbj_BAA19103_ (AB000410) hOGG1 [Homo sapiens] >gi_2197083 (AF003595) 8-oxoguanine DNA glycosylase 1 [Homo sapiens] >gi_2351704 (U88527) 8-hydroxyguanine glycosylase/lyase [Homo sapiens] >gi_4505495_ref_NP_002533.1_pOGG1_ 8-oxoguanine DNA glycosylase

Seq. No.	229289
Seq. ID	LIB3196-029-P1-M1-B4
Method	BLASTX
NCBI GI	g2894378
BLAST score	140
E value	4.0e-09
Match length	67
% identity	38
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	229290
Seq. ID	LIB3196-029-P1-M1-B7
Method	BLASTX
NCBI GI	g4539660
BLAST score	186
E value	5.0e-14
Match length	77
% identity	47
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	229291
Seq. ID	LIB3196-029-P1-M1-B8
Method	BLASTX
NCBI GI	g121567
BLAST score	654
E value	8.0e-69
Match length	127
% identity	100
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN) (BIP) >gi_87528_pir__A29821 Ig heavy chain-binding protein precursor - human >gi_386758 (M19645) GRP78 precursor [Homo sapiens] >gi_1143492_emb_CAA61201_ (X87949) BiP [Homo sapiens]

Seq. No.	229292
Seq. ID	LIB3196-029-P1-M1-C1

Method	BLASTX
NCBI GI	g683553
BLAST score	229
E value	5.0e-19
Match length	104
% identity	50
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	229293
Seq. ID	LIB3196-029-P1-M1-C10
Method	BLASTX
NCBI GI	g167367
BLAST score	556
E value	2.0e-57
Match length	119
% identity	90
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	229294
Seq. ID	LIB3196-029-P1-M1-C12
Method	BLASTX
NCBI GI	g416662
BLAST score	326
E value	2.0e-30
Match length	116
% identity	54
NCBI Description	21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin inhibitor homolog - soybean >gi_21909_emb_CAA39860_ (X56509) 21 kDa seed protein [Theobroma cacao]

Seq. No.	229295
Seq. ID	LIB3196-029-P1-M1-C6
Method	BLASTX
NCBI GI	g3513294
BLAST score	307
E value	3.0e-28
Match length	118
% identity	50
NCBI Description	(AC005591) PkB-like [Homo sapiens]

Seq. No.	229296
Seq. ID	LIB3196-029-P1-M1-C8
Method	BLASTX
NCBI GI	g1173027
BLAST score	380
E value	1.0e-36
Match length	103
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	229297
Seq. ID	LIB3196-029-P1-M1-C9
Method	BLASTX
NCBI GI	g2266994
BLAST score	663

E value	7.0e-70
Match length	127
% identity	98
NCBI Description	(U77413) O-linked GlcNAc transferase [Homo sapiens] >gi_4505499_ref_NP_003596.1_pOGT_ O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase)

Seq. No.	229298
Seq. ID	LIB3196-029-P1-M1-D10
Method	BLASTX
NCBI GI	g71625
BLAST score	641
E value	2.0e-67
Match length	125
% identity	99
NCBI Description	actin gamma - bovine (tentative sequence)

Seq. No.	229299
Seq. ID	LIB3196-029-P1-M1-D5
Method	BLASTX
NCBI GI	g2500399
BLAST score	428
E value	2.0e-42
Match length	99
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098) ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls, embryos, Peptide, 253 aa] [Ambystoma mexicanum]

Seq. No.	229300
Seq. ID	LIB3196-029-P1-M1-D9
Method	BLASTX
NCBI GI	g266691
BLAST score	179
E value	4.0e-13
Match length	81
% identity	48
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	229301
Seq. ID	LIB3196-029-P1-M1-E1
Method	BLASTX
NCBI GI	g3901014
BLAST score	234
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	229302
Seq. ID	LIB3196-029-P1-M1-E3
Method	BLASTX
NCBI GI	g1905998
BLAST score	526

E value	8.0e-54
Match length	119
% identity	87
NCBI Description	(U90426) nuclear RNA helicase [Homo sapiens]

Seq. No.	229303
Seq. ID	LIB3196-029-P1-M1-E5
Method	BLASTX
NCBI GI	g120669
BLAST score	391
E value	5.0e-38
Match length	77
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	229304
Seq. ID	LIB3196-029-P1-M1-E6
Method	BLASTX
NCBI GI	g3688177
BLAST score	318
E value	2.0e-29
Match length	93
% identity	65
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	229305
Seq. ID	LIB3196-029-P1-M1-E8
Method	BLASTX
NCBI GI	g1304668
BLAST score	395
E value	2.0e-38
Match length	77
% identity	96
NCBI Description	(U42376) RIG-E precursor [Homo sapiens] >gi_1465747 (U56145) thymic shared antigen-1/stem cell antigen-2 [Homo sapiens] >gi_1519440 (U66711) 9804 [Homo sapiens] >gi_4454267_emb_CAA92321_ (Z68179) retinoic acid induced gene E [Homo sapiens] >gi_4505049_ref_NP_002337.1_pLY6E_ lymphocyte antigen 6 complex, locus E

Seq. No.	229306
Seq. ID	LIB3196-029-P1-M1-F1
Method	BLASTX
NCBI GI	g4107099
BLAST score	178
E value	5.0e-13
Match length	116
% identity	29
NCBI Description	(AB015141) AHP1 [Arabidopsis thaliana] >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No. 229307

Seq. ID	LIB3196-029-P1-M1-F11
Method	BLASTX
NCBI GI	g2961178
BLAST score	171
E value	3.0e-12
Match length	41
% identity	76
NCBI Description	(AF050675) GTP-binding protein [Oryza sativa]

Seq. No.	229308
Seq. ID	LIB3196-029-P1-M1-F12
Method	BLASTX
NCBI GI	g137578
BLAST score	514
E value	2.0e-52
Match length	119
% identity	87
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229309
Seq. ID	LIB3196-029-P1-M1-F5
Method	BLASTX
NCBI GI	g2558501
BLAST score	167
E value	7.0e-12
Match length	104
% identity	38
NCBI Description	(D63850) hepatoma-derived growth factor [Mus musculus]

Seq. No.	229310
Seq. ID	LIB3196-029-P1-M1-F7
Method	BLASTX
NCBI GI	g1710401
BLAST score	442
E value	4.0e-44
Match length	99
% identity	82
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	229311
Seq. ID	LIB3196-029-P1-M1-F9
Method	BLASTX
NCBI GI	g3860255
BLAST score	283
E value	2.0e-25
Match length	112
% identity	63
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229312
Seq. ID	LIB3196-029-P1-M1-G2
Method	BLASTX
NCBI GI	g137578
BLAST score	455
E value	2.0e-45
Match length	119
% identity	47
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229313
Seq. ID	LIB3196-029-P1-M1-G3
Method	BLASTX
NCBI GI	g4417309
BLAST score	168
E value	6.0e-12
Match length	108
% identity	35
NCBI Description	(AC006446) putative pol polyprotein with a reverse transcriptase domain [Arabidopsis thaliana]

Seq. No.	229314
Seq. ID	LIB3196-029-P1-M1-G4
Method	BLASTX
NCBI GI	g2921447
BLAST score	395
E value	2.0e-38
Match length	100
% identity	78
NCBI Description	(AF037260) non-receptor protein tyrosine kinase Ack [Mus musculus]

Seq. No.	229315
Seq. ID	LIB3196-029-P1-M1-G5
Method	BLASTX
NCBI GI	g1708624
BLAST score	98
E value	1.0e-08
Match length	41
% identity	78
NCBI Description	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE) >gi_606757 (L38707) diacylglycerol kinase [Homo sapiens] >gi_1589110_prf__2210300A diacylglycerol kinase 4 [Homo sapiens] >gi_4557519_ref_NP_001338.1_pDGKQ_ diacylglycerol kinase, theta (110kD)

Seq. No.	229316
Seq. ID	LIB3196-029-P1-M1-G6
Method	BLASTX
NCBI GI	g1703018
BLAST score	577

E value	7.0e-60
Match length	120
% identity	95
NCBI Description	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING >gi_984325 (U30255) phosphogluconate dehydrogenase [Homo sapiens] >gi_4505759_ref_NP_002622.1_pPGD_ phosphogluconate dehydrogenase

Seq. No.	229317
Seq. ID	LIB3196-029-P1-M1-H3
Method	BLASTX
NCBI GI	g4140326
BLAST score	240
E value	3.0e-20
Match length	52
% identity	83
NCBI Description	(AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins) [Homo sapiens]

Seq. No.	229318
Seq. ID	LIB3196-029-P1-M1-H5
Method	BLASTX
NCBI GI	g729022
BLAST score	399
E value	4.0e-39
Match length	94
% identity	84
NCBI Description	MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) >gi_346234_pir__A43358 macrophage capping protein - human >gi_187456 (M94345) macrophage capping protein [Homo sapiens] >gi_4502561_ref_NP_001738.1_pCAPG_ capping protein (actin filament), gelsolin-like

Seq. No.	229319
Seq. ID	LIB3196-029-P1-M1-H7
Method	BLASTX
NCBI GI	g3023512
BLAST score	308
E value	3.0e-28
Match length	119
% identity	53
NCBI Description	PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT PRECURSOR (ENDOPEPTIDASE CLP) >gi_2134793_pir__S68421 ATP-dependent Clp proteinase (EC 3.4.21.92) chain P homolog - human >gi_963048_emb_CAA90705_ (Z50853) CLPP [Homo sapiens]

Seq. No.	229320
Seq. ID	LIB3196-030-P1-M1-A11
Method	BLASTX
NCBI GI	g2344889
BLAST score	172
E value	2.0e-12
Match length	114
% identity	33
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	229321
Seq. ID	LIB3196-030-P1-M1-A2
Method	BLASTX
NCBI GI	g2764583
BLAST score	495
E value	3.0e-50
Match length	112
% identity	79
NCBI Description	(AJ001043) metastasis-associated GPI-anchored protein [Rattus norvegicus]

Seq. No.	229322
Seq. ID	LIB3196-030-P1-M1-A3
Method	BLASTX
NCBI GI	g72287
BLAST score	647
E value	5.0e-68
Match length	121
% identity	100
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	229323
Seq. ID	LIB3196-030-P1-M1-A5
Method	BLASTX
NCBI GI	g126156
BLAST score	298
E value	4.0e-27
Match length	101
% identity	61
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229324
Seq. ID	LIB3196-030-P1-M1-B1
Method	BLASTX
NCBI GI	g665584
BLAST score	531
E value	2.0e-54
Match length	107
% identity	99
NCBI Description	(D16561) ATP synthase gamma-subunit [Homo sapiens] >gi_665585_dbj_BAA03997_ (D16563) ATP synthase gamma-subunit [Homo sapiens]

Seq. No.	229325
Seq. ID	LIB3196-030-P1-M1-B10
Method	BLASTX
NCBI GI	g4467804
BLAST score	286
E value	7.0e-26

Match length	82
% identity	71
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No.	229326
Seq. ID	LIB3196-030-P1-M1-B11
Method	BLASTX
NCBI GI	g2132930
BLAST score	180
E value	3.0e-13
Match length	48
% identity	67
NCBI Description	probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) >gi_1420591_emb_CAA99484_ (Z75170) ORF YOR262w [Saccharomyces cerevisiae]

Seq. No.	229327
Seq. ID	LIB3196-030-P1-M1-B2
Method	BLASTX
NCBI GI	g81546
BLAST score	267
E value	8.0e-24
Match length	70
% identity	70
NCBI Description	alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No.	229328
Seq. ID	LIB3196-030-P1-M1-B4
Method	BLASTX
NCBI GI	g386849
BLAST score	621
E value	6.0e-65
Match length	126
% identity	99
NCBI Description	(L00205) keratin type II [Homo sapiens]

Seq. No.	229329
Seq. ID	LIB3196-030-P1-M1-B7
Method	BLASTX
NCBI GI	g137578
BLAST score	437
E value	2.0e-43
Match length	117
% identity	45
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229330
Seq. ID	LIB3196-030-P1-M1-B9
Method	BLASTX

NCBI GI	g2388689
BLAST score	356
E value	6.0e-34
Match length	91
% identity	79
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	229331
Seq. ID	LIB3196-030-P1-M1-C1
Method	BLASTX
NCBI GI	g125887
BLAST score	160
E value	6.0e-11
Match length	83
% identity	47
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	229332
Seq. ID	LIB3196-030-P1-M1-C10
Method	BLASTX
NCBI GI	g4539944
BLAST score	356
E value	6.0e-34
Match length	97
% identity	65
NCBI Description	(AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]

Seq. No.	229333
Seq. ID	LIB3196-030-P1-M1-C11
Method	BLASTX
NCBI GI	g113463
BLAST score	369
E value	2.0e-35
Match length	76
% identity	99
NCBI Description	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) >gi_86757_pir__S03894 ADP,ATP carrier protein T2 - human

Seq. No.	229334
Seq. ID	LIB3196-030-P1-M1-C12
Method	BLASTX
NCBI GI	g3915742
BLAST score	596
E value	4.0e-62
Match length	114
% identity	99
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229335
Seq. ID	LIB3196-030-P1-M1-C2

Method	BLASTX
NCBI GI	g2501719
BLAST score	233
E value	2.0e-19
Match length	44
% identity	100
NCBI Description	ZINC FINGER PROTEIN 177 >gi_1049301 (U37263) KRAB zinc finger protein; Method: conceptual translation supplied by author [Homo sapiens] >gi_4508009_ref_NP_003442.1_pZNF177_ zinc finger protein

Seq. No.	229336
Seq. ID	LIB3196-030-P1-M1-C4
Method	BLASTX
NCBI GI	g2842486
BLAST score	209
E value	1.0e-16
Match length	71
% identity	61
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No.	229337
Seq. ID	LIB3196-030-P1-M1-C6
Method	BLASTX
NCBI GI	g267072
BLAST score	615
E value	3.0e-64
Match length	119
% identity	97
NCBI Description	TUBULIN BETA-1 CHAIN >gi_100072_pir__S20868 tubulin beta-1 chain - garden pea >gi_20758_emb_CAA38613_ (X54844) beta-tubulin 1 [Pisum sativum]

Seq. No.	229338
Seq. ID	LIB3196-030-P1-M1-C8
Method	BLASTX
NCBI GI	g2213558
BLAST score	217
E value	1.0e-17
Match length	118
% identity	42
NCBI Description	(Z97052) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	229339
Seq. ID	LIB3196-030-P1-M1-C9
Method	BLASTX
NCBI GI	g3834321
BLAST score	554
E value	3.0e-57
Match length	117
% identity	93
NCBI Description	(AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	229340

Seq. ID	LIB3196-030-P1-M1-D10
Method	BLASTX
NCBI GI	g1399329
BLAST score	629
E value	6.0e-66
Match length	122
% identity	92
NCBI Description	(U41834) MHC class I antigen Mamu A*06 [Macaca mulatta]

Seq. No.	229341
Seq. ID	LIB3196-030-P1-M1-D11
Method	BLASTX
NCBI GI	g481821
BLAST score	358
E value	3.0e-34
Match length	113
% identity	64
NCBI Description	probable glutathione transferase (EC 2.5.1.18) (clone ERD11) - Arabidopsis thaliana >gi_497788_dbj_BAA04553_ (D17672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	229342
Seq. ID	LIB3196-030-P1-M1-D2
Method	BLASTX
NCBI GI	g167367
BLAST score	646
E value	6.0e-68
Match length	122
% identity	100
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	229343
Seq. ID	LIB3196-030-P1-M1-D3
Method	BLASTX
NCBI GI	g1706518
BLAST score	631
E value	4.0e-66
Match length	127
% identity	99
NCBI Description	DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN DRG >gi_1082424_pir__A55014 GTP-binding protein - human >gi_577779_emb_CAA56730_ (X80754) GTP-binding protein [Homo sapiens] >gi_4557537_ref_NP_001379.1_pDRG2_ developmentally regulated GTP-binding protein

Seq. No.	229344
Seq. ID	LIB3196-030-P1-M1-D4
Method	BLASTX
NCBI GI	g121116
BLAST score	646
E value	6.0e-68
Match length	123
% identity	53
NCBI Description	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi_71649_pir__FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf__1211330A

gelsolin [Homo sapiens] >gi_4504165_ref_NP_000168.1_pGSN_
gelsolin (amyloidosis, Finnish type)

Seq. No.	229345
Seq. ID	LIB3196-030-P1-M1-D5
Method	BLASTX
NCBI GI	g120672
BLAST score	552
E value	6.0e-57
Match length	114
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66016_pir__DEPZG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - parsley >gi_20549_emb_CAA42902_ (X60344) glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]

Seq. No.	229346
Seq. ID	LIB3196-030-P1-M1-D7
Method	BLASTX
NCBI GI	g4206785
BLAST score	662
E value	8.0e-70
Match length	125
% identity	98
NCBI Description	(AF107848) guanine nucleotide-binding protein [Mus musculus]

Seq. No.	229347
Seq. ID	LIB3196-030-P1-M1-E10
Method	BLASTX
NCBI GI	g88044
BLAST score	563
E value	3.0e-58
Match length	123
% identity	97
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	229348
Seq. ID	LIB3196-030-P1-M1-E5
Method	BLASTX
NCBI GI	g3152595
BLAST score	482
E value	1.0e-48
Match length	118
% identity	75
NCBI Description	(AC002986) Similar to D. melanogaster sno gene gb_U95760. EST gb_N97148 and gb_Z26221 come from this gene. [Arabidopsis thaliana]

Seq. No.	229349
Seq. ID	LIB3196-030-P1-M1-E6
Method	BLASTX
NCBI GI	g4454467
BLAST score	280

E value 5.0e-25
Match length 116
% identity 46
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 229350
Seq. ID LIB3196-030-P1-M1-E7
Method BLASTX
NCBI GI g421960
BLAST score 381
E value 7.0e-37
Match length 100
% identity 73
NCBI Description small nuclear ribonucleoprotein U2B'' - potato >gi_169589 (M72892) spliceosomal protein [Solanum tuberosum]

Seq. No. 229351
Seq. ID LIB3196-030-P1-M1-E8
Method BLASTX
NCBI GI g4539660
BLAST score 324
E value 3.0e-30
Match length 116
% identity 53
NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 229352
Seq. ID LIB3196-030-P1-M1-F2
Method BLASTX
NCBI GI g4008159
BLAST score 557
E value 2.0e-57
Match length 115
% identity 90
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]

Seq. No. 229353
Seq. ID LIB3196-030-P1-M1-F3
Method BLASTX
NCBI GI g2245069
BLAST score 435
E value 3.0e-43
Match length 117
% identity 66
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 229354
Seq. ID LIB3196-030-P1-M1-F8
Method BLASTX
NCBI GI g4204684
BLAST score 284
E value 1.0e-25
Match length 58
% identity 90
NCBI Description (AF102542) beta-1,6-N-acetylglucosaminyltransferase [Homo sapiens] >gi_4511881_gb_AAD21525.1_ (AF038650) core 2/core 4 beta-1,6-N-acetylglucosaminyltransferase; core 2/4-GnT

[Homo sapiens]

Seq. No.	229355
Seq. ID	LIB3196-030-P1-M1-F9
Method	BLASTX
NCBI GI	g4336205
BLAST score	530
E value	2.0e-54
Match length	113
% identity	84
NCBI Description	(AF077372) cytochrome b5 reductase [Zea mays]

Seq. No.	229356
Seq. ID	LIB3196-030-P1-M1-G10
Method	BLASTX
NCBI GI	g1076291
BLAST score	175
E value	1.0e-12
Match length	117
% identity	36
NCBI Description	amino acid transporter AAT1 - Arabidopsis thaliana >gi_2911069_emb_CAA17531_ (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]

Seq. No.	229357
Seq. ID	LIB3196-030-P1-M1-G12
Method	BLASTX
NCBI GI	g3122072
BLAST score	530
E value	2.0e-54
Match length	105
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]

Seq. No.	229358
Seq. ID	LIB3196-030-P1-M1-G2
Method	BLASTX
NCBI GI	g3915742
BLAST score	488
E value	2.0e-49
Match length	116
% identity	84
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229359
Seq. ID	LIB3196-030-P1-M1-G5
Method	BLASTX
NCBI GI	g136479
BLAST score	461
E value	3.0e-46
Match length	90

% identity	100
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23) >gi_88948_pir__S06590 IgE-dependent histamine-releasing factor - human >gi_37496_emb_CAA34200_ (X16064) tumor protein (AA 1 - 172) [Homo sapiens] >gi_4507669_ref_NP_003286.1_pTPT1_ tumor protein, translationally-controlled

Seq. No.	229360
Seq. ID	LIB3196-030-P1-M1-G6
Method	BLASTX
NCBI GI	g2811001
BLAST score	508
E value	1.0e-51
Match length	99
% identity	100
NCBI Description	NUCLEOLAR PROTEIN NOP56 >gi_2230878_emb_CAA72789_ (Y12065) hNop56 [Homo sapiens]

Seq. No.	229361
Seq. ID	LIB3196-030-P1-M1-G9
Method	BLASTX
NCBI GI	g117501
BLAST score	513
E value	2.0e-52
Match length	95
% identity	100
NCBI Description	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A) >gi_87015_pir__A37047 calreticulin precursor - human >gi_179882 (M84739) calreticulin [Homo sapiens] >gi_337487 (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A) precursor [Homo sapiens] >gi_1905911 (AD000092) calreticulin [Homo sapiens]

Seq. No.	229362
Seq. ID	LIB3196-030-P1-M1-H11
Method	BLASTX
NCBI GI	g2306917
BLAST score	371
E value	1.0e-35
Match length	83
% identity	89
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	229363
Seq. ID	LIB3196-030-P1-M1-H5
Method	BLASTX
NCBI GI	g2995405
BLAST score	472
E value	1.0e-47
Match length	117
% identity	74
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	229364

Seq. ID	LIB3196-030-P1-M1-H6
Method	BLASTX
NCBI GI	g1346344
BLAST score	636
E value	1.0e-66
Match length	126
% identity	100
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II - human >gi_908779 (L42583) keratin type II [Homo sapiens]

Seq. No.	229365
Seq. ID	LIB3196-030-P1-M1-H8
Method	BLASTX
NCBI GI	g284691
BLAST score	204
E value	4.0e-16
Match length	51
% identity	80
NCBI Description	transcription factor ATF-4 - mouse >gi_50050_emb_CAA43723_ (X61507) activating transcriptionn factor 4 [Mus musculus]

Seq. No.	229366
Seq. ID	LIB3196-031-P1-M1-A4
Method	BLASTX
NCBI GI	g432977
BLAST score	584
E value	1.0e-60
Match length	124
% identity	93
NCBI Description	(M75884) sterol carrier protein-2 [Homo sapiens] >gi_4506823_ref_NP_002970.1_pSCP2_ sterol carrier protein

Seq. No.	229367
Seq. ID	LIB3196-031-P1-M1-A5
Method	BLASTX
NCBI GI	g2605714
BLAST score	448
E value	1.0e-44
Match length	124
% identity	47
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	229368
Seq. ID	LIB3196-031-P1-M1-B11
Method	BLASTX
NCBI GI	g122085
BLAST score	527
E value	6.0e-54
Match length	124
% identity	85
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3

(AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	229369
Seq. ID	LIB3196-031-P1-M1-B3
Method	BLASTX
NCBI GI	g2497539
BLAST score	604
E value	5.0e-63
Match length	122
% identity	98
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	229370
Seq. ID	LIB3196-031-P1-M1-B4
Method	BLASTX
NCBI GI	g125077
BLAST score	158
E value	1.0e-10
Match length	31
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	229371
Seq. ID	LIB3196-031-P1-M1-B6
Method	BLASTX
NCBI GI	g167311
BLAST score	492
E value	7.0e-50
Match length	93
% identity	100
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	229372
Seq. ID	LIB3196-031-P1-M1-B8
Method	BLASTX

NCBI GI	g4200327
BLAST score	485
E value	4.0e-49
Match length	94
% identity	97
NCBI Description	(AL022313) thioredoxin [Homo sapiens]

Seq. No.	229373
Seq. ID	LIB3196-031-P1-M1-C1
Method	BLASTX
NCBI GI	g2652938
BLAST score	248
E value	3.0e-21
Match length	62
% identity	45
NCBI Description	(Z47554) orf [Zea mays]

Seq. No.	229374
Seq. ID	LIB3196-031-P1-M1-C10
Method	BLASTX
NCBI GI	g87333
BLAST score	383
E value	4.0e-37
Match length	115
% identity	70
NCBI Description	DNA-binding protein B - human (fragment) >gi_181486 (M24070) DNA-binding protein B [Homo sapiens]

Seq. No.	229375
Seq. ID	LIB3196-031-P1-M1-C12
Method	BLASTX
NCBI GI	g125080
BLAST score	353
E value	1.0e-33
Match length	69
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	229376
Seq. ID	LIB3196-031-P1-M1-C5
Method	BLASTX
NCBI GI	g1363944
BLAST score	669
E value	1.0e-70
Match length	133
% identity	99
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	229377
Seq. ID	LIB3196-031-P1-M1-C7
Method	BLASTX

NCBI GI g4432821
BLAST score 161
E value 3.0e-11
Match length 80
% identity 50
NCBI Description (AC006593) putative transmembrane protein [Arabidopsis thaliana]

Seq. No. 229378
Seq. ID LIB3196-031-P1-M1-D11
Method BLASTX
NCBI GI g137580
BLAST score 407
E value 6.0e-40
Match length 78
% identity 100
NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No. 229379
Seq. ID LIB3196-031-P1-M1-D12
Method BLASTX
NCBI GI g2492517
BLAST score 352
E value 1.0e-60
Match length 127
% identity 98
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6B (TAT-BINDING PROTEIN-7) (TBP-7) >gi_1395186_dbj_BAA09340_ (D50695) proteasomal ATPase (Tat-binding protein7) [Rattus norvegicus]

Seq. No. 229380
Seq. ID LIB3196-031-P1-M1-D3
Method BLASTX
NCBI GI g125077
BLAST score 154
E value 3.0e-10
Match length 30
% identity 100
NCBI Description KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No. 229381
Seq. ID LIB3196-031-P1-M1-D4
Method BLASTX
NCBI GI g4539005
BLAST score 592
E value 1.0e-61
Match length 125
% identity 86
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 229382

Seq. ID	LIB3196-031-P1-M1-D6
Method	BLASTX
NCBI GI	g3334147
BLAST score	228
E value	1.0e-35
Match length	117
% identity	60
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	229383
Seq. ID	LIB3196-031-P1-M1-D7
Method	BLASTX
NCBI GI	g3549652
BLAST score	246
E value	5.0e-21
Match length	88
% identity	66
NCBI Description	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No.	229384
Seq. ID	LIB3196-031-P1-M1-D9
Method	BLASTX
NCBI GI	g3738288
BLAST score	163
E value	3.0e-11
Match length	105
% identity	43
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	229385
Seq. ID	LIB3196-031-P1-M1-E10
Method	BLASTX
NCBI GI	g137473
BLAST score	264
E value	4.0e-23
Match length	100
% identity	61
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) (V-ATPASE 31 KD SUBUNIT) (P31) >gi_89601_pir__A31335 H+-transporting ATPase (EC 3.6.1.35) 31K chain, vacuolar - bovine >gi_163132 (J03244) H+ ATPase 31kDa subunit (EC 3.6.1.3) [Bos taurus]

Seq. No.	229386
Seq. ID	LIB3196-031-P1-M1-E12
Method	BLASTX
NCBI GI	g3319882
BLAST score	383
E value	5.0e-37
Match length	77
% identity	95
NCBI Description	(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No.	229387
Seq. ID	LIB3196-031-P1-M1-E2
Method	BLASTX
NCBI GI	g992706
BLAST score	174
E value	1.0e-12
Match length	36
% identity	86
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	229388
Seq. ID	LIB3196-031-P1-M1-E3
Method	BLASTX
NCBI GI	g28595
BLAST score	552
E value	7.0e-57
Match length	107
% identity	100
NCBI Description	(X06352) aldolase A protein [Homo sapiens]

Seq. No.	229389
Seq. ID	LIB3196-031-P1-M1-E4
Method	BLASTX
NCBI GI	g4220532
BLAST score	262
E value	7.0e-23
Match length	123
% identity	50
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	229390
Seq. ID	LIB3196-031-P1-M1-E6
Method	BLASTX
NCBI GI	g129916
BLAST score	601
E value	1.0e-62
Match length	124
% identity	95
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No.	229391
Seq. ID	LIB3196-031-P1-M1-E7
Method	BLASTX
NCBI GI	g683553
BLAST score	220
E value	5.0e-18
Match length	102
% identity	49
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	229392
Seq. ID	LIB3196-031-P1-M1-F10
Method	BLASTX

NCBI GI	g2500813
BLAST score	606
E value	3.0e-63
Match length	131
% identity	93
NCBI Description	NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) >gi_1236986 (U51432) nuclear protein Skip [Homo sapiens] >gi_3417599 (AF045184) nuclear receptor coactivator NCoA-62 [Homo sapiens]

Seq. No.	229393
Seq. ID	LIB3196-031-P1-M1-F2
Method	BLASTX
NCBI GI	g112925
BLAST score	146
E value	3.0e-09
Match length	93
% identity	39
NCBI Description	41-2 PROTEIN ANTIGEN PRECURSOR >gi_320938_pir__A45503 41-2 protein antigen precursor - Plasmodium falciparum >gi_160039 (J04656) 41-2 protein antigen [Plasmodium falciparum]

Seq. No.	229394
Seq. ID	LIB3196-031-P1-M1-F4
Method	BLASTX
NCBI GI	g167367
BLAST score	435
E value	4.0e-43
Match length	95
% identity	87
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	229395
Seq. ID	LIB3196-031-P1-M1-F6
Method	BLASTX
NCBI GI	g137578
BLAST score	610
E value	1.0e-63
Match length	129
% identity	89
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229396
Seq. ID	LIB3196-031-P1-M1-F7
Method	BLASTX
NCBI GI	g1351722
BLAST score	220
E value	6.0e-18
Match length	121
% identity	39
NCBI Description	HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I >gi_1122371_emb_CAA92386_ (Z68198) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No.	229397
Seq. ID	LIB3196-031-P1-M1-G4
Method	BLASTX
NCBI GI	g1518540
BLAST score	591
E value	2.0e-61
Match length	127
% identity	89
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	229398
Seq. ID	LIB3196-031-P1-M1-G6
Method	BLASTX
NCBI GI	g4567303
BLAST score	382
E value	6.0e-37
Match length	77
% identity	86
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	229399
Seq. ID	LIB3196-031-P1-M1-G7
Method	BLASTX
NCBI GI	g1336807
BLAST score	268
E value	1.0e-23
Match length	96
% identity	60
NCBI Description	(S81193) CEN=GTP-binding protein homolog [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum] >gi_1587482_prf__2206476A CEN gene [Antirrhinum sp.]

Seq. No.	229400
Seq. ID	LIB3196-031-P1-M1-G8
Method	BLASTX
NCBI GI	g137578
BLAST score	643
E value	1.0e-67
Match length	124
% identity	99
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229401
Seq. ID	LIB3196-031-P1-M1-H1
Method	BLASTX
NCBI GI	g4539660
BLAST score	449
E value	8.0e-45
Match length	124
% identity	66

NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	229402
Seq. ID	LIB3196-031-P1-M1-H11
Method	BLASTX
NCBI GI	g137578
BLAST score	503
E value	4.0e-51
Match length	129
% identity	78
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229403
Seq. ID	LIB3196-031-P1-M1-H5
Method	BLASTX
NCBI GI	g3386610
BLAST score	160
E value	1.0e-20
Match length	85
% identity	58
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229404
Seq. ID	LIB3196-031-P1-M1-H7
Method	BLASTX
NCBI GI	g386850
BLAST score	250
E value	9.0e-22
Match length	74
% identity	72
NCBI Description	(M19723) keratin K5 [Homo sapiens]

Seq. No.	229405
Seq. ID	LIB3196-032-P1-M1-A10
Method	BLASTX
NCBI GI	g2072972
BLAST score	483
E value	2.0e-58
Match length	122
% identity	85
NCBI Description	(U93572) putative p150 [Homo sapiens]

Seq. No.	229406
Seq. ID	LIB3196-032-P1-M1-A11
Method	BLASTX
NCBI GI	g3192969
BLAST score	570
E value	4.0e-59
Match length	109
% identity	99
NCBI Description	(AF043106) sarco/endoplasmic reticulum Ca2+-ATPase [Rattus norvegicus]

Seq. No.	229407
Seq. ID	LIB3196-032-P1-M1-A2
Method	BLASTX
NCBI GI	g126156
BLAST score	520
E value	4.0e-53
Match length	100
% identity	100
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229408
Seq. ID	LIB3196-032-P1-M1-A3
Method	BLASTX
NCBI GI	g129034
BLAST score	523
E value	2.0e-53
Match length	102
% identity	96
NCBI Description	2-OXOISOVALERATE DEHYDROGENASE BETA SUBUNIT PRECURSOR (BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPONENT BETA CHAIN (E1)) (BCKDH E1-BETA) >gi_105120_pir__A37157 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) E1-beta chain precursor - human >gi_179362 (M55575) branched chain alpha-keto acid dehydrogenase E1-beta subunit [Homo sapiens] >gi_219493_dbj_BAA14389_ (D90391) E-1-beta subunit [Homo sapiens] >gi_1480477 (U50708) branched chain alpha-ketoacid dehydrogenase E1 beta subunit [Homo sapiens] >gi_4557353_ref_NP_000047.1_pBCKDHB_ branched chain keto acid dehydrogenase E1, beta polypeptide precursor

Seq. No.	229409
Seq. ID	LIB3196-032-P1-M1-A5
Method	BLASTX
NCBI GI	g399365
BLAST score	459
E value	3.0e-46
Match length	89
% identity	100
NCBI Description	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (CLASS 3) >gi_178402 (M74542) aldehyde dehydrogenase type III [Homo sapiens] >gi_4502035_ref_NP_000682.1_pALDH3_ aldehyde dehydrogenase

Seq. No.	229410
Seq. ID	LIB3196-032-P1-M1-A9
Method	BLASTX
NCBI GI	g683553
BLAST score	203
E value	6.0e-16
Match length	98

% identity	48
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
Seq. No.	229411
Seq. ID	LIB3196-032-P1-M1-B11
Method	BLASTX
NCBI GI	g3914977
BLAST score	265
E value	3.0e-23
Match length	52
% identity	96
NCBI Description	SERINE/THREONINE-PROTEIN KINASE SGK (SERUM/GLUCOCORTICOID-REGULATED KINASE) >gi_1834511_emb_CAA71138_ (Y10032) serine/threonine protein kinase [Homo sapiens] >gi_2463201_emb_CAA04146_ (AJ000512) serine/threonine protein kinase [Homo sapiens]
Seq. No.	229412
Seq. ID	LIB3196-032-P1-M1-B3
Method	BLASTX
NCBI GI	g4406801
BLAST score	192
E value	1.0e-14
Match length	57
% identity	63
NCBI Description	(AC006304) unknown protein [Arabidopsis thaliana]
Seq. No.	229413
Seq. ID	LIB3196-032-P1-M1-B4
Method	BLASTX
NCBI GI	g266691
BLAST score	168
E value	4.0e-12
Match length	68
% identity	53
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]
Seq. No.	229414
Seq. ID	LIB3196-032-P1-M1-C2
Method	BLASTX
NCBI GI	g1703375
BLAST score	490
E value	1.0e-49
Match length	96
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]
Seq. No.	229415
Seq. ID	LIB3196-032-P1-M1-C4
Method	BLASTX
NCBI GI	g685073
BLAST score	174
E value	8.0e-13
Match length	39

% identity	11
NCBI Description	SPRC=small proline-rich protein [human, odontogenic keratocysts, Peptide Partial, 161 aa]

Seq. No.	229416
Seq. ID	LIB3196-032-P1-M1-D10
Method	BLASTX
NCBI GI	g730922
BLAST score	573
E value	2.0e-59
Match length	113
% identity	97
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (TCP20) (HTR3) >gi_627402_pir__S48087 chaperonin TCP20 - human >gi_517065 (L27706) chaperonin-like protein [Homo sapiens] >gi_4502643_ref_NP_001753.1_pCCT6_ chaperonin containing T-complex subunit

Seq. No.	229417
Seq. ID	LIB3196-032-P1-M1-D12
Method	BLASTX
NCBI GI	g730922
BLAST score	321
E value	3.0e-49
Match length	130
% identity	81
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (TCP20) (HTR3) >gi_627402_pir__S48087 chaperonin TCP20 - human >gi_517065 (L27706) chaperonin-like protein [Homo sapiens] >gi_4502643_ref_NP_001753.1_pCCT6_ chaperonin containing T-complex subunit

Seq. No.	229418
Seq. ID	LIB3196-032-P1-M1-D6
Method	BLASTX
NCBI GI	g4185819
BLAST score	192
E value	1.0e-14
Match length	47
% identity	68
NCBI Description	(AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No.	229419
Seq. ID	LIB3196-032-P1-M1-D7
Method	BLASTX
NCBI GI	g4220474
BLAST score	451
E value	4.0e-45
Match length	102
% identity	90
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	229420
Seq. ID	LIB3196-032-P1-M1-D8
Method	BLASTX

NCBI GI	g1336807
BLAST score	293
E value	1.0e-26
Match length	106
% identity	58
NCBI Description	(S81193) CEN=GTP-binding protein homolog [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum] >gi_1587482_prf__2206476A CEN gene [Antirrhinum sp.]

Seq. No.	229421
Seq. ID	LIB3196-032-P1-M1-D9
Method	BLASTX
NCBI GI	g2137308
BLAST score	272
E value	9.0e-45
Match length	99
% identity	95
NCBI Description	G protein beta subuit like - mouse >gi_475012_dbj_BAA06185_ (D29802) G protein beta subuit like [Mus musculus]

Seq. No.	229422
Seq. ID	LIB3196-032-P1-M1-E1
Method	BLASTX
NCBI GI	g3062801
BLAST score	347
E value	4.0e-33
Match length	93
% identity	68
NCBI Description	(AB012873) arginine decarboxylase [Nicotiana sylvestris]

Seq. No.	229423
Seq. ID	LIB3196-032-P1-M1-E2
Method	BLASTX
NCBI GI	g1263291
BLAST score	412
E value	1.0e-40
Match length	85
% identity	95
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	229424
Seq. ID	LIB3196-032-P1-M1-E5
Method	BLASTX
NCBI GI	g1256259
BLAST score	427
E value	3.0e-42
Match length	96
% identity	83
NCBI Description	(U50900) voltage-dependent anion channel protein [Spinacia oleracea]

Seq. No.	229425
Seq. ID	LIB3196-032-P1-M1-E7
Method	BLASTX
NCBI GI	g2662341
BLAST score	489
E value	1.0e-49

Match length	93
% identity	100
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	229426
Seq. ID	LIB3196-032-P1-M1-E9
Method	BLASTX
NCBI GI	g2833280
BLAST score	542
E value	8.0e-56
Match length	110
% identity	94
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (COMPLEX I-39KD) (CI-39KD)

Seq. No.	229427
Seq. ID	LIB3196-032-P1-M1-F1
Method	BLASTX
NCBI GI	g119354
BLAST score	215
E value	9.0e-18
Match length	49
% identity	90
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	229428
Seq. ID	LIB3196-032-P1-M1-F10
Method	BLASTX
NCBI GI	g2879811
BLAST score	481
E value	2.0e-48
Match length	94
% identity	95
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	229429
Seq. ID	LIB3196-032-P1-M1-F2
Method	BLASTX
NCBI GI	g291888
BLAST score	283
E value	1.0e-39
Match length	84
% identity	88
NCBI Description	(L16510) cathepsin B [Homo sapiens] >gi_4503139_ref_NP_001899.1_pCTSB_ cathepsin B

Seq. No.	229430
Seq. ID	LIB3196-032-P1-M1-F6
Method	BLASTX
NCBI GI	g106323

BLAST score	477
E value	4.0e-48
Match length	129
% identity	65
NCBI Description	hypothetical protein (L1H 5' region) - human

Seq. No.	229431
Seq. ID	LIB3196-032-P1-M1-F8
Method	BLASTX
NCBI GI	g3915742
BLAST score	372
E value	4.0e-53
Match length	119
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229432
Seq. ID	LIB3196-032-P1-M1-G11
Method	BLASTX
NCBI GI	g137578
BLAST score	455
E value	1.0e-45
Match length	110
% identity	85
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229433
Seq. ID	LIB3196-032-P1-M1-G12
Method	BLASTX
NCBI GI	g4432846
BLAST score	454
E value	2.0e-45
Match length	124
% identity	68
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	229434
Seq. ID	LIB3196-032-P1-M1-G3
Method	BLASTX
NCBI GI	g3212869
BLAST score	201
E value	3.0e-16
Match length	41
% identity	83
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	229435
Seq. ID	LIB3196-032-P1-M1-G4
Method	BLASTX

NCBI GI	g2623304
BLAST score	148
E value	8.0e-10
Match length	66
% identity	48
NCBI Description	(AC002409) similar to Medicago nodulin N21 [Arabidopsis thaliana]

Seq. No.	229436
Seq. ID	LIB3196-032-P1-M1-G7
Method	BLASTX
NCBI GI	g1171035
BLAST score	171
E value	2.0e-12
Match length	43
% identity	72
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504 >gi_1086021_pir__S48038 metallothionein-like protein - kiwi fruit >gi_450245 (L27813) metallothionein-like protein [Actinidia deliciosa]

Seq. No.	229437
Seq. ID	LIB3196-032-P1-M1-G9
Method	BLASTX
NCBI GI	g662366
BLAST score	172
E value	1.0e-12
Match length	60
% identity	55
NCBI Description	(L39786) conglutin gamma [Lupinus angustifolius] >gi_666056_emb_CAA46552_ (X65601) conglutin gamma [Lupinus angustifolius]

Seq. No.	229438
Seq. ID	LIB3196-032-P1-M1-H1
Method	BLASTX
NCBI GI	g2149640
BLAST score	648
E value	4.0e-68
Match length	132
% identity	92
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	229439
Seq. ID	LIB3196-032-P1-M1-H2
Method	BLASTX
NCBI GI	g1304227
BLAST score	544
E value	5.0e-56
Match length	116
% identity	84
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	229440
Seq. ID	LIB3196-032-P1-M1-H6

Method	BLASTX
NCBI GI	g3023847
BLAST score	402
E value	2.0e-39
Match length	90
% identity	45
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	229441
Seq. ID	LIB3196-033-P1-M1-A11
Method	BLASTX
NCBI GI	g3334115
BLAST score	381
E value	7.0e-37
Match length	78
% identity	95
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	229442
Seq. ID	LIB3196-033-P1-M1-A12
Method	BLASTX
NCBI GI	g2980784
BLAST score	224
E value	1.0e-18
Match length	91
% identity	53
NCBI Description	(AL022198) puative protein [Arabidopsis thaliana]

Seq. No.	229443
Seq. ID	LIB3196-033-P1-M1-A3
Method	BLASTX
NCBI GI	g126156
BLAST score	488
E value	2.0e-49
Match length	97
% identity	100
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229444
Seq. ID	LIB3196-033-P1-M1-A4
Method	BLASTX
NCBI GI	g126156
BLAST score	488
E value	2.0e-49
Match length	97
% identity	100
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)

	>gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]
Seq. No.	229445
Seq. ID	LIB3196-033-P1-M1-A5
Method	BLASTX
NCBI GI	g106322
BLAST score	205
E value	2.0e-16
Match length	104
% identity	45
NCBI Description	hypothetical protein (L1H 3' region) - human
Seq. No.	229446
Seq. ID	LIB3196-033-P1-M1-A7
Method	BLASTX
NCBI GI	g4539335
BLAST score	430
E value	1.0e-42
Match length	116
% identity	69
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	229447
Seq. ID	LIB3196-033-P1-M1-B10
Method	BLASTX
NCBI GI	g3868758
BLAST score	347
E value	7.0e-33
Match length	87
% identity	75
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.	229448
Seq. ID	LIB3196-033-P1-M1-B2
Method	BLASTX
NCBI GI	g4097712
BLAST score	719
E value	2.0e-76
Match length	125
% identity	99
NCBI Description	(U67322) HBV associated factor [Homo sapiens]
Seq. No.	229449
Seq. ID	LIB3196-033-P1-M1-B3
Method	BLASTX
NCBI GI	g1469930
BLAST score	286
E value	1.0e-25
Match length	92
% identity	68
NCBI Description	(U48777) fiber-specific acyl carrier protein [Gossypium hirsutum]

Seq. No.	229450
Seq. ID	LIB3196-033-P1-M1-B6
Method	BLASTX
NCBI GI	g137580
BLAST score	561
E value	5.0e-58
Match length	120
% identity	91
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No.	229451
Seq. ID	LIB3196-033-P1-M1-B8
Method	BLASTX
NCBI GI	g2736288
BLAST score	574
E value	2.0e-59
Match length	118
% identity	87
NCBI Description	(AF031080) isopentenyl diphosphate isomerase II [Camptotheca acuminata]

Seq. No.	229452
Seq. ID	LIB3196-033-P1-M1-B9
Method	BLASTX
NCBI GI	g3914449
BLAST score	606
E value	3.0e-63
Match length	118
% identity	100
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No.	229453
Seq. ID	LIB3196-033-P1-M1-C1
Method	BLASTX
NCBI GI	g4566614
BLAST score	328
E value	1.0e-30
Match length	89
% identity	71
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	229454
Seq. ID	LIB3196-033-P1-M1-C10
Method	BLASTX
NCBI GI	g3953471
BLAST score	384
E value	3.0e-37
Match length	109
% identity	61
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	229455
Seq. ID	LIB3196-033-P1-M1-C11
Method	BLASTX
NCBI GI	g1709990
BLAST score	239
E value	3.0e-20
Match length	50
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L35A

Seq. No.	229456
Seq. ID	LIB3196-033-P1-M1-C3
Method	BLASTX
NCBI GI	g130582
BLAST score	186
E value	5.0e-14
Match length	107
% identity	36
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi_100342_pir__S04273 hypothetical protein - common tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana tabacum]

Seq. No.	229457
Seq. ID	LIB3196-033-P1-M1-C4
Method	BLASTX
NCBI GI	g3769300
BLAST score	203
E value	5.0e-16
Match length	58
% identity	66
NCBI Description	(AB018552) AtRER1C [Arabidopsis thaliana]

Seq. No.	229458
Seq. ID	LIB3196-033-P1-M1-C5
Method	BLASTX
NCBI GI	g1352440
BLAST score	262
E value	6.0e-23
Match length	56
% identity	79
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT) (EIF-4F P26 SUBUNIT) >gi_1002915 (U34597) p26 [Oryza sativa]

Seq. No.	229459
Seq. ID	LIB3196-033-P1-M1-C6
Method	BLASTX
NCBI GI	g137580
BLAST score	554
E value	4.0e-57
Match length	107
% identity	100
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone

C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No.	229460
Seq. ID	LIB3196-033-P1-M1-C9
Method	BLASTX
NCBI GI	g2119228
BLAST score	188
E value	3.0e-14
Match length	67
% identity	60
NCBI Description	keratin K4a - human (fragment) >gi_313159_emb_CAA47914_ (X67683) keratin K4a [Homo sapiens]

Seq. No.	229461
Seq. ID	LIB3196-033-P1-M1-D10
Method	BLASTX
NCBI GI	g122106
BLAST score	370
E value	1.0e-35
Match length	75
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	229462
Seq. ID	LIB3196-033-P1-M1-D11
Method	BLASTX
NCBI GI	g1843527
BLAST score	319
E value	1.0e-29
Match length	91
% identity	74
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	229463
Seq. ID	LIB3196-033-P1-M1-D2
Method	BLASTX
NCBI GI	g178685
BLAST score	265
E value	3.0e-23
Match length	82
% identity	65
NCBI Description	(J03569) lymphocyte activation antigen [Homo sapiens]

	>gi_4505141_ref_NP_002385.1_pMDU1_ antigen identified by monoclonal antibodies 4F2, TRA1.10, TROP4, and T43
Seq. No.	229464
Seq. ID	LIB3196-033-P1-M1-D4
Method	BLASTX
NCBI GI	g88044
BLAST score	589
E value	3.0e-61
Match length	125
% identity	94
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]
Seq. No.	229465
Seq. ID	LIB3196-033-P1-M1-D5
Method	BLASTX
NCBI GI	g3914191
BLAST score	335
E value	2.0e-31
Match length	115
% identity	58
NCBI Description	UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT) >gi_1931579 (U76557) O-GlcNAc transferase, p110 subunit [Rattus norvegicus]
Seq. No.	229466
Seq. ID	LIB3196-033-P1-M1-D6
Method	BLASTX
NCBI GI	g4325338
BLAST score	558
E value	1.0e-57
Match length	119
% identity	88
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]
Seq. No.	229467
Seq. ID	LIB3196-033-P1-M1-E11
Method	BLASTX
NCBI GI	g3702339
BLAST score	353
E value	1.0e-33
Match length	109
% identity	60
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	229468
Seq. ID	LIB3196-033-P1-M1-E3
Method	BLASTX
NCBI GI	g3510297
BLAST score	171
E value	3.0e-12
Match length	31
% identity	97
NCBI Description	(AB006746) hMmTRA1b [Homo sapiens] >gi_4092081 (AF098642)

phospholipid scramblase; plasma membrane phospholipid scramblase [Homo sapiens]

Seq. No.	229469
Seq. ID	LIB3196-033-P1-M1-E4
Method	BLASTX
NCBI GI	g225581
BLAST score	370
E value	1.0e-35
Match length	88
% identity	86
NCBI Description	storage protein C94 [Saguinus oedipus]

Seq. No.	229470
Seq. ID	LIB3196-033-P1-M1-F1
Method	BLASTX
NCBI GI	g2739008
BLAST score	389
E value	7.0e-38
Match length	110
% identity	71
NCBI Description	(AF022463) CYP78A3p [Glycine max]

Seq. No.	229471
Seq. ID	LIB3196-033-P1-M1-F11
Method	BLASTX
NCBI GI	g1049086
BLAST score	330
E value	7.0e-31
Match length	62
% identity	100
NCBI Description	(U30829) SRp55-3 [Homo sapiens]

Seq. No.	229472
Seq. ID	LIB3196-033-P1-M1-F6
Method	BLASTX
NCBI GI	g3128225
BLAST score	220
E value	5.0e-18
Match length	66
% identity	68
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	229473
Seq. ID	LIB3196-033-P1-M1-F8
Method	BLASTX
NCBI GI	g120676
BLAST score	351
E value	2.0e-41
Match length	113
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82165_pir__C24430 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) C, cytosolic - common tobacco (fragment) >gi_170241 (M14419) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	229474
Seq. ID	LIB3196-033-P1-M1-F9
Method	BLASTX
NCBI GI	g4097579
BLAST score	290
E value	2.0e-26
Match length	63
% identity	87
NCBI Description	(U64922) NTGP1 [Nicotiana tabacum]

Seq. No.	229475
Seq. ID	LIB3196-033-P1-M1-G1
Method	BLASTX
NCBI GI	g4335731
BLAST score	205
E value	3.0e-16
Match length	90
% identity	41
NCBI Description	(AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No.	229476
Seq. ID	LIB3196-033-P1-M1-G11
Method	BLASTX
NCBI GI	g4263787
BLAST score	318
E value	2.0e-29
Match length	112
% identity	57
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	229477
Seq. ID	LIB3196-033-P1-M1-G12
Method	BLASTX
NCBI GI	g4263787
BLAST score	218
E value	9.0e-18
Match length	109
% identity	48
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	229478
Seq. ID	LIB3196-033-P1-M1-G3
Method	BLASTX
NCBI GI	g2961300
BLAST score	486
E value	3.0e-49
Match length	100
% identity	92
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	229479
Seq. ID	LIB3196-033-P1-M1-G8
Method	BLASTX
NCBI GI	g4006829
BLAST score	374
E value	2.0e-36

Match length	84
% identity	86
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	229480
Seq. ID	LIB3196-033-P1-M1-G9
Method	BLASTX
NCBI GI	g1710401
BLAST score	167
E value	3.0e-12
Match length	56
% identity	55
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	229481
Seq. ID	LIB3196-033-P1-M1-H10
Method	BLASTX
NCBI GI	g4240315
BLAST score	178
E value	3.0e-16
Match length	101
% identity	53
NCBI Description	(AB020720) KIAA0913 protein [Homo sapiens]

Seq. No.	229482
Seq. ID	LIB3196-033-P1-M1-H11
Method	BLASTX
NCBI GI	g81546
BLAST score	535
E value	6.0e-55
Match length	106
% identity	99
NCBI Description	alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No.	229483
Seq. ID	LIB3196-033-P1-M1-H12
Method	BLASTX
NCBI GI	g1169475
BLAST score	332
E value	4.0e-31
Match length	63
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_556301 (M22432) elongation factor Tu [Mus musculus]

Seq. No.	229484
Seq. ID	LIB3196-033-P1-M1-H3
Method	BLASTX
NCBI GI	g4455179
BLAST score	239
E value	3.0e-20
Match length	112

% identity	47
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]
Seq. No.	229485
Seq. ID	LIB3196-033-P1-M1-H6
Method	BLASTX
NCBI GI	g2498434
BLAST score	511
E value	5.0e-52
Match length	110
% identity	14
NCBI Description	HIGH DENSITY LIPOPROTEIN BINDING PROTEIN (HDL-BINDING PROTEIN) >gi_345882_pir__A44125 high density lipoprotein-binding protein, 110K - human >gi_183892 (M64098) high density lipoprotein binding protein [Homo sapiens]
Seq. No.	229486
Seq. ID	LIB3196-033-P1-M1-H9
Method	BLASTX
NCBI GI	g1346766
BLAST score	195
E value	4.0e-15
Match length	108
% identity	38
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi_1362741_pir__S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 - human >gi_1037164_dbj_BAA07237_ (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi_3702282 (AC005789) PP31_HUMAN [Homo sapiens] >gi_4506233_ref_NP_002803.1_pPSMD8_ proteasome (prosome, macropain) 26S subunit, non-ATPase,
Seq. No.	229487
Seq. ID	LIB3196-034-P1-M1-A1
Method	BLASTX
NCBI GI	g137578
BLAST score	411
E value	2.0e-40
Match length	100
% identity	45
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	229488
Seq. ID	LIB3196-034-P1-M1-A11
Method	BLASTX
NCBI GI	g4467804
BLAST score	600
E value	2.0e-62
Match length	122
% identity	95
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3

PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No.	229489
Seq. ID	LIB3196-034-P1-M1-A2
Method	BLASTX
NCBI GI	g4415908
BLAST score	391
E value	5.0e-38
Match length	111
% identity	63
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	229490
Seq. ID	LIB3196-034-P1-M1-A6
Method	BLASTX
NCBI GI	g125077
BLAST score	142
E value	4.0e-09
Match length	90
% identity	43
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	229491
Seq. ID	LIB3196-034-P1-M1-A7
Method	BLASTX
NCBI GI	g118458
BLAST score	408
E value	5.0e-40
Match length	119
% identity	73
NCBI Description	DESMOPLAKIN I AND II (DPI AND DPII) >gi_181608 (J05211) desmoplakin [Homo sapiens]

Seq. No.	229492
Seq. ID	LIB3196-034-P1-M1-A8
Method	BLASTX
NCBI GI	g730645
BLAST score	400
E value	4.0e-39
Match length	91
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	229493
Seq. ID	LIB3196-034-P1-M1-A9
Method	BLASTX

NCBI GI g3811383
BLAST score 169
E value 5.0e-12
Match length 115
% identity 34
NCBI Description (AF100956) Sacm21 [Mus musculus]

Seq. No. 229494
Seq. ID LIB3196-034-P1-M1-B11
Method BLASTX
NCBI GI g3549657
BLAST score 213
E value 3.0e-17
Match length 89
% identity 46
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 229495
Seq. ID LIB3196-034-P1-M1-B2
Method BLASTX
NCBI GI g4490728
BLAST score 286
E value 1.0e-25
Match length 75
% identity 71
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 229496
Seq. ID LIB3196-034-P1-M1-B4
Method BLASTX
NCBI GI g1352450
BLAST score 561
E value 6.0e-58
Match length 112
% identity 100
NCBI Description INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA) (HEMATOPOIETIN-1) >gi_644806 (U19844) interleukin-1 alpha [Macaca mulatta]

Seq. No. 229497
Seq. ID LIB3196-034-P1-M1-B5
Method BLASTX
NCBI GI g1352450
BLAST score 561
E value 6.0e-58
Match length 112
% identity 100
NCBI Description INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA) (HEMATOPOIETIN-1) >gi_644806 (U19844) interleukin-1 alpha [Macaca mulatta]

Seq. No. 229498
Seq. ID LIB3196-034-P1-M1-B6
Method BLASTX
NCBI GI g4240175
BLAST score 328
E value 1.0e-30

Match length	121
% identity	43
NCBI Description	(AB020650) KIAA0843 protein [Homo sapiens]

Seq. No.	229499
Seq. ID	LIB3196-034-P1-M1-B7
Method	BLASTX
NCBI GI	g231723
BLAST score	381
E value	8.0e-37
Match length	73
% identity	100
NCBI Description	CD9 ANTIGEN (27 KD DIPHTHERIA TOXIN RECEPTOR-ASSOCIATED PROTEIN) (DRAP27) >gi_104994_pir__A42929 CD9 antigen - green monkey >gi_218566_dbj_BAA01569_ (D10726) diphtheria toxin receptor associated protein [Chlorocebus aethiops]

Seq. No.	229500
Seq. ID	LIB3196-034-P1-M1-B8
Method	BLASTX
NCBI GI	g137578
BLAST score	437
E value	2.0e-43
Match length	114
% identity	76
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha-globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229501
Seq. ID	LIB3196-034-P1-M1-B9
Method	BLASTX
NCBI GI	g167367
BLAST score	274
E value	7.0e-36
Match length	105
% identity	79
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	229502
Seq. ID	LIB3196-034-P1-M1-C1
Method	BLASTX
NCBI GI	g225580
BLAST score	521
E value	3.0e-53
Match length	119
% identity	87
NCBI Description	storage protein C72 [Saguinus oedipus]

Seq. No.	229503
Seq. ID	LIB3196-034-P1-M1-C12
Method	BLASTX
NCBI GI	g3702293
BLAST score	519

E value	4.0e-53
Match length	104
% identity	99
NCBI Description	(AC005784) RFX2_HUMAN, [AA 620-723] [Homo sapiens]

Seq. No.	229504
Seq. ID	LIB3196-034-P1-M1-C4
Method	BLASTX
NCBI GI	g441457
BLAST score	481
E value	1.0e-48
Match length	90
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	229505
Seq. ID	LIB3196-034-P1-M1-C5
Method	BLASTX
NCBI GI	g441457
BLAST score	481
E value	1.0e-48
Match length	90
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	229506
Seq. ID	LIB3196-034-P1-M1-C6
Method	BLASTX
NCBI GI	g2431769
BLAST score	234
E value	1.0e-19
Match length	57
% identity	81
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	229507
Seq. ID	LIB3196-034-P1-M1-D11
Method	BLASTX
NCBI GI	g2160158
BLAST score	153
E value	3.0e-10
Match length	35
% identity	83
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	229508
Seq. ID	LIB3196-034-P1-M1-D3
Method	BLASTX
NCBI GI	g4220541
BLAST score	261
E value	8.0e-23
Match length	112
% identity	55

NCBI Description	(AL035356) Rab geranylgeranyl transferase like protein [Arabidopsis thaliana]
Seq. No.	229509
Seq. ID	LIB3196-034-P1-M1-D4
Method	BLASTX
NCBI GI	g3334115
BLAST score	288
E value	6.0e-26
Match length	117
% identity	59
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]
Seq. No.	229510
Seq. ID	LIB3196-034-P1-M1-D8
Method	BLASTX
NCBI GI	g2687726
BLAST score	314
E value	5.0e-29
Match length	101
% identity	57
NCBI Description	(AJ003246) 2'-hydroxydihydrodaidzein reductase [Glycine max]
Seq. No.	229511
Seq. ID	LIB3196-034-P1-M1-D9
Method	BLASTX
NCBI GI	g126156
BLAST score	395
E value	2.0e-38
Match length	74
% identity	100
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]
Seq. No.	229512
Seq. ID	LIB3196-034-P1-M1-E10
Method	BLASTX
NCBI GI	g1346772
BLAST score	527
E value	6.0e-54
Match length	106
% identity	95
NCBI Description	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM (PTDINS TRANSFER PROTEIN BETA) (PTDINSTP) (PI-TP-BETA) >gi_1060905_dbj_BAA06277_ (D30037) phosphatidylinositol transfer protein [Homo sapiens]
Seq. No.	229513
Seq. ID	LIB3196-034-P1-M1-E11

Method	BLASTX
NCBI GI	g2833242
BLAST score	240
E value	3.0e-20
Match length	122
% identity	49
NCBI Description	G PROTEIN PATHWAY SUPPRESSOR 2 (GPS2 PROTEIN)

Seq. No.	229514
Seq. ID	LIB3196-034-P1-M1-E2
Method	BLASTX
NCBI GI	g1346772
BLAST score	392
E value	5.0e-38
Match length	106
% identity	74
NCBI Description	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM (PTDINS TRANSFER PROTEIN BETA) (PTDINSTP) (PI-TP-BETA) >gi_1060905_dbj_BAA06277_ (D30037) phosphatidylinositol transfer protein [Homo sapiens]

Seq. No.	229515
Seq. ID	LIB3196-034-P1-M1-E4
Method	BLASTX
NCBI GI	g126156
BLAST score	410
E value	3.0e-40
Match length	117
% identity	70
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229516
Seq. ID	LIB3196-034-P1-M1-E5
Method	BLASTX
NCBI GI	g126156
BLAST score	148
E value	8.0e-10
Match length	53
% identity	60
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229517
Seq. ID	LIB3196-034-P1-M1-E7
Method	BLASTX
NCBI GI	g1420936
BLAST score	554
E value	3.0e-57

Match length	117
% identity	85
NCBI Description	(U61396) Vigna unguiculata aspartic proteinase mRNA, complete cds. [Vigna unguiculata]

Seq. No.	229518
Seq. ID	LIB3196-034-P1-M1-F1
Method	BLASTX
NCBI GI	g136060
BLAST score	545
E value	2.0e-62
Match length	123
% identity	97
NCBI Description	TRIOSEPHOSPHATE ISOMERASE (TIM) >gi_68420_pir__ISCZT1 triose-phosphate isomerase (EC 5.3.1.1) 1 - chimpanzee >gi_2144541_pir__ISHUT triose-phosphate isomerase (EC 5.3.1.1) - human >gi_37247_emb_CAA49379_ (X69723) triosephosphate isomerase [Homo sapiens] >gi_176960 (M57946) triose-phosphate isomerase [Pan troglodytes] >gi_339841 (M10036) triosephosphate isomerase (EC 5.3.1.1) [Homo sapiens] >gi_1200507 (U47924) triosephosphate isomerase [Homo sapiens] >gi_4507645_ref_NP_000356.1_pTPI1_ triosephosphate isomerase

Seq. No.	229519
Seq. ID	LIB3196-034-P1-M1-F11
Method	BLASTX
NCBI GI	g2398807
BLAST score	222
E value	2.0e-18
Match length	69
% identity	62
NCBI Description	(Z99091) succinate dehydrogenase [Schizosaccharomyces pombe]

Seq. No.	229520
Seq. ID	LIB3196-034-P1-M1-F2
Method	BLASTX
NCBI GI	g136117
BLAST score	433
E value	6.0e-43
Match length	76
% identity	100
NCBI Description	ORPHAN RECEPTOR TR2 >gi_87334_pir__A31521 DNA-binding protein TR2 - human >gi_338486 (M21985) steroid receptor TR2 [Homo sapiens]

Seq. No.	229521
Seq. ID	LIB3196-034-P1-M1-F4
Method	BLASTX
NCBI GI	g136091
BLAST score	232
E value	2.0e-19
Match length	96
% identity	56
NCBI Description	TROPOMYOSIN BETA CHAIN, SKELETAL MUSCLE >gi_71600_pir__TMRBB tropomyosin beta chain, skeletal

NCBI GI	g1619300
BLAST score	315
E value	3.0e-29
Match length	79
% identity	73
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	230002
Seq. ID	LIB3196-047-P1-M1-C2
Method	BLASTX
NCBI GI	g2605714
BLAST score	238
E value	2.0e-20
Match length	60
% identity	82
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	230003
Seq. ID	LIB3196-047-P1-M1-C4
Method	BLASTX
NCBI GI	g226407
BLAST score	218
E value	5.0e-18
Match length	89
% identity	48
NCBI Description	retrotransposon del1-46 [Lilium henryi]

Seq. No.	230004
Seq. ID	LIB3196-047-P1-M1-C7
Method	BLASTX
NCBI GI	g1363944
BLAST score	441
E value	6.0e-44
Match length	115
% identity	80
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230005
Seq. ID	LIB3196-047-P1-M1-D3
Method	BLASTX
NCBI GI	g4056432
BLAST score	187
E value	2.0e-14
Match length	54
% identity	74
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	230006
Seq. ID	LIB3196-047-P1-M1-D5
Method	BLASTX
NCBI GI	g1363944

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BLAST score	668
E value	2.0e-70
Match length	133
% identity	100
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230007
Seq. ID	LIB3196-047-P1-M1-D8
Method	BLASTX
NCBI GI	g2270990
BLAST score	203
E value	6.0e-16
Match length	123
% identity	41
NCBI Description	(AF004807) dehydrin [Glycine max]

Seq. No.	230008
Seq. ID	LIB3196-047-P1-M1-D9
Method	BLASTX
NCBI GI	g4056432
BLAST score	175
E value	3.0e-13
Match length	60
% identity	60
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	230009
Seq. ID	LIB3196-047-P1-M1-E2
Method	BLASTX
NCBI GI	g3273828
BLAST score	220
E value	5.0e-18
Match length	95
% identity	55
NCBI Description	(AF068686) nodule-enhanced malate dehydrogenase [Glycine max]

Seq. No.	230010
Seq. ID	LIB3196-047-P1-M1-F1
Method	BLASTX
NCBI GI	g730932
BLAST score	511
E value	5.0e-52
Match length	132
% identity	78
NCBI Description	PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (TGASE E3) (TRANSGLUTAMINASE 3) >gi_307504 (L10386) transglutaminase E3 [Homo sapiens] >gi_4507477_ref_NP_003236.1_pTGM3_ transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)

Seq. No.	230011

Seq. ID	LIB3196-047-P1-M1-F12
Method	BLASTX
NCBI GI	g481131
BLAST score	395
E value	1.0e-38
Match length	93
% identity	80
NCBI Description	sucrose transport protein SUC2 - Arabidopsis thaliana >gi_407092_emb_CAA53150_ (X75382) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No.	230012
Seq. ID	LIB3196-047-P1-M1-F5
Method	BLASTX
NCBI GI	g2813965
BLAST score	675
E value	3.0e-71
Match length	135
% identity	96
NCBI Description	(Z97053) adenosine deaminase (ADA) [Homo sapiens]

Seq. No.	230013
Seq. ID	LIB3196-047-P1-M1-F9
Method	BLASTX
NCBI GI	g3123050
BLAST score	510
E value	8.0e-52
Match length	119
% identity	77
NCBI Description	HYPOTHETICAL PROTEIN KIAA0064 (HA1355) >gi_498154_dbj_BAA06542_ (D31764) KIAA0064 [Homo sapiens]

Seq. No.	230014
Seq. ID	LIB3196-047-P1-M1-G1
Method	BLASTX
NCBI GI	g294668
BLAST score	550
E value	1.0e-56
Match length	113
% identity	93
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	230015
Seq. ID	LIB3196-047-P1-M1-G10
Method	BLASTX
NCBI GI	g4406763
BLAST score	147
E value	2.0e-09
Match length	99
% identity	39
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	230016
Seq. ID	LIB3196-047-P1-M1-G4
Method	BLASTX
NCBI GI	g3935151
BLAST score	525

E value	1.0e-53
Match length	126
% identity	73
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	230017
Seq. ID	LIB3196-047-P1-M1-G5
Method	BLASTX
NCBI GI	g2492901
BLAST score	504
E value	3.0e-51
Match length	100
% identity	55
NCBI Description	THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9) >gi_703118 (L40407) thyroid receptor interactor [Homo sapiens] >gi_4505385_ref_NP_002494.1_pNFKBIB_ nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta

Seq. No.	230018
Seq. ID	LIB3196-047-P1-M1-G6
Method	BLASTX
NCBI GI	g1778294
BLAST score	294
E value	1.0e-26
Match length	95
% identity	64
NCBI Description	(U70475) p45 NF-E2 related factor 2 [Mus musculus]

Seq. No.	230019
Seq. ID	LIB3196-047-P1-M1-H4
Method	BLASTX
NCBI GI	g1688233
BLAST score	155
E value	2.0e-10
Match length	94
% identity	46
NCBI Description	(U77655) DNA binding protein homolog [Solanum tuberosum]

Seq. No.	230020
Seq. ID	LIB3196-047-P1-M1-H6
Method	BLASTX
NCBI GI	g1703447
BLAST score	310
E value	2.0e-28
Match length	127
% identity	57
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_496102 (L19141) L-asparaginase [Lupinus albus]

Seq. No.	230021
Seq. ID	LIB3196-047-P1-M1-H7
Method	BLASTX
NCBI GI	g225242
BLAST score	476
E value	5.0e-48
Match length	97

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% identity	93
NCBI Description	ORF 1708 [Nicotiana tabacum]
Seq. No.	230022
Seq. ID	LIB3196-047-P1-M1-H8
Method	BLASTX
NCBI GI	g728837
BLAST score	149
E value	2.0e-09
Match length	64
% identity	13
NCBI Description	ALU SUBFAMILY SQ WARNING ENTRY !!!!
Seq. No.	230023
Seq. ID	LIB3196-047-P1-M1-H9
Method	BLASTX
NCBI GI	g548900
BLAST score	302
E value	1.0e-27
Match length	127
% identity	45
NCBI Description	SUCROSE-BINDING PROTEIN PRECURSOR (SBP) >gi_322691_pir__JQ1730 62K sucrose-binding protein precursor - soybean >gi_170064 (L06038) glucose binding protein [Glycine max]
Seq. No.	230024
Seq. ID	LIB3196-048-P1-M1-A3
Method	BLASTX
NCBI GI	g113471
BLAST score	541
E value	1.0e-55
Match length	128
% identity	83
NCBI Description	ADRENODOXIN PRECURSOR (ADRENAL FERREDOXIN) >gi_476388_pir__AXHU adrenodoxin precursor - human >gi_178086 (J03548) adrenodoxin [Homo sapiens] >gi_182494 (M18003) ferredoxin [Homo sapiens] >gi_182496 (M34788) ferredoxin [Homo sapiens] >gi_557734 (M23668) adrenodoxin [Homo sapiens]
Seq. No.	230025
Seq. ID	LIB3196-048-P1-M1-A4
Method	BLASTX
NCBI GI	g49868
BLAST score	662
E value	9.0e-70
Match length	129
% identity	100
NCBI Description	(X03765) put. beta-actin (aa 27-375) [Mus musculus] >gi_387083 (M12481) cytoplasmic beta-actin [Mus musculus]
Seq. No.	230026
Seq. ID	LIB3196-048-P1-M1-A6
Method	BLASTX
NCBI GI	g730832
BLAST score	169

E value	5.0e-12
Match length	53
% identity	57
NCBI Description	8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN) (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi_18748_emb_CAA78359_ (Z13956) a protein similar to potato tuber protein p322 homolgous to Bowman-Birk Proteinase Inhibitor [Glycine max]

Seq. No.	230027
Seq. ID	LIB3196-048-P1-M1-A9
Method	BLASTX
NCBI GI	g2062167
BLAST score	268
E value	1.0e-23
Match length	72
% identity	69
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	230028
Seq. ID	LIB3196-048-P1-M1-B1
Method	BLASTX
NCBI GI	g1706562
BLAST score	142
E value	2.0e-09
Match length	34
% identity	74
NCBI Description	EMBRYOGENIC-CELL PROTEIN 40 (ECP40) >gi_485500_pir__S33538 embryogenic cell protein ecp40 - carrot >gi_311368_emb_CAA43906_ (X61914) ECP40 [Daucus carota]

Seq. No.	230029
Seq. ID	LIB3196-048-P1-M1-B11
Method	BLASTX
NCBI GI	g3122072
BLAST score	599
E value	2.0e-62
Match length	114
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]

Seq. No.	230030
Seq. ID	LIB3196-048-P1-M1-B12
Method	BLASTX
NCBI GI	g462333
BLAST score	648
E value	4.0e-68
Match length	129
% identity	100
NCBI Description	HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR 1) (HSTF 1) >gi_87630_pir__A41137 heat shock transcription factor 1 - human >gi_184403 (M64673)

heat shock factor 1 [Homo sapiens]

Seq. No.	230031
Seq. ID	LIB3196-048-P1-M1-B3
Method	BLASTX
NCBI GI	g225581
BLAST score	406
E value	9.0e-40
Match length	96
% identity	83
NCBI Description	storage protein C94 [Saguinus oedipus]

Seq. No.	230032
Seq. ID	LIB3196-048-P1-M1-B5
Method	BLASTX
NCBI GI	g1076755
BLAST score	176
E value	7.0e-13
Match length	104
% identity	33
NCBI Description	protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]

Seq. No.	230033
Seq. ID	LIB3196-048-P1-M1-B7
Method	BLASTX
NCBI GI	g4103490
BLAST score	171
E value	1.0e-12
Match length	40
% identity	90
NCBI Description	(AF024519) glucocorticoid-induced leucine zipper GILZ protein [Mus musculus]

Seq. No.	230034
Seq. ID	LIB3196-048-P1-M1-B9
Method	BLASTX
NCBI GI	g167367
BLAST score	516
E value	1.0e-52
Match length	115
% identity	89
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230035
Seq. ID	LIB3196-048-P1-M1-C11
Method	BLASTX
NCBI GI	g231505
BLAST score	573
E value	2.0e-59
Match length	116
% identity	96
NCBI Description	ACTIN 101 >gi_100419_pir__S20093 actin - potato >gi_21534_emb_CAA39281_ (X55752) actin [Solanum tuberosum]

Seq. No.	230036
Seq. ID	LIB3196-048-P1-M1-C12

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Method	BLASTX
NCBI GI	g3913425
BLAST score	317
E value	1.0e-43
Match length	116
% identity	83
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	230037
Seq. ID	LIB3196-048-P1-M1-C2
Method	BLASTX
NCBI GI	g2129946
BLAST score	340
E value	3.0e-32
Match length	69
% identity	99
NCBI Description	ADP-ribosylation factor homolog GTP-binding protein NTGB1 - common tobacco (fragment) >gi_1184987 (U46927) NTGB1 [Nicotiana tabacum]

Seq. No.	230038
Seq. ID	LIB3196-048-P1-M1-C3
Method	BLASTX
NCBI GI	g3915742
BLAST score	365
E value	3.0e-35
Match length	80
% identity	85
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	230039
Seq. ID	LIB3196-048-P1-M1-C4
Method	BLASTX
NCBI GI	g2135267
BLAST score	679
E value	9.0e-72
Match length	129
% identity	56
NCBI Description	glucose-regulated protein ERp57/GRP58 - human

Seq. No.	230040
Seq. ID	LIB3196-048-P1-M1-C9
Method	BLASTX
NCBI GI	g285057
BLAST score	588
E value	4.0e-61
Match length	106
% identity	100
NCBI Description	zinc finger protein - mouse (fragment) >gi_403020_emb_CAA47353_ (X66902) En-2/lacZ fusion protein [Mus musculus]

Seq. No.	230041
Seq. ID	LIB3196-048-P1-M1-D1
Method	BLASTX
NCBI GI	g1064828
BLAST score	247
E value	1.0e-21
Match length	62
% identity	84
NCBI Description	(D78205) Actin [Ipomoea nil]

Seq. No.	230042
Seq. ID	LIB3196-048-P1-M1-D10
Method	BLASTX
NCBI GI	g72287
BLAST score	526
E value	7.0e-54
Match length	116
% identity	91
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	230043
Seq. ID	LIB3196-048-P1-M1-D4
Method	BLASTX
NCBI GI	g1351867
BLAST score	559
E value	1.0e-57
Match length	103
% identity	100
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi_761724 (U20114) beta-actin [Cricetulus griseus]

Seq. No.	230044
Seq. ID	LIB3196-048-P1-M1-D7
Method	BLASTX
NCBI GI	g137578
BLAST score	461
E value	3.0e-46
Match length	116
% identity	76
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230045
Seq. ID	LIB3196-048-P1-M1-D8
Method	BLASTX
NCBI GI	g567121
BLAST score	171
E value	2.0e-12
Match length	77
% identity	48
NCBI Description	(M34024) immunoglobulin heavy chain [Homo sapiens]

Seq. No.	230046
Seq. ID	LIB3196-048-P1-M1-E1
Method	BLASTX
NCBI GI	g280816
BLAST score	612
E value	6.0e-64
Match length	127
% identity	97
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin

Seq. No.	230047
Seq. ID	LIB3196-048-P1-M1-E11
Method	BLASTX
NCBI GI	g2129832
BLAST score	578
E value	6.0e-60
Match length	111
% identity	94
NCBI Description	heat shock transcription factor 5 - soybean >gi_671868_emb_CAA87080_ (Z46956) heat shock transcription factor 5 [Glycine max]

Seq. No.	230048
Seq. ID	LIB3196-048-P1-M1-E12
Method	BLASTX
NCBI GI	g3915742
BLAST score	570
E value	5.0e-59
Match length	119
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	230049
Seq. ID	LIB3196-048-P1-M1-E2
Method	BLASTX
NCBI GI	g4220534
BLAST score	411
E value	2.0e-40
Match length	104
% identity	70
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	230050
Seq. ID	LIB3196-048-P1-M1-E6
Method	BLASTX
NCBI GI	g3913425
BLAST score	515
E value	1.0e-52
Match length	106
% identity	93

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NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.	230051
Seq. ID	LIB3196-048-P1-M1-F10
Method	BLASTX
NCBI GI	g3894190
BLAST score	240
E value	3.0e-20
Match length	81
% identity	54
NCBI Description	(AC005662) putative RNA polymerase [Arabidopsis thaliana]
Seq. No.	230052
Seq. ID	LIB3196-048-P1-M1-F11
Method	BLASTX
NCBI GI	g1669533
BLAST score	260
E value	1.0e-22
Match length	93
% identity	54
NCBI Description	(D63643) clathrin coat assembly protein-like [Homo sapiens] >gi_1770513_emb_CAA67823_ (X99458) sigma 3A protein [Homo sapiens] >gi_1923270 (U91932) AP-3 complex sigma3A subunit [Homo sapiens] >gi_3462900 (AF084575) adaptor protein complex-3 sigma3A subunit isoform [Mus musculus] >gi_4502861_ref_NP_001275.1_pCLAPS3_ clathrin-associated/assembly/adaptor protein, small 3 (22kD)
Seq. No.	230053
Seq. ID	LIB3196-048-P1-M1-F12
Method	BLASTX
NCBI GI	g207905
BLAST score	644
E value	1.0e-67
Match length	123
% identity	100
NCBI Description	(M18027) alpha globulin B [Artificial gene]
Seq. No.	230054
Seq. ID	LIB3196-048-P1-M1-F2
Method	BLASTX
NCBI GI	g4049344
BLAST score	138
E value	1.0e-08
Match length	95
% identity	43
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	230055
Seq. ID	LIB3196-048-P1-M1-F7
Method	BLASTX
NCBI GI	g2369714
BLAST score	503
E value	3.0e-51

Match length	102
% identity	93
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	230056
Seq. ID	LIB3196-048-P1-M1-F8
Method	BLASTX
NCBI GI	g115492
BLAST score	462
E value	2.0e-46
Match length	90
% identity	52
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	230057
Seq. ID	LIB3196-048-P1-M1-G1
Method	BLASTX
NCBI GI	g416585
BLAST score	191
E value	6.0e-24
Match length	124
% identity	49
NCBI Description	ALCOHOL DEHYDROGENASE, MAJOR >gi_410008_bbs_137224 alcohol dehydrogenase {EC 1.1.1.1} [Alligator mississippiensis=American alligators, liver, Peptide, 374 aa]

Seq. No.	230058
Seq. ID	LIB3196-048-P1-M1-G10
Method	BLASTX
NCBI GI	g2499946
BLAST score	473
E value	1.0e-47
Match length	120
% identity	78
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	230059
Seq. ID	LIB3196-048-P1-M1-G2
Method	BLASTX
NCBI GI	g167311
BLAST score	248
E value	2.0e-21
Match length	78
% identity	64
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	230060
Seq. ID	LIB3196-048-P1-M1-G4
Method	BLASTX
NCBI GI	g2661840
BLAST score	454
E value	2.0e-45

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Match length	125
% identity	66
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	230061
Seq. ID	LIB3196-048-P1-M1-G5
Method	BLASTX
NCBI GI	g1856971
BLAST score	575
E value	1.0e-59
Match length	123
% identity	89
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	230062
Seq. ID	LIB3196-048-P1-M1-G6
Method	BLASTX
NCBI GI	g3913791
BLAST score	598
E value	3.0e-62
Match length	121
% identity	93
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum]

Seq. No.	230063
Seq. ID	LIB3196-048-P1-M1-G9
Method	BLASTX
NCBI GI	g266690
BLAST score	348
E value	5.0e-33
Match length	100
% identity	72
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	230064
Seq. ID	LIB3196-048-P1-M1-H10
Method	BLASTX
NCBI GI	g125080
BLAST score	649
E value	3.0e-68
Match length	129
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	230065
Seq. ID	LIB3196-048-P1-M1-H11

Method	BLASTX
NCBI GI	g1694673
BLAST score	416
E value	6.0e-41
Match length	95
% identity	85
NCBI Description	(D89052) proton-ATPase-like protein [Homo sapiens]

Seq. No.	230066
Seq. ID	LIB3196-048-P1-M1-H2
Method	BLASTX
NCBI GI	g547752
BLAST score	196
E value	4.0e-15
Match length	70
% identity	47
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 2 ORAL (CYTOKERATIN 2P) (K2P) (CK 2P) >gi_2119218_pir__I53169 cytokeratin 2 - human >gi_181390 (M99063) cytokeratin 2 [Homo sapiens]

Seq. No.	230067
Seq. ID	LIB3196-048-P1-M1-H3
Method	BLASTX
NCBI GI	g133041
BLAST score	522
E value	2.0e-53
Match length	102
% identity	99
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi_71137_pir__R5HUP0 acidic ribosomal protein P0 - human >gi_190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041) [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_ ribosomal protein, large, P0

Seq. No.	230068
Seq. ID	LIB3196-048-P1-M1-H5
Method	BLASTX
NCBI GI	g549063
BLAST score	370
E value	1.0e-35
Match length	94
% identity	73
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	230069
Seq. ID	LIB3196-048-P1-M1-H7
Method	BLASTX
NCBI GI	g2388585
BLAST score	295
E value	3.0e-38
Match length	119
% identity	80

NCBI Description	(AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No.	230070
Seq. ID	LIB3196-049-P1-M1-A1
Method	BLASTX
NCBI GI	g1220196
BLAST score	521
E value	3.0e-53
Match length	121
% identity	85
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	230071
Seq. ID	LIB3196-049-P1-M1-A12
Method	BLASTX
NCBI GI	g3421134
BLAST score	478
E value	3.0e-48
Match length	126
% identity	79
NCBI Description	(AF045666) arginine decarboxylase [Theobroma cacao]

Seq. No.	230072
Seq. ID	LIB3196-049-P1-M1-A3
Method	BLASTX
NCBI GI	g1778370
BLAST score	512
E value	4.0e-52
Match length	130
% identity	74
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	230073
Seq. ID	LIB3196-049-P1-M1-A4
Method	BLASTX
NCBI GI	g2493852
BLAST score	291
E value	3.0e-26
Match length	63
% identity	84
NCBI Description	CYTOCHROME C OXIDASE POLYPEPTIDE VC >gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc subunit [Hordeum vulgare]

Seq. No.	230074
Seq. ID	LIB3196-049-P1-M1-A7
Method	BLASTX
NCBI GI	g3641837
BLAST score	176
E value	3.0e-13
Match length	58
% identity	69
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	230075

Seq. ID	LIB3196-049-P1-M1-A9
Method	BLASTX
NCBI GI	g72287
BLAST score	292
E value	2.0e-26
Match length	71
% identity	85
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	230076
Seq. ID	LIB3196-049-P1-M1-B11
Method	BLASTX
NCBI GI	g126156
BLAST score	625
E value	2.0e-65
Match length	127
% identity	91
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	230077
Seq. ID	LIB3196-049-P1-M1-B12
Method	BLASTX
NCBI GI	g2369714
BLAST score	617
E value	2.0e-64
Match length	127
% identity	93
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	230078
Seq. ID	LIB3196-049-P1-M1-B2
Method	BLASTX
NCBI GI	g2894611
BLAST score	148
E value	2.0e-09
Match length	50
% identity	66
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	230079
Seq. ID	LIB3196-049-P1-M1-B3
Method	BLASTX
NCBI GI	g476850
BLAST score	610
E value	1.0e-63
Match length	136
% identity	90
NCBI Description	heat shock cognate protein 70 - mouse >gi_309319 (M19141) heat shock protein 70 cognate [Mus musculus] >gi_1661134_gb_AAB18391.1_ (U73744) heat shock 70 protein

[Mus musculus]

Seq. No.	230080
Seq. ID	LIB3196-049-P1-M1-B4
Method	BLASTX
NCBI GI	g476850
BLAST score	234
E value	1.0e-19
Match length	83
% identity	64
NCBI Description	heat shock cognate protein 70 - mouse >gi_309319 (M19141) heat shock protein 70 cognate [Mus musculus] >gi_1661134_gb_AAB18391.1_ (U73744) heat shock 70 protein [Mus musculus]

Seq. No.	230081
Seq. ID	LIB3196-049-P1-M1-C2
Method	BLASTX
NCBI GI	g3452572
BLAST score	227
E value	1.0e-18
Match length	47
% identity	94
NCBI Description	(AB011399) AF-6 [Homo sapiens]

Seq. No.	230082
Seq. ID	LIB3196-049-P1-M1-C3
Method	BLASTX
NCBI GI	g4204303
BLAST score	310
E value	2.0e-28
Match length	70
% identity	81
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	230083
Seq. ID	LIB3196-049-P1-M1-C4
Method	BLASTX
NCBI GI	g2460200
BLAST score	170
E value	4.0e-12
Match length	61
% identity	48
NCBI Description	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]

Seq. No.	230084
Seq. ID	LIB3196-049-P1-M1-C6
Method	BLASTX
NCBI GI	g4206196
BLAST score	241
E value	2.0e-20
Match length	80
% identity	55
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230085
Seq. ID	LIB3196-049-P1-M1-C8
Method	BLASTX
NCBI GI	g167311
BLAST score	413
E value	6.0e-48
Match length	111
% identity	89
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	230086
Seq. ID	LIB3196-049-P1-M1-D1
Method	BLASTX
NCBI GI	g3702286
BLAST score	251
E value	1.0e-21
Match length	50
% identity	98
NCBI Description	(AC005787) R33374_1 [Homo sapiens]

Seq. No.	230087
Seq. ID	LIB3196-049-P1-M1-D11
Method	BLASTX
NCBI GI	g3646426
BLAST score	394
E value	3.0e-38
Match length	79
% identity	92
NCBI Description	(AJ223355) mitochondrial dicarboxylate carrier [Rattus norvegicus]

Seq. No.	230088
Seq. ID	LIB3196-049-P1-M1-D6
Method	BLASTX
NCBI GI	g1170644
BLAST score	342
E value	3.0e-32
Match length	132
% identity	17
NCBI Description	RING CANAL PROTEIN (KELCH PROTEIN) >gi_577276 (L08483) ring canal protein [Drosophila melanogaster]

Seq. No.	230089
Seq. ID	LIB3196-049-P1-M1-E6
Method	BLASTX
NCBI GI	g3193299
BLAST score	442
E value	6.0e-44
Match length	116
% identity	71
NCBI Description	(AF069298) Arabidopsis poly(ADP-ribose) polymerase (GB:Z48243) [Arabidopsis thaliana]

Seq. No.	230090
Seq. ID	LIB3196-049-P1-M1-E9
Method	BLASTX
NCBI GI	g2129842

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BLAST score	174
E value	1.0e-12
Match length	53
% identity	58
NCBI Description	SE60 protein - soybean >gi_509769_emb_CAA79164_ (Z18359) seed-specific low molecular weight sulfur-rich protein [Glycine max]

Seq. No.	230091
Seq. ID	LIB3196-049-P1-M1-F11
Method	BLASTX
NCBI GI	g2708738
BLAST score	210
E value	9.0e-17
Match length	60
% identity	65
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230092
Seq. ID	LIB3196-049-P1-M1-F12
Method	BLASTX
NCBI GI	g549063
BLAST score	426
E value	4.0e-42
Match length	99
% identity	81
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	230093
Seq. ID	LIB3196-049-P1-M1-F2
Method	BLASTX
NCBI GI	g4033735
BLAST score	596
E value	5.0e-62
Match length	125
% identity	90
NCBI Description	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No.	230094
Seq. ID	LIB3196-049-P1-M1-F6
Method	BLASTX
NCBI GI	g4098129
BLAST score	652
E value	1.0e-68
Match length	127
% identity	94
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	230095
Seq. ID	LIB3196-049-P1-M1-F7
Method	BLASTX
NCBI GI	g2244734
BLAST score	512
E value	3.0e-52

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Match length	102
% identity	98
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	230096
Seq. ID	LIB3196-049-P1-M1-F9
Method	BLASTX
NCBI GI	g4210948
BLAST score	505
E value	2.0e-51
Match length	118
% identity	82
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	230097
Seq. ID	LIB3196-049-P1-M1-G1
Method	BLASTX
NCBI GI	g123571
BLAST score	583
E value	2.0e-60
Match length	123
% identity	88
NCBI Description	HEAT SHOCK 27 KD PROTEIN (HSP 27) (STRESS-RESPONSIVE PROTEIN 27) (SRP27) (ESTROGEN-REGULATED 24 KD PROTEIN) (28 KD HEAT SHOCK PROTEIN) >gi_662841 (L39370) heat shock protein 27 [Homo sapiens]

Seq. No.	230098
Seq. ID	LIB3196-049-P1-M1-G10
Method	BLASTX
NCBI GI	g3201969
BLAST score	446
E value	2.0e-44
Match length	109
% identity	71
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	230099
Seq. ID	LIB3196-049-P1-M1-G11
Method	BLASTX
NCBI GI	g72287
BLAST score	691
E value	3.0e-73
Match length	127
% identity	100
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	230100
Seq. ID	LIB3196-049-P1-M1-G4
Method	BLASTX
NCBI GI	g3258569
BLAST score	338
E value	8.0e-32
Match length	73
% identity	89

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NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	230101
Seq. ID	LIB3196-049-P1-M1-G5
Method	BLASTX
NCBI GI	g2244734
BLAST score	649
E value	3.0e-68
Match length	128
% identity	100
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	230102
Seq. ID	LIB3196-049-P1-M1-G6
Method	BLASTX
NCBI GI	g1363944
BLAST score	662
E value	1.0e-69
Match length	134
% identity	99
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230103
Seq. ID	LIB3196-049-P1-M1-G7
Method	BLASTX
NCBI GI	g3746652
BLAST score	239
E value	4.0e-20
Match length	48
% identity	100
NCBI Description	(AF070523) JWA protein [Homo sapiens]

Seq. No.	230104
Seq. ID	LIB3196-049-P1-M1-G9
Method	BLASTX
NCBI GI	g4417306
BLAST score	277
E value	1.0e-24
Match length	119
% identity	49
NCBI Description	(AC006446) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]

Seq. No.	230105
Seq. ID	LIB3196-049-P1-M1-H1
Method	BLASTX
NCBI GI	g107554
BLAST score	612
E value	6.0e-64
Match length	121
% identity	98
NCBI Description	pyruvate kinase (EC 2.7.1.40) isozyme M2 - human >gi_338827 (M26252) cytosolic thyroid hormone-binding protein (EC 2.7.1.40) [Homo sapiens]

Seq. No.	230106
Seq. ID	LIB3196-049-P1-M1-H10
Method	BLASTX
NCBI GI	g3757517
BLAST score	181
E value	2.0e-13
Match length	118
% identity	5
NCBI Description	(AC005167) putative salt-inducible protein [Arabidopsis thaliana]

Seq. No.	230107
Seq. ID	LIB3196-049-P1-M1-H11
Method	BLASTX
NCBI GI	g137578
BLAST score	496
E value	3.0e-50
Match length	126
% identity	78
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230108
Seq. ID	LIB3196-049-P1-M1-H6
Method	BLASTX
NCBI GI	g3329386
BLAST score	605
E value	5.0e-63
Match length	117
% identity	97
NCBI Description	(AF038958) synaptic glycoprotein SC2 spliced variant [Homo sapiens]

Seq. No.	230109
Seq. ID	LIB3196-049-P1-M1-H7
Method	BLASTX
NCBI GI	g2072626
BLAST score	380
E value	1.0e-36
Match length	123
% identity	64
NCBI Description	(Y12904) hypothetical protein [Arabidopsis thaliana] >gi_3281856_emb_CAA19751_ (AL031004) Transcription factor II homolog [Arabidopsis thaliana]

Seq. No.	230110
Seq. ID	LIB3196-049-P1-M1-H8
Method	BLASTX
NCBI GI	g1565225
BLAST score	150
E value	9.0e-10
Match length	29

% identity	90
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	230111
Seq. ID	LIB3196-050-P1-M1-A1
Method	BLASTX
NCBI GI	g547753
BLAST score	511
E value	4.0e-52
Match length	110
% identity	94
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	230112
Seq. ID	LIB3196-050-P1-M1-A10
Method	BLASTX
NCBI GI	g1346342
BLAST score	314
E value	6.0e-29
Match length	63
% identity	97
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo sapiens]

Seq. No.	230113
Seq. ID	LIB3196-050-P1-M1-A11
Method	BLASTX
NCBI GI	g417440
BLAST score	525
E value	1.0e-53
Match length	125
% identity	88
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE ... >gi_423821_pir__A46295 delta 1-pyrroline-5-carboxylate synthetase - moth bean

Seq. No.	230114
Seq. ID	LIB3196-050-P1-M1-A4
Method	BLASTX
NCBI GI	g3334320
BLAST score	518
E value	2.0e-56
Match length	119
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	230115
Seq. ID	LIB3196-050-P1-M1-A8
Method	BLASTX
NCBI GI	g2499575
BLAST score	547
E value	2.0e-56

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Match length	112
% identity	92
NCBI Description	PROTEIN KINASE C, MU TYPE (NPKC-MU) >gi_1362911_pir__A53215 protein kinase C (EC 2.7.1.-) mu - human >gi_438373_emb_CAA53384_ (X75756) protein kinase C mu [Homo sapiens] >gi_4506075_ref_NP_002733.1_pPRKCM_ protein kinase C, mu
Seq. No.	230116
Seq. ID	LIB3196-050-P1-M1-A9
Method	BLASTX
NCBI GI	g547753
BLAST score	685
E value	2.0e-72
Match length	141
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
Seq. No.	230117
Seq. ID	LIB3196-050-P1-M1-B2
Method	BLASTX
NCBI GI	g1163177
BLAST score	670
E value	1.0e-70
Match length	132
% identity	29
NCBI Description	(U33818) inducible poly(A)-binding protein [Homo sapiens] >gi_2801403 (U75686) polyadenylate binding protein [Homo sapiens] >gi_1585757_prf__2201474A inducible poly(A)-binding protein [Homo sapiens] >gi_4504715_ref_NP_003810.1_pIPABP_ UNKNOWN
Seq. No.	230118
Seq. ID	LIB3196-050-P1-M1-B3
Method	BLASTX
NCBI GI	g4204277
BLAST score	522
E value	3.0e-53
Match length	110
% identity	81
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	230119
Seq. ID	LIB3196-050-P1-M1-B7
Method	BLASTX
NCBI GI	g3745822
BLAST score	592
E value	1.0e-61
Match length	114
% identity	100
NCBI Description	Chain B, Tubulin Alpha-Beta Dimer, Electron Diffraction
Seq. No.	230120
Seq. ID	LIB3196-050-P1-M1-B8
Method	BLASTX
NCBI GI	g3687243
BLAST score	245

E value	7.0e-21
Match length	61
% identity	79
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	230121
Seq. ID	LIB3196-050-P1-M1-B9
Method	BLASTX
NCBI GI	g2739383
BLAST score	450
E value	7.0e-45
Match length	103
% identity	79
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	230122
Seq. ID	LIB3196-050-P1-M1-C1
Method	BLASTX
NCBI GI	g126156
BLAST score	585
E value	1.0e-60
Match length	136
% identity	84
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	230123
Seq. ID	LIB3196-050-P1-M1-C2
Method	BLASTX
NCBI GI	g2792220
BLAST score	320
E value	1.0e-29
Match length	134
% identity	47
NCBI Description	(AF032688) NBS-LRR type resistance protein [Oryza sativa]

Seq. No.	230124
Seq. ID	LIB3196-050-P1-M1-C3
Method	BLASTX
NCBI GI	g117501
BLAST score	553
E value	6.0e-57
Match length	104
% identity	98
NCBI Description	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A) >gi_87015_pir__A37047 calreticulin precursor - human >gi_179882 (M84739) calreticulin [Homo sapiens] >gi_337487 (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A) precursor [Homo sapiens] >gi_1905911 (AD000092) calreticulin [Homo sapiens]

Seq. No.	230125
Seq. ID	LIB3196-050-P1-M1-C4
Method	BLASTX
NCBI GI	g2493144
BLAST score	391
E value	5.0e-38
Match length	96
% identity	83
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	230126
Seq. ID	LIB3196-050-P1-M1-C5
Method	BLASTX
NCBI GI	g2584787
BLAST score	231
E value	3.0e-19
Match length	104
% identity	45
NCBI Description	(X95762) Aminopeptidase P-like [Homo sapiens]

Seq. No.	230127
Seq. ID	LIB3196-050-P1-M1-C6
Method	BLASTX
NCBI GI	g126156
BLAST score	567
E value	1.0e-58
Match length	109
% identity	100
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	230128
Seq. ID	LIB3196-050-P1-M1-C8
Method	BLASTX
NCBI GI	g1174621
BLAST score	166
E value	1.0e-11
Match length	78
% identity	47
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	230129
Seq. ID	LIB3196-050-P1-M1-C9
Method	BLASTX

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NCBI GI	g88047
BLAST score	193
E value	7.0e-15
Match length	40
% identity	100
NCBI Description	keratin, 46K type I cytoskeletal - human

Seq. No.	230130
Seq. ID	LIB3196-050-P1-M1-D1
Method	BLASTX
NCBI GI	g4455177
BLAST score	485
E value	5.0e-49
Match length	132
% identity	68
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	230131
Seq. ID	LIB3196-050-P1-M1-D10
Method	BLASTX
NCBI GI	g120649
BLAST score	467
E value	5.0e-47
Match length	89
% identity	99
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_182863 (J02642) glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_224880_prf__1203217A dehydrogenase,glyceraldehydephosphate [Homo sapiens]

Seq. No.	230132
Seq. ID	LIB3196-050-P1-M1-D11
Method	BLASTX
NCBI GI	g2369714
BLAST score	588
E value	4.0e-61
Match length	118
% identity	92
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	230133
Seq. ID	LIB3196-050-P1-M1-D12
Method	BLASTX
NCBI GI	g137578
BLAST score	473
E value	1.0e-47
Match length	134
% identity	44
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor -

upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230134
Seq. ID	LIB3196-050-P1-M1-D3
Method	BLASTX
NCBI GI	g1351867
BLAST score	715
E value	6.0e-76
Match length	133
% identity	100
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi_761724 (U20114) beta-actin [Cricetulus griseus]

Seq. No.	230135
Seq. ID	LIB3196-050-P1-M1-D4
Method	BLASTX
NCBI GI	g3860275
BLAST score	147
E value	3.0e-15
Match length	88
% identity	51
NCBI Description	(AC005824) putative GTP-binding protein [Arabidopsis thaliana] >gi_4314395_gb_AAD15605_ (AC006232) putative terminal flower 1 (TFL1) [Arabidopsis thaliana] >gi_4521159_dbj_BAA75933.1_ (AB024712) ATC [Arabidopsis thaliana] >gi_4521161_dbj_BAA75931.1_ (AB024714) ATC [Arabidopsis thaliana] >gi_4521163_dbj_BAA75932.1_ (AB024715) ATC [Arabidopsis thaliana]

Seq. No.	230136
Seq. ID	LIB3196-050-P1-M1-D5
Method	BLASTX
NCBI GI	g137578
BLAST score	715
E value	6.0e-76
Match length	134
% identity	100
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230137
Seq. ID	LIB3196-050-P1-M1-D8
Method	BLASTX
NCBI GI	g3746127
BLAST score	403
E value	2.0e-39
Match length	98
% identity	79
NCBI Description	(U76253) E25B protein [Mus musculus]

Seq. No.	230138
Seq. ID	LIB3196-050-P1-M1-D9
Method	BLASTX
NCBI GI	g2078298
BLAST score	563
E value	4.0e-58
Match length	133
% identity	82
NCBI Description	(U97257) glyceraldehyde 3-phosphate dehydrogenase [Lycopersicon esculentum]

Seq. No.	230139
Seq. ID	LIB3196-050-P1-M1-E11
Method	BLASTX
NCBI GI	g1754538
BLAST score	450
E value	7.0e-45
Match length	93
% identity	94
NCBI Description	(U66894) ESX [Homo sapiens] >gi_1841523 (U73843) ESE-1b [Homo sapiens] >gi_2338756 (AF017307) Ets-related transcription factor [Homo sapiens] >gi_2384740 (AF016295) Ets transcription factor [Homo sapiens] >gi_2459797 (U97156) epthelial-specific ets protein [Homo sapiens]

Seq. No.	230140
Seq. ID	LIB3196-050-P1-M1-E12
Method	BLASTX
NCBI GI	g4006924
BLAST score	162
E value	1.0e-11
Match length	76
% identity	41
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	230141
Seq. ID	LIB3196-050-P1-M1-E2
Method	BLASTX
NCBI GI	g1169534
BLAST score	451
E value	1.0e-61
Match length	130
% identity	86
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus communis]

Seq. No.	230142
Seq. ID	LIB3196-050-P1-M1-E6
Method	BLASTX
NCBI GI	g106903
BLAST score	213
E value	5.0e-17
Match length	82

% identity	67
NCBI Description	line-1 protein ORF2 - human

Seq. No.	230143
Seq. ID	LIB3196-050-P1-M1-E9
Method	BLASTX
NCBI GI	g2431769
BLAST score	227
E value	6.0e-19
Match length	58
% identity	76
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	230144
Seq. ID	LIB3196-050-P1-M1-F1
Method	BLASTX
NCBI GI	g167367
BLAST score	525
E value	9.0e-54
Match length	115
% identity	90
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230145
Seq. ID	LIB3196-050-P1-M1-F10
Method	BLASTX
NCBI GI	g683553
BLAST score	238
E value	5.0e-20
Match length	109
% identity	50
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	230146
Seq. ID	LIB3196-050-P1-M1-F3
Method	BLASTX
NCBI GI	g3915742
BLAST score	539
E value	2.0e-55
Match length	114
% identity	90
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	230147
Seq. ID	LIB3196-050-P1-M1-F5
Method	BLASTX
NCBI GI	g4539335
BLAST score	427
E value	3.0e-42
Match length	131
% identity	62
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	230148
Seq. ID	LIB3196-050-P1-M1-F7
Method	BLASTX
NCBI GI	g547751
BLAST score	632
E value	3.0e-66
Match length	129
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (39.1) (VERSION 1) >gi_422802_pir__S30433 keratin 17, cytoskeletal - human >gi_30379_emb_CAA79626_ (Z19574) cytokeratin 17 [Homo sapiens] >gi_34075_emb_CAA44451_ (X62571) keratin related product [Homo sapiens] >gi_4557701_ref_NP_000413.1_pKRT17_ keratin

Seq. No.	230149
Seq. ID	LIB3196-050-P1-M1-G1
Method	BLASTX
NCBI GI	g3288823
BLAST score	376
E value	3.0e-36
Match length	84
% identity	83
NCBI Description	(AF063852) FUS5 [Arabidopsis thaliana]

Seq. No.	230150
Seq. ID	LIB3196-050-P1-M1-G3
Method	BLASTX
NCBI GI	g478818
BLAST score	231
E value	3.0e-19
Match length	109
% identity	40
NCBI Description	strictosidine synthase - Rauvolfia mannii (fragment) >gi_21097_emb_CAA45025_ (X63431) strictosidine synthase [Rauvolfia mannii]

Seq. No.	230151
Seq. ID	LIB3196-050-P1-M1-G5
Method	BLASTX
NCBI GI	g464707
BLAST score	570
E value	5.0e-59
Match length	116
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and

gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	230152
Seq. ID	LIB3196-050-P1-M1-G9
Method	BLASTX
NCBI GI	g1350944
BLAST score	389
E value	8.0e-38
Match length	80
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	230153
Seq. ID	LIB3196-050-P1-M1-H1
Method	BLASTX
NCBI GI	g1663706
BLAST score	529
E value	4.0e-54
Match length	100
% identity	94
NCBI Description	(D87685) similar to human transcription factor TFIIS (S34159). [Homo sapiens]

Seq. No.	230154
Seq. ID	LIB3196-050-P1-M1-H10
Method	BLASTX
NCBI GI	g71533
BLAST score	158
E value	3.0e-11
Match length	53
% identity	68
NCBI Description	keratin, 56K type II cytoskeletal - human

Seq. No.	230155
Seq. ID	LIB3196-050-P1-M1-H12
Method	BLASTX
NCBI GI	g232139
BLAST score	282
E value	2.0e-25
Match length	62
% identity	87
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-15 SUBUNIT (ALPHA-16) >gi_106195_pir__A41096 GTP-binding regulatory protein alpha-16 chain - human >gi_182892 (M63904) G-alpha-16 protein [Homo sapiens] >gi_4504039_ref_NP_002059.1_pGNA15_ guanine nucleotide binding protein (G protein), alpha 15 (Gq class)

Seq. No.	230156
Seq. ID	LIB3196-050-P1-M1-H3
Method	BLASTX
NCBI GI	g3319958
BLAST score	445
E value	3.0e-44
Match length	137

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% identity	6
NCBI Description	(AJ228139) VAKTI precursor [Homo sapiens]
Seq. No.	230157
Seq. ID	LIB3196-050-P1-M1-H5
Method	BLASTX
NCBI GI	g3510462
BLAST score	141
E value	6.0e-09
Match length	27
% identity	93
NCBI Description	(AF019767) zinc finger protein [Homo sapiens] >gi_4508021_ref_NP_003895.1_pZNF259_ UNKNOWN
Seq. No.	230158
Seq. ID	LIB3196-050-P1-M1-H6
Method	BLASTX
NCBI GI	g125080
BLAST score	677
E value	2.0e-71
Match length	138
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.	230159
Seq. ID	LIB3196-050-P1-M1-H7
Method	BLASTX
NCBI GI	g125080
BLAST score	581
E value	2.0e-60
Match length	115
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.	230160
Seq. ID	LIB3196-050-P1-M1-H8
Method	BLASTX
NCBI GI	g125887
BLAST score	224
E value	2.0e-18
Match length	125
% identity	42
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]
Seq. No.	230161
Seq. ID	LIB3196-050-P1-M1-H9

Method	BLASTX
NCBI GI	g2655037
BLAST score	627
E value	1.0e-65
Match length	133
% identity	84
NCBI Description	(AF019952) tumor suppressing STF cDNA 1 [Homo sapiens] >gi_4507703_ref_NP_003301.1_pTSSC1_ tumor suppressing subtransferable candidate

Seq. No.	230162
Seq. ID	LIB3196-052-P1-M1-A11
Method	BLASTX
NCBI GI	g2605714
BLAST score	221
E value	4.0e-18
Match length	59
% identity	80
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	230163
Seq. ID	LIB3196-052-P1-M1-A4
Method	BLASTX
NCBI GI	g1346348
BLAST score	665
E value	4.0e-70
Match length	135
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E) (K6E KERATIN) >gi_2119223_pir__I61770 keratin type II - human >gi_908803 (L42611) keratin type II [Homo sapiens]

Seq. No.	230164
Seq. ID	LIB3196-052-P1-M1-B1
Method	BLASTX
NCBI GI	g2982259
BLAST score	504
E value	2.0e-51
Match length	101
% identity	94
NCBI Description	(AF051212) probable 60s ribosomal protein L13a [Picea mariana]

Seq. No.	230165
Seq. ID	LIB3196-052-P1-M1-B11
Method	BLASTX
NCBI GI	g1173267
BLAST score	241
E value	1.0e-20
Match length	91
% identity	59
NCBI Description	40S RIBOSOMAL PROTEIN S5 >gi_1362935_pir__S55916 ribosomal protein S5 - human >gi_550021 (U14970) ribosomal protein S5 [Homo sapiens] >gi_1096942_prf__2113200E ribosomal protein S5 [Homo sapiens] >gi_4506729_ref_NP_001000.1_pRPS5_ ribosomal protein S5

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Seq. No.	230166
Seq. ID	LIB3196-052-P1-M1-B2
Method	BLASTX
NCBI GI	g1169475
BLAST score	255
E value	1.0e-23
Match length	87
% identity	71
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_556301 (M22432) elongation factor Tu [Mus musculus]

Seq. No.	230167
Seq. ID	LIB3196-052-P1-M1-B4
Method	BLASTX
NCBI GI	g2492860
BLAST score	511
E value	4.0e-52
Match length	127
% identity	76
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2 PRECURSOR (GSA 2) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 2) (GSA-AT 2) >gi_498914 (U10278) glutamate-1-semialdehyde aminotransferase [Arabidopsis thaliana]

Seq. No.	230168
Seq. ID	LIB3196-052-P1-M1-B6
Method	BLASTX
NCBI GI	g3122833
BLAST score	365
E value	3.0e-35
Match length	81
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S5 >gi_1685071 (U78085) ribosomal protein S5 [Mus musculus]

Seq. No.	230169
Seq. ID	LIB3196-052-P1-M1-C1
Method	BLASTX
NCBI GI	g1587477
BLAST score	347
E value	6.0e-33
Match length	107
% identity	71
NCBI Description	TCOF1 gene [Homo sapiens]

Seq. No.	230170
Seq. ID	LIB3196-052-P1-M1-C11
Method	BLASTX
NCBI GI	g207905
BLAST score	558
E value	1.0e-57
Match length	126
% identity	89
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	230171
Seq. ID	LIB3196-052-P1-M1-C12
Method	BLASTX
NCBI GI	g1465772
BLAST score	592
E value	1.0e-61
Match length	130
% identity	85
NCBI Description	(U61232) cofactor E [Homo sapiens] >gi_4507375_ref_NP_003184.1_pTBCE_ tubulin-specific chaperone e

Seq. No.	230172
Seq. ID	LIB3196-052-P1-M1-C2
Method	BLASTX
NCBI GI	g1363944
BLAST score	264
E value	1.0e-38
Match length	115
% identity	80
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230173
Seq. ID	LIB3196-052-P1-M1-C4
Method	BLASTX
NCBI GI	g1346348
BLAST score	656
E value	4.0e-69
Match length	132
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E) (K6E KERATIN) >gi_2119223_pir__I61770 keratin type II - human >gi_908803 (L42611) keratin type II [Homo sapiens]

Seq. No.	230174
Seq. ID	LIB3196-052-P1-M1-C6
Method	BLASTX
NCBI GI	g4469023
BLAST score	523
E value	2.0e-53
Match length	116
% identity	88
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	230175
Seq. ID	LIB3196-052-P1-M1-C7
Method	BLASTX
NCBI GI	g1587477
BLAST score	151
E value	5.0e-10
Match length	83
% identity	49
NCBI Description	TCOF1 gene [Homo sapiens]

Seq. No. 230176

Seq. ID	LIB3196-052-P1-M1-C8
Method	BLASTX
NCBI GI	g1363944
BLAST score	583
E value	1.0e-60
Match length	118
% identity	98
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230177
Seq. ID	LIB3196-052-P1-M1-D11
Method	BLASTX
NCBI GI	g2982303
BLAST score	564
E value	3.0e-58
Match length	127
% identity	82
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	230178
Seq. ID	LIB3196-052-P1-M1-D12
Method	BLASTX
NCBI GI	g1705654
BLAST score	630
E value	5.0e-66
Match length	128
% identity	96
NCBI Description	80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80) >gi_1082651_pir__S50082 nuclear cap binding protein - human >gi_563368_emb_CAA56334_ (X80030) cap binding protein [Homo sapiens] >gi_577628_dbj_BAA06769_ (D32002) nuclear cap binding protein [Homo sapiens] >gi_4505343_ref_NP_002477.1_pNCBP_ nuclear cap binding protein, 80kD

Seq. No.	230179
Seq. ID	LIB3196-052-P1-M1-D2
Method	BLASTX
NCBI GI	g730565
BLAST score	646
E value	7.0e-68
Match length	122
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_423069_pir__S34195 ribosomal protein L3 - human >gi_313659_emb_CAA51839_ (X73460) ribosomal protein L3 [Homo sapiens] >gi_3850177_emb_CAA18450_ (AL022326) dJ333H23.1.1 (60S Ribosomal Protein L3) [Homo sapiens] >gi_4506649_ref_NP_000958.1_pRPL3_ ribosomal protein L3

Seq. No.	230180
Seq. ID	LIB3196-052-P1-M1-D3
Method	BLASTX
NCBI GI	g1173104
BLAST score	438

E value	2.0e-43
Match length	93
% identity	77
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	230181
Seq. ID	LIB3196-052-P1-M1-D6
Method	BLASTX
NCBI GI	g553182
BLAST score	332
E value	5.0e-31
Match length	78
% identity	81
NCBI Description	(M99703) class II AP endonuclease [Homo sapiens]

Seq. No.	230182
Seq. ID	LIB3196-052-P1-M1-E1
Method	BLASTX
NCBI GI	g170354
BLAST score	231
E value	2.0e-19
Match length	53
% identity	18
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	230183
Seq. ID	LIB3196-052-P1-M1-E10
Method	BLASTX
NCBI GI	g3860247
BLAST score	549
E value	1.0e-56
Match length	123
% identity	88
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	230184
Seq. ID	LIB3196-052-P1-M1-E4
Method	BLASTX
NCBI GI	g2160694
BLAST score	623
E value	3.0e-65
Match length	126
% identity	94
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	230185
Seq. ID	LIB3196-052-P1-M1-E5
Method	BLASTX
NCBI GI	g116026
BLAST score	450
E value	7.0e-45
Match length	113
% identity	83
NCBI Description	CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491)

(LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP-3) (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H) (GRANULOPHYSIN) >gi_2144873_pir__I38016 melanoma-associated antigen CD63 - human >gi_34527_emb_CAA30792_ (X07982) ME491 antigen precursor (AA -1 to 237) [Homo sapiens] >gi_189384 (M59907) melanoma-associated antigen [Homo sapiens] >gi_246539_bbs_93790 (S93788) ocular melanoma-associated antigen, OMA81H [human, uveal melanoma, Peptide, 238 aa] [Homo sapiens] >gi_430756_emb_CAA44519_ (X62654) ME491 /CD63 antigen [Homo sapiens] >gi_4502679_ref_NP_001771.1_pCD63_ CD63 antigen (melanoma 1 antigen)

Seq. No.	230186
Seq. ID	LIB3196-052-P1-M1-E6
Method	BLASTX
NCBI GI	g2245108
BLAST score	441
E value	6.0e-44
Match length	110
% identity	75
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	230187
Seq. ID	LIB3196-052-P1-M1-E7
Method	BLASTX
NCBI GI	g167311
BLAST score	563
E value	4.0e-58
Match length	126
% identity	87
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	230188
Seq. ID	LIB3196-052-P1-M1-F11
Method	BLASTX
NCBI GI	g3435312
BLAST score	497
E value	1.0e-51
Match length	131
% identity	84
NCBI Description	(AF083255) RNA helicase-related protein [Homo sapiens]

Seq. No.	230189
Seq. ID	LIB3196-052-P1-M1-F12
Method	BLASTX
NCBI GI	g2493439
BLAST score	230
E value	4.0e-19
Match length	46
% identity	100
NCBI Description	CALCYPHOSINE >gi_1359717_emb_CAA66609_ (X97966) calcyphosine [Homo sapiens] >gi_3075376 (AC004602) CAYP_HUMAN; RD25 [Homo sapiens]

Seq. No.	230190
Seq. ID	LIB3196-052-P1-M1-F3

Method	BLASTX
NCBI GI	g266690
BLAST score	357
E value	5.0e-34
Match length	106
% identity	71
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	230191
Seq. ID	LIB3196-052-P1-M1-F4
Method	BLASTX
NCBI GI	g728837
BLAST score	146
E value	8.0e-10
Match length	90
% identity	25
NCBI Description	ALU SUBFAMILY SQ WARNING ENTRY !!!!

Seq. No.	230192
Seq. ID	LIB3196-052-P1-M1-F7
Method	BLASTX
NCBI GI	g4138912
BLAST score	270
E value	8.0e-24
Match length	55
% identity	84
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No.	230193
Seq. ID	LIB3196-052-P1-M1-F9
Method	BLASTX
NCBI GI	g2317910
BLAST score	460
E value	4.0e-46
Match length	127
% identity	65
NCBI Description	(U89959) CER1 protein [Arabidopsis thaliana]

Seq. No.	230194
Seq. ID	LIB3196-052-P1-M1-G10
Method	BLASTX
NCBI GI	g2145023
BLAST score	225
E value	2.0e-18
Match length	112
% identity	44
NCBI Description	(U97700) 15.5 kDa oleosin [Sesamum indicum]

Seq. No.	230195
Seq. ID	LIB3196-052-P1-M1-G11
Method	BLASTX
NCBI GI	g2145023
BLAST score	178
E value	5.0e-13
Match length	97

% identity	43
NCBI Description	(U97700) 15.5 kDa oleosin [Sesamum indicum]

Seq. No.	230196
Seq. ID	LIB3196-052-P1-M1-G12
Method	BLASTX
NCBI GI	g1076457
BLAST score	484
E value	7.0e-49
Match length	107
% identity	88
NCBI Description	small GTP-binding protein - rape >gi_289370 (L12395) small GTP-binding protein [Brassica napus]

Seq. No.	230197
Seq. ID	LIB3196-052-P1-M1-G4
Method	BLASTX
NCBI GI	g4115931
BLAST score	248
E value	3.0e-21
Match length	104
% identity	54
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	230198
Seq. ID	LIB3196-052-P1-M1-G5
Method	BLASTX
NCBI GI	g2459441
BLAST score	277
E value	1.0e-24
Match length	80
% identity	70
NCBI Description	(AC002332) putative SWI/SNF complex subunit BAF170 [Arabidopsis thaliana]

Seq. No.	230199
Seq. ID	LIB3196-052-P1-M1-G8
Method	BLASTX
NCBI GI	g125080
BLAST score	581
E value	3.0e-60
Match length	116
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	230200
Seq. ID	LIB3196-052-P1-M1-H10
Method	BLASTX
NCBI GI	g1732511
BLAST score	176
E value	4.0e-13
Match length	43

% identity	79
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	230201
Seq. ID	LIB3196-052-P1-M1-H4
Method	BLASTX
NCBI GI	g126156
BLAST score	411
E value	2.0e-40
Match length	82
% identity	100
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	230202
Seq. ID	LIB3196-052-P1-M1-H5
Method	BLASTX
NCBI GI	g741804
BLAST score	474
E value	1.0e-47
Match length	113
% identity	80
NCBI Description	protein RAKc [Rattus norvegicus]

Seq. No.	230203
Seq. ID	LIB3196-052-P1-M1-H6
Method	BLASTX
NCBI GI	g167311
BLAST score	521
E value	3.0e-53
Match length	114
% identity	89
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	230204
Seq. ID	LIB3196-052-P1-M1-H7
Method	BLASTX
NCBI GI	g3915961
BLAST score	597
E value	4.0e-62
Match length	128
% identity	92
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	230205
Seq. ID	LIB3196-052-P1-M1-H9
Method	BLASTX
NCBI GI	g137578
BLAST score	527

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E value	6.0e-54
Match length	123
% identity	88
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230206
Seq. ID	LIB3196-053-P1-M1-A11
Method	BLASTX
NCBI GI	g4469019
BLAST score	421
E value	2.0e-41
Match length	89
% identity	92
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	230207
Seq. ID	LIB3196-053-P1-M1-A2
Method	BLASTX
NCBI GI	g136140
BLAST score	151
E value	8.0e-10
Match length	86
% identity	37
NCBI Description	PUTATIVE AC9 TRANSPOSASE >gi_72973_pir__TQZMCA probable transposase - maize transposon Ac9

Seq. No.	230208
Seq. ID	LIB3196-053-P1-M1-A5
Method	BLASTX
NCBI GI	g2147165
BLAST score	529
E value	4.0e-54
Match length	103
% identity	58
NCBI Description	calmodulin - Bidens pilosa >gi_939860_emb_CAA61980_ (X89890) Calmodulin [Bidens pilosa]

Seq. No.	230209
Seq. ID	LIB3196-053-P1-M1-A6
Method	BLASTX
NCBI GI	g1916850
BLAST score	187
E value	5.0e-14
Match length	113
% identity	47
NCBI Description	(U83463) scaffold protein Pbp1 [Homo sapiens]

Seq. No.	230210
Seq. ID	LIB3196-053-P1-M1-A8
Method	BLASTX
NCBI GI	g3283166
BLAST score	299

E value	4.0e-27
Match length	112
% identity	54
NCBI Description	(AF057526) erythrocyte membrane protein Rh50 [Mus musculus] >gi_3329467 (AF065395) Rh50-like protein [Mus musculus] >gi_3445508_dbj_BAA32441_ (AB015192) 50 kD glycoprotein (Rh50) [Mus musculus]

Seq. No.	230211
Seq. ID	LIB3196-053-P1-M1-B10
Method	BLASTX
NCBI GI	g2970051
BLAST score	579
E value	4.0e-60
Match length	122
% identity	92
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	230212
Seq. ID	LIB3196-053-P1-M1-B11
Method	BLASTX
NCBI GI	g2078529
BLAST score	527
E value	6.0e-54
Match length	123
% identity	80
NCBI Description	(U89505) Hlark [Homo sapiens] >gi_4506445_ref_NP_002887.1_pRBM4_ RNA binding motif protein

Seq. No.	230213
Seq. ID	LIB3196-053-P1-M1-B2
Method	BLASTX
NCBI GI	g3193222
BLAST score	169
E value	6.0e-12
Match length	37
% identity	89
NCBI Description	(AF068687) malate dehydrogenase [Glycine max]

Seq. No.	230214
Seq. ID	LIB3196-053-P1-M1-B5
Method	BLASTX
NCBI GI	g2191175
BLAST score	160
E value	7.0e-11
Match length	125
% identity	52
NCBI Description	(AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No.	230215
Seq. ID	LIB3196-053-P1-M1-B8
Method	BLASTX
NCBI GI	g2443869
BLAST score	518
E value	7.0e-53

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Match length	104
% identity	99
NCBI Description	(AC002985) epsilon-COP [Homo sapiens]

Seq. No.	230216
Seq. ID	LIB3196-053-P1-M1-B9
Method	BLASTX
NCBI GI	g4097714
BLAST score	656
E value	5.0e-69
Match length	139
% identity	90
NCBI Description	(U67734) cPLA2 interacting protein [Homo sapiens]

Seq. No.	230217
Seq. ID	LIB3196-053-P1-M1-C1
Method	BLASTX
NCBI GI	g1381394
BLAST score	432
E value	4.0e-43
Match length	89
% identity	91
NCBI Description	(U40989) tat interactive protein [Homo sapiens]

Seq. No.	230218
Seq. ID	LIB3196-053-P1-M1-C12
Method	BLASTX
NCBI GI	g4467128
BLAST score	280
E value	6.0e-25
Match length	79
% identity	68
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	230219
Seq. ID	LIB3196-053-P1-M1-C3
Method	BLASTX
NCBI GI	g1161926
BLAST score	575
E value	1.0e-59
Match length	119
% identity	87
NCBI Description	(U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine max]

Seq. No.	230220
Seq. ID	LIB3196-053-P1-M1-C4
Method	BLASTX
NCBI GI	g2558938
BLAST score	286
E value	1.0e-25
Match length	131
% identity	49
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	230221
Seq. ID	LIB3196-053-P1-M1-C6

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Method	BLASTX
NCBI GI	g2244847
BLAST score	147
E value	2.0e-09
Match length	91
% identity	42
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	230222
Seq. ID	LIB3196-053-P1-M1-C9
Method	BLASTX
NCBI GI	g2654435
BLAST score	565
E value	6.0e-61
Match length	133
% identity	82
NCBI Description	(U68187) extracellular matrix protein 1 [Homo sapiens]

Seq. No.	230223
Seq. ID	LIB3196-053-P1-M1-D1
Method	BLASTX
NCBI GI	g88052
BLAST score	694
E value	2.0e-73
Match length	139
% identity	100
NCBI Description	keratin K5, 58K type II, epidermal (version 2) - human (fragment)

Seq. No.	230224
Seq. ID	LIB3196-053-P1-M1-D10
Method	BLASTX
NCBI GI	g2642448
BLAST score	156
E value	2.0e-10
Match length	43
% identity	47
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230225
Seq. ID	LIB3196-053-P1-M1-D12
Method	BLASTX
NCBI GI	g266691
BLAST score	398
E value	8.0e-39
Match length	119
% identity	71
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	230226
Seq. ID	LIB3196-053-P1-M1-D2
Method	BLASTX
NCBI GI	g1653016

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BLAST score	154
E value	4.0e-10
Match length	87
% identity	40
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	230227
Seq. ID	LIB3196-053-P1-M1-D4
Method	BLASTX
NCBI GI	g4510363
BLAST score	212
E value	2.0e-34
Match length	89
% identity	84
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	230228
Seq. ID	LIB3196-053-P1-M1-D9
Method	BLASTX
NCBI GI	g1085384
BLAST score	299
E value	3.0e-27
Match length	79
% identity	65
NCBI Description	Sm protein F - human >gi_806564_emb_CAA59688_ (X85372) Sm protein F [Homo sapiens] >gi_4507131_ref_NP_003086.1_pSNRPF_ small nuclear ribonucleoprotein polypeptide F

Seq. No.	230229
Seq. ID	LIB3196-053-P1-M1-E10
Method	BLASTX
NCBI GI	g2662343
BLAST score	633
E value	2.0e-66
Match length	126
% identity	96
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	230230
Seq. ID	LIB3196-053-P1-M1-E12
Method	BLASTX
NCBI GI	g464707
BLAST score	521
E value	3.0e-53
Match length	106
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A

[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	230231
Seq. ID	LIB3196-053-P1-M1-E4
Method	BLASTX
NCBI GI	g2134892
BLAST score	340
E value	2.0e-32
Match length	76
% identity	89
NCBI Description	cell surface glycoprotein - human >gi_188256 (M60334) cell surface glycoprotein [Homo sapiens] >gi_1834460_emb_CAB06609_ (Z84814) HLA-DRA*0102 [Homo sapiens]

Seq. No.	230232
Seq. ID	LIB3196-053-P1-M1-E5
Method	BLASTX
NCBI GI	g30851
BLAST score	192
E value	4.0e-15
Match length	38
% identity	97
NCBI Description	(X62421) homologue to E.coli DnaJ protein [Homo sapiens]

Seq. No.	230233
Seq. ID	LIB3196-053-P1-M1-E6
Method	BLASTX
NCBI GI	g3414809
BLAST score	150
E value	4.0e-10
Match length	76
% identity	49
NCBI Description	(AF061529) rjs [Mus musculus]

Seq. No.	230234
Seq. ID	LIB3196-053-P1-M1-F10
Method	BLASTX
NCBI GI	g2245138
BLAST score	185
E value	7.0e-14
Match length	63
% identity	62
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230235
Seq. ID	LIB3196-053-P1-M1-F12
Method	BLASTX
NCBI GI	g4539005
BLAST score	250
E value	2.0e-21
Match length	112

% identity	45
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.	230236
Seq. ID	LIB3196-053-P1-M1-G11
Method	BLASTX
NCBI GI	g126156
BLAST score	313
E value	7.0e-29
Match length	109
% identity	60
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]
Seq. No.	230237
Seq. ID	LIB3196-053-P1-M1-G12
Method	BLASTX
NCBI GI	g226120
BLAST score	218
E value	1.0e-17
Match length	83
% identity	54
NCBI Description	vicilin gene B [Saguinus oedipus]
Seq. No.	230238
Seq. ID	LIB3196-053-P1-M1-G3
Method	BLASTX
NCBI GI	g1346347
BLAST score	498
E value	2.0e-50
Match length	102
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]
Seq. No.	230239
Seq. ID	LIB3196-053-P1-M1-G5
Method	BLASTX
NCBI GI	g122106
BLAST score	398
E value	6.0e-39
Match length	80
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503

(M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	230240
Seq. ID	LIB3196-053-P1-M1-G6
Method	BLASTX
NCBI GI	g4263779
BLAST score	353
E value	2.0e-33
Match length	104
% identity	66
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230241
Seq. ID	LIB3196-053-P1-M1-H10
Method	BLASTX
NCBI GI	g106322
BLAST score	197
E value	2.0e-21
Match length	87
% identity	59
NCBI Description	hypothetical protein (L1H 3' region) - human

Seq. No.	230242
Seq. ID	LIB3196-053-P1-M1-H4
Method	BLASTX
NCBI GI	g1363944
BLAST score	695
E value	1.0e-73
Match length	139
% identity	99
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230243
Seq. ID	LIB3196-053-P1-M1-H8
Method	BLASTX
NCBI GI	g4512699
BLAST score	396
E value	1.0e-38
Match length	115
% identity	73
NCBI Description	(AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No.	230244
Seq. ID	LIB3196-053-P1-M1-H9
Method	BLASTX
NCBI GI	g3861068
BLAST score	145
E value	4.0e-09

Match length 65
% identity 45
NCBI Description (AJ235272) unknown [Rickettsia prowazekii]

Seq. No. 230245
Seq. ID LIB3196-054-P1-M1-A1
Method BLASTX
NCBI GI g1236083
BLAST score 398
E value 8.0e-39
Match length 123
% identity 69
NCBI Description (U49507) Lisch7 [Mus musculus]

Seq. No. 230246
Seq. ID LIB3196-054-P1-M1-A11
Method BLASTX
NCBI GI g2578033
BLAST score 544
E value 6.0e-56
Match length 109
% identity 92
NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 230247
Seq. ID LIB3196-054-P1-M1-A12
Method BLASTX
NCBI GI g2443751
BLAST score 136
E value 7.0e-09
Match length 83
% identity 54
NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi_2529676 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 230248
Seq. ID LIB3196-054-P1-M1-A4
Method BLASTX
NCBI GI g1336807
BLAST score 337
E value 1.0e-31
Match length 119
% identity 58
NCBI Description (S81193) CEN=GTP-binding protein homolog [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum] >gi_1587482_prf__2206476A CEN gene [Antirrhinum sp.]

Seq. No. 230249
Seq. ID LIB3196-054-P1-M1-A6
Method BLASTX
NCBI GI g2702281
BLAST score 147
E value 2.0e-09
Match length 59
% identity 51
NCBI Description (AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	230250
Seq. ID	LIB3196-054-P1-M1-A7
Method	BLASTX
NCBI GI	g225280
BLAST score	339
E value	5.0e-32
Match length	72
% identity	90
NCBI Description	rpoC-like ORF 548 [Nicotiana tabacum]

Seq. No.	230251
Seq. ID	LIB3196-054-P1-M1-A8
Method	BLASTX
NCBI GI	g3024646
BLAST score	602
E value	1.0e-62
Match length	119
% identity	98
NCBI Description	STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) >gi_1082805_pir__A54962 sterol regulatory element binding protein 2 precursor - human >gi_451330 (U02031) sterol regulatory element binding protein-2 [Homo sapiens]

Seq. No.	230252
Seq. ID	LIB3196-054-P1-M1-B1
Method	BLASTX
NCBI GI	g113950
BLAST score	623
E value	3.0e-65
Match length	126
% identity	61
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II - human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo sapiens]

Seq. No.	230253
Seq. ID	LIB3196-054-P1-M1-B11
Method	BLASTX
NCBI GI	g1136402
BLAST score	326
E value	3.0e-30
Match length	112
% identity	62
NCBI Description	(D79993) similar to hypothetical protein L8167.6 of Saccharomyces cerevisiae. [Homo sapiens]

Seq. No.	230254
Seq. ID	LIB3196-054-P1-M1-B12
Method	BLASTX
NCBI GI	g399413
BLAST score	691
E value	4.0e-73
Match length	130

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% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_72869_pir__EFRB1 translation elongation factor eEF-1 alpha chain - rabbit >gi_1070665_pir__EFHU1 translation elongation factor eEF-1 alpha-1 chain - human >gi_1551_emb_CAA44162_ (X62245) elongation factor 1 alpha [Oryctolagus cuniculus] >gi_31098_emb_CAA27245_ (X03558) EF-1 alpha (aa 1-463) [Homo sapiens] >gi_181963 (J04617) elongation factor EF-1-alpha [Homo sapiens] >gi_495221 (U09823) elongation factor 1 alpha [Oryctolagus cuniculus] >gi_4503471_ref_NP_001393.1_pEEF1A1_ eukaryotic translation elongation factor 1 alpha
Seq. No.	230255
Seq. ID	LIB3196-054-P1-M1-B2
Method	BLASTX
NCBI GI	g280816
BLAST score	661
E value	1.0e-69
Match length	134
% identity	99
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin
Seq. No.	230256
Seq. ID	LIB3196-054-P1-M1-B6
Method	BLASTX
NCBI GI	g3282092
BLAST score	165
E value	1.0e-11
Match length	108
% identity	38
NCBI Description	(AJ007446) hypothetical protein [Thermotoga neapolitana]
Seq. No.	230257
Seq. ID	LIB3196-054-P1-M1-B7
Method	BLASTX
NCBI GI	g3309082
BLAST score	544
E value	6.0e-56
Match length	125
% identity	84
NCBI Description	(AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]
Seq. No.	230258
Seq. ID	LIB3196-054-P1-M1-B8
Method	BLASTX
NCBI GI	g183663
BLAST score	167
E value	1.0e-11
Match length	32
% identity	100
NCBI Description	(M99422) glutathione transferase [Homo sapiens]

Seq. No.	230259
Seq. ID	LIB3196-054-P1-M1-C11
Method	BLASTX
NCBI GI	g2921213
BLAST score	462
E value	2.0e-46
Match length	123
% identity	73
NCBI Description	(AF026150) beta-ketoacyl-ACP synthase IIIA [Perilla frutescens]

Seq. No.	230260
Seq. ID	LIB3196-054-P1-M1-C3
Method	BLASTX
NCBI GI	g2244975
BLAST score	499
E value	1.0e-50
Match length	125
% identity	73
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230261
Seq. ID	LIB3196-054-P1-M1-C4
Method	BLASTX
NCBI GI	g125077
BLAST score	367
E value	4.0e-35
Match length	76
% identity	91
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	230262
Seq. ID	LIB3196-054-P1-M1-C6
Method	BLASTX
NCBI GI	g2583129
BLAST score	297
E value	5.0e-27
Match length	81
% identity	70
NCBI Description	(AC002387) putative methionine aminopeptidase [Arabidopsis thaliana]

Seq. No.	230263
Seq. ID	LIB3196-054-P1-M1-C7
Method	BLASTX
NCBI GI	g2145023
BLAST score	167
E value	1.0e-11
Match length	71
% identity	48
NCBI Description	(U97700) 15.5 kDa oleosin [Sesamum indicum]

Seq. No.	230264

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Seq. ID	LIB3196-054-P1-M1-D1
Method	BLASTX
NCBI GI	g3024665
BLAST score	199
E value	2.0e-15
Match length	116
% identity	40
NCBI Description	STRICTOSIDINE SYNTHASE 3 PRECURSOR >gi_1754987 (U43946) strictosidine synthase [Arabidopsis thaliana]

Seq. No.	230265
Seq. ID	LIB3196-054-P1-M1-D10
Method	BLASTX
NCBI GI	g3128168
BLAST score	171
E value	3.0e-12
Match length	43
% identity	60
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	230266
Seq. ID	LIB3196-054-P1-M1-D11
Method	BLASTX
NCBI GI	g1223922
BLAST score	305
E value	6.0e-28
Match length	67
% identity	81
NCBI Description	(U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata]

Seq. No.	230267
Seq. ID	LIB3196-054-P1-M1-D12
Method	BLASTX
NCBI GI	g3875242
BLAST score	207
E value	2.0e-16
Match length	85
% identity	52
NCBI Description	(Z75532) similar to mitochrondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	230268
Seq. ID	LIB3196-054-P1-M1-D2
Method	BLASTX
NCBI GI	g137578
BLAST score	547
E value	2.0e-56
Match length	125
% identity	86
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

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Seq. No.	230269
Seq. ID	LIB3196-054-P1-M1-D3
Method	BLASTX
NCBI GI	g115833
BLAST score	460
E value	4.0e-46
Match length	117
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No.	230270
Seq. ID	LIB3196-054-P1-M1-D4
Method	BLASTX
NCBI GI	g3080405
BLAST score	290
E value	4.0e-26
Match length	100
% identity	57
NCBI Description	(AL022603) Lsd1 like protein [Arabidopsis thaliana] >gi_4455269_emb_CAB36805.1_ (AL035527) Lsd1 like protein [Arabidopsis thaliana]

Seq. No.	230271
Seq. ID	LIB3196-054-P1-M1-D6
Method	BLASTX
NCBI GI	g3885334
BLAST score	596
E value	5.0e-62
Match length	125
% identity	84
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	230272
Seq. ID	LIB3196-054-P1-M1-D9
Method	BLASTX
NCBI GI	g421876
BLAST score	364
E value	8.0e-35
Match length	114
% identity	66
NCBI Description	probable ATP synthase chain - soybean >gi_396230_emb_CAA52349_ (X74296) putative ATP synthase subunit [Glycine max]

Seq. No.	230273
Seq. ID	LIB3196-054-P1-M1-E1
Method	BLASTX
NCBI GI	g4415936
BLAST score	218
E value	1.0e-17
Match length	55
% identity	71

NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana]

Seq. No.	230274
Seq. ID	LIB3196-054-P1-M1-E10
Method	BLASTX
NCBI GI	g3080416
BLAST score	182
E value	1.0e-13
Match length	41
% identity	85
NCBI Description	(AL022604) UDP-galactose transporter - like protein [Arabidopsis thaliana]

Seq. No.	230275
Seq. ID	LIB3196-054-P1-M1-E11
Method	BLASTX
NCBI GI	g1888357
BLAST score	515
E value	1.0e-52
Match length	123
% identity	75
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	230276
Seq. ID	LIB3196-054-P1-M1-E2
Method	BLASTX
NCBI GI	g125080
BLAST score	238
E value	5.0e-20
Match length	120
% identity	45
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	230277
Seq. ID	LIB3196-054-P1-M1-E4
Method	BLASTX
NCBI GI	g3540195
BLAST score	604
E value	5.0e-63
Match length	122
% identity	44
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	230278
Seq. ID	LIB3196-054-P1-M1-E7
Method	BLASTX
NCBI GI	g2160158
BLAST score	213
E value	3.0e-17
Match length	48
% identity	81

NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	230279
Seq. ID	LIB3196-054-P1-M1-E8
Method	BLASTX
NCBI GI	g115421
BLAST score	685
E value	2.0e-72
Match length	133
% identity	30
NCBI Description	NEURAL-CADHERIN PRECURSOR (N-CADHERIN) >gi_319925_pir__IJBOCN N-cadherin precursor - bovine (fragment) >gi_664894_emb_CAA37677_ (X53615) N-cadherin [Bos taurus]

Seq. No.	230280
Seq. ID	LIB3196-054-P1-M1-E9
Method	BLASTX
NCBI GI	g1703377
BLAST score	246
E value	6.0e-21
Match length	45
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_951146 (U31350) ADP-ribosylation factor 1 [Xenopus laevis]

Seq. No.	230281
Seq. ID	LIB3196-054-P1-M1-F5
Method	BLASTX
NCBI GI	g2443314
BLAST score	158
E value	7.0e-21
Match length	98
% identity	59
NCBI Description	(D63774) keratin 14 [Rattus norvegicus]

Seq. No.	230282
Seq. ID	LIB3196-054-P1-M1-F8
Method	BLASTX
NCBI GI	g3128177
BLAST score	528
E value	4.0e-54
Match length	125
% identity	82
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	230283
Seq. ID	LIB3196-054-P1-M1-F9
Method	BLASTX
NCBI GI	g1199772
BLAST score	245
E value	7.0e-21
Match length	51
% identity	86
NCBI Description	(D83226) extensin like protein [Populus nigra]

09845.47000

	>gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]
Seq. No.	230284
Seq. ID	LIB3196-054-P1-M1-G1
Method	BLASTX
NCBI GI	g559703
BLAST score	605
E value	4.0e-63
Match length	133
% identity	89
NCBI Description	(D38549) hal025 is new [Homo sapiens]
Seq. No.	230285
Seq. ID	LIB3196-054-P1-M1-G11
Method	BLASTX
NCBI GI	g2459421
BLAST score	411
E value	2.0e-40
Match length	110
% identity	68
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]
Seq. No.	230286
Seq. ID	LIB3196-054-P1-M1-G3
Method	BLASTX
NCBI GI	g100001
BLAST score	450
E value	6.0e-45
Match length	121
% identity	72
NCBI Description	endopeptidase C1 - kidney bean >gi_1345573_emb_CAA40073_ (X56753) endopeptidase (EP-C1) [Phaseolus vulgaris]
Seq. No.	230287
Seq. ID	LIB3196-054-P1-M1-G7
Method	BLASTX
NCBI GI	g2655420
BLAST score	440
E value	9.0e-44
Match length	109
% identity	76
NCBI Description	(AF035414) heat shock cognate protein HSC70 [Brassica napus]
Seq. No.	230288
Seq. ID	LIB3196-054-P1-M1-G8
Method	BLASTX
NCBI GI	g2507455
BLAST score	578
E value	6.0e-60
Match length	125
% identity	92
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach

>gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	230289
Seq. ID	LIB3196-054-P1-M1-H2
Method	BLASTX
NCBI GI	g799177
BLAST score	163
E value	3.0e-11
Match length	122
% identity	39
NCBI Description	(U22055) 100 kDa coactivator [Homo sapiens]

Seq. No.	230290
Seq. ID	LIB3196-054-P1-M1-H3
Method	BLASTX
NCBI GI	g473949
BLAST score	182
E value	2.0e-13
Match length	36
% identity	97
NCBI Description	(D29958) KIAA0116 [Homo sapiens]

Seq. No.	230291
Seq. ID	LIB3196-054-P1-M1-H7
Method	BLASTX
NCBI GI	g266690
BLAST score	360
E value	2.0e-34
Match length	101
% identity	73
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	230292
Seq. ID	LIB3196-055-P1-M1-A12
Method	BLASTX
NCBI GI	g2462749
BLAST score	403
E value	2.0e-39
Match length	81
% identity	94
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	230293
Seq. ID	LIB3196-055-P1-M1-A2
Method	BLASTX
NCBI GI	g135858
BLAST score	467
E value	6.0e-47
Match length	119
% identity	78
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi_99760_pir__S22201 tonoplast intrinsic protein alpha - Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)

	tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.	230294
Seq. ID	LIB3196-055-P1-M1-A6
Method	BLASTX
NCBI GI	g730526
BLAST score	358
E value	4.0e-34
Match length	117
% identity	62
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]
Seq. No.	230295
Seq. ID	LIB3196-055-P1-M1-A7
Method	BLASTX
NCBI GI	g4006875
BLAST score	197
E value	2.0e-15
Match length	91
% identity	48
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]
Seq. No.	230296
Seq. ID	LIB3196-055-P1-M1-A8
Method	BLASTX
NCBI GI	g2388689
BLAST score	136
E value	9.0e-12
Match length	86
% identity	53
NCBI Description	(AF016633) GH1 protein [Glycine max]
Seq. No.	230297
Seq. ID	LIB3196-055-P1-M1-B1
Method	BLASTX
NCBI GI	g2137162
BLAST score	288
E value	5.0e-26
Match length	97
% identity	70
NCBI Description	BAP31 protein - mouse >gi_1487986_emb_CAA57414_ (X81816) BAP31 [Mus musculus]
Seq. No.	230298
Seq. ID	LIB3196-055-P1-M1-B3
Method	BLASTX
NCBI GI	g1742951
BLAST score	278
E value	1.0e-24
Match length	61
% identity	89

NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	230299
Seq. ID	LIB3196-055-P1-M1-B5
Method	BLASTX
NCBI GI	g129899
BLAST score	302
E value	4.0e-28
Match length	78
% identity	77
NCBI Description	PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (CYCLOOXYGENASE -1) (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1) (PROSTAGLANDIN H2 SYNTHASE 1) (PGH SYNTHASE 1) (PGHS-1) (PHS 1) >gi_88488_pir__JH0259 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 1 precursor - human >gi_189887 (M59979) prostaglandin endoperoxide synthase [Homo sapiens] >gi_243972_bbs_78221 (S78220) prostaglandin endoperoxide synthase, cyclooxygenase [human, platelets, Peptide, 599 aa] [Homo sapiens] >gi_249626_bbs_103946 (S36271) prostaglandin G/H synthase, PGG/HS [human, lung fibroblast, Peptide, 599 aa] [Homo sapiens]

Seq. No.	230300
Seq. ID	LIB3196-055-P1-M1-C1
Method	BLASTX
NCBI GI	g1524121
BLAST score	157
E value	2.0e-10
Match length	56
% identity	57
NCBI Description	(X96539) malate dehydrogenase [Mesembryanthemum crystallinum]

Seq. No.	230301
Seq. ID	LIB3196-055-P1-M1-C12
Method	BLASTX
NCBI GI	g1809248
BLAST score	319
E value	1.0e-29
Match length	124
% identity	56
NCBI Description	(U51586) siah binding protein 1 [Homo sapiens]

Seq. No.	230302
Seq. ID	LIB3196-055-P1-M1-C3
Method	BLASTX
NCBI GI	g2739383
BLAST score	377
E value	2.0e-36
Match length	119
% identity	68
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	230303
Seq. ID	LIB3196-055-P1-M1-C5
Method	BLASTX
NCBI GI	g1708480

BLAST score	233
E value	2.0e-33
Match length	108
% identity	76
NCBI Description	IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT) (SRP1-ALPHA) (RAG COHORT PROTEIN 1) >gi_2135835_pir__A56516 nuclear localization sequence receptor SRP1 alpha - human >gi_791185 (U09559) Rch1 [Homo sapiens] >gi_899539 (U28386) hSRP1alpha [Homo sapiens] >gi_4504897_ref_NP_002257.1_pKPNA2_ karyopherin alpha 2 (RAG cohort 1, importin alpha 1)

Seq. No.	230304
Seq. ID	LIB3196-055-P1-M1-D12
Method	BLASTX
NCBI GI	g126396
BLAST score	644
E value	1.0e-67
Match length	125
% identity	94
NCBI Description	ARACHIDONATE 15-LIPOXYGENASE (ARACHIDONATE OMEGA-6 LIPOXYGENASE) (15-LOX) >gi_86878_pir__A31349 arachidonate 15-lipoxygenase (EC 1.13.11.33) - human >gi_307135 (M23892) 15-lipoxygenase [Homo sapiens] >gi_1872525 (U88317) 15-lipoxygenase [Homo sapiens] >gi_4502055_ref_NP_001131.1_pALOX15_ arachidonate 15-lipoxygenase

Seq. No.	230305
Seq. ID	LIB3196-055-P1-M1-D5
Method	BLASTX
NCBI GI	g72287
BLAST score	629
E value	6.0e-66
Match length	121
% identity	99
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	230306
Seq. ID	LIB3196-055-P1-M1-E12
Method	BLASTX
NCBI GI	g125887
BLAST score	164
E value	2.0e-11
Match length	89
% identity	45
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	230307
Seq. ID	LIB3196-055-P1-M1-E2
Method	BLASTX
NCBI GI	g683553

BLAST score	210
E value	8.0e-17
Match length	97
% identity	48
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	230308
Seq. ID	LIB3196-055-P1-M1-E8
Method	BLASTX
NCBI GI	g167311
BLAST score	316
E value	3.0e-29
Match length	71
% identity	85
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	230309
Seq. ID	LIB3196-055-P1-M1-F1
Method	BLASTX
NCBI GI	g4262140
BLAST score	143
E value	2.0e-12
Match length	77
% identity	58
NCBI Description	(AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No.	230310
Seq. ID	LIB3196-055-P1-M1-F11
Method	BLASTX
NCBI GI	g3643595
BLAST score	303
E value	1.0e-27
Match length	110
% identity	54
NCBI Description	(AC005395) putative oleosin protein [Arabidopsis thaliana]

Seq. No.	230311
Seq. ID	LIB3196-055-P1-M1-F12
Method	BLASTX
NCBI GI	g125105
BLAST score	562
E value	5.0e-58
Match length	122
% identity	92
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	230312
Seq. ID	LIB3196-055-P1-M1-F3
Method	BLASTX
NCBI GI	g1732417
BLAST score	246
E value	6.0e-21

Match length 98
% identity 56
NCBI Description (U47924) DRPLA [Homo sapiens]

Seq. No. 230313
Seq. ID LIB3196-055-P1-M1-F5
Method BLASTX
NCBI GI g2746719
BLAST score 149
E value 1.0e-09
Match length 45
% identity 64
NCBI Description (AF038386) histone H2B [Capsicum annuum]

Seq. No. 230314
Seq. ID LIB3196-055-P1-M1-G1
Method BLASTX
NCBI GI g4102715
BLAST score 454
E value 2.0e-45
Match length 113
% identity 77
NCBI Description (AF015287) serine protease [Homo sapiens]

Seq. No. 230315
Seq. ID LIB3196-055-P1-M1-G11
Method BLASTX
NCBI GI g113287
BLAST score 498
E value 2.0e-50
Match length 96
% identity 95
NCBI Description ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1)
>gi_71610_pir__ATHU actin, skeletal muscle - human
>gi_71612_pir__ATRT actin, skeletal muscle - rat
>gi_71613_pir__ATCH actin alpha, skeletal muscle - chicken
>gi_90264_pir__A24904 actin, skeletal muscle - mouse
>gi_55577_emb_CAA24529_ (V01218) actin [Rattus norvegicus]
>gi_63029_emb_CAA24753_ (V01507) a-actin [Gallus gallus]
>gi_178029 (J00068) alpha-actin [Homo sapiens] >gi_309088
(M12866) actin [Mus musculus] >gi_337746 (M20543)
alpha-skeletal actin precursor [Homo sapiens] >gi_387081
(M12347) alpha-actin [Mus musculus] >gi_790202 (U16368)
skeletal alpha actin [Sus scrofa] >gi_223503_prf__0809315A
actin [Rattus norvegicus]
>gi_4501881_ref_NP_001091.1_pACTA1_ actin, alpha 1,
skeletal muscle

Seq. No. 230316
Seq. ID LIB3196-055-P1-M1-G12
Method BLASTX
NCBI GI g4263711
BLAST score 203
E value 2.0e-16
Match length 44
% identity 86
NCBI Description (AC006223) putative CCR4-associated transcription factor

0005470-0005569

[Arabidopsis thaliana]

Seq. No.	230317
Seq. ID	LIB3196-055-P1-M1-G2
Method	BLASTX
NCBI GI	g137578
BLAST score	461
E value	5.0e-58
Match length	120
% identity	97
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230318
Seq. ID	LIB3196-055-P1-M1-G6
Method	BLASTX
NCBI GI	g2960216
BLAST score	355
E value	2.0e-36
Match length	114
% identity	71
NCBI Description	(AJ223384) 26S proteasome regulatory ATPase subunit 10b (S10b) [Manduca sexta]

Seq. No.	230319
Seq. ID	LIB3196-055-P1-M1-H1
Method	BLASTX
NCBI GI	g3869127
BLAST score	282
E value	3.0e-25
Match length	81
% identity	63
NCBI Description	(AB019527) LDOC1 protein [Homo sapiens]

Seq. No.	230320
Seq. ID	LIB3196-055-P1-M1-H2
Method	BLASTX
NCBI GI	g3869127
BLAST score	170
E value	5.0e-12
Match length	77
% identity	47
NCBI Description	(AB019527) LDOC1 protein [Homo sapiens]

Seq. No.	230321
Seq. ID	LIB3196-055-P1-M1-H3
Method	BLASTX
NCBI GI	g2586082
BLAST score	339
E value	6.0e-32
Match length	110
% identity	56
NCBI Description	(U72725) retrofit [Oryza longistaminata]

0004504.0095

Seq. No.	230322
Seq. ID	LIB3196-056-P1-M1-A1
Method	BLASTX
NCBI GI	g2583135
BLAST score	436
E value	3.0e-43
Match length	99
% identity	88
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana] >gi_3822216 (AF074948) FIL [Arabidopsis thaliana] >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs protein [Arabidopsis thaliana]

Seq. No.	230323
Seq. ID	LIB3196-056-P1-M1-A2
Method	BLASTX
NCBI GI	g1170373
BLAST score	355
E value	3.0e-34
Match length	78
% identity	90
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	230324
Seq. ID	LIB3196-056-P1-M1-B7
Method	BLASTX
NCBI GI	g3915742
BLAST score	296
E value	4.0e-27
Match length	69
% identity	81
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	230325
Seq. ID	LIB3196-056-P1-M1-C10
Method	BLASTX
NCBI GI	g3915742
BLAST score	259
E value	1.0e-39
Match length	90
% identity	93
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	230326
Seq. ID	LIB3196-056-P1-M1-C12
Method	BLASTX
NCBI GI	g4539292

09604016.1060000

BLAST score	438
E value	1.0e-43
Match length	92
% identity	87
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	230327
Seq. ID	LIB3196-056-P1-M1-C2
Method	BLASTX
NCBI GI	g1800317
BLAST score	187
E value	5.0e-17
Match length	73
% identity	77
NCBI Description	(U83896) Rat homologues of yeast sec7p [Rattus norvegicus] >gi_3660538_dbj_BAA33429_ (AB013466) cytohesin 2 [Mus musculus] >gi_3885503 (AF079971) cytohesin-2 [Mus musculus]

Seq. No.	230328
Seq. ID	LIB3196-056-P1-M1-C3
Method	BLASTX
NCBI GI	g1223922
BLAST score	486
E value	4.0e-49
Match length	113
% identity	74
NCBI Description	(U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata]

Seq. No.	230329
Seq. ID	LIB3196-056-P1-M1-C8
Method	BLASTX
NCBI GI	g4538997
BLAST score	167
E value	8.0e-12
Match length	75
% identity	47
NCBI Description	(AL049481) AIG1-like protein [Arabidopsis thaliana]

Seq. No.	230330
Seq. ID	LIB3196-056-P1-M1-C9
Method	BLASTX
NCBI GI	g1107696
BLAST score	457
E value	6.0e-46
Match length	94
% identity	90
NCBI Description	(X86691) Mi-2 protein [Homo sapiens] >gi_4557453_ref_NP_001264.1_pCHD4_ chromodomain helicase DNA binding protein

Seq. No.	230331
Seq. ID	LIB3196-056-P1-M1-D3
Method	BLASTX
NCBI GI	g3868758
BLAST score	320

09568405.1050000

E value 2.0e-32
Match length 94
% identity 67
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 230332
Seq. ID LIB3196-056-P1-M1-D9
Method BLASTX
NCBI GI g2624326
BLAST score 338
E value 6.0e-32
Match length 93
% identity 74
NCBI Description (AJ002893) OsGRP1 [Oryza sativa]

Seq. No. 230333
Seq. ID LIB3196-056-P1-M1-E1
Method BLASTX
NCBI GI g137580
BLAST score 199
E value 1.0e-15
Match length 44
% identity 89
NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No. 230334
Seq. ID LIB3196-056-P1-M1-E12
Method BLASTX
NCBI GI g3695408
BLAST score 229
E value 5.0e-19
Match length 87
% identity 48
NCBI Description (AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable wound-induced protein [Arabidopsis thaliana]

Seq. No. 230335
Seq. ID LIB3196-056-P1-M1-E9
Method BLASTX
NCBI GI g3915742
BLAST score 530
E value 2.0e-54
Match length 117
% identity 89
NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No. 230336
Seq. ID LIB3196-056-P1-M1-F12
Method BLASTX

NCBI GI	g113944
BLAST score	525
E value	9.0e-54
Match length	105
% identity	99
NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi_71756_pir__LUHU annexin I - human >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I (lipocortin I)

Seq. No.	230337
Seq. ID	LIB3196-056-P1-M1-F2
Method	BLASTX
NCBI GI	g113944
BLAST score	434
E value	5.0e-43
Match length	100
% identity	88
NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi_71756_pir__LUHU annexin I - human >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I (lipocortin I)

Seq. No.	230338
Seq. ID	LIB3196-056-P1-M1-F3
Method	BLASTX
NCBI GI	g2832237
BLAST score	469
E value	4.0e-47
Match length	122
% identity	84
NCBI Description	(AF022655) cep250 centrosome associated protein [Homo sapiens]

Seq. No.	230339
Seq. ID	LIB3196-056-P1-M1-F5
Method	BLASTX
NCBI GI	g130224
BLAST score	645
E value	8.0e-68
Match length	124
% identity	56
NCBI Description	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148) >gi_89333_pir__S00666 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) isozyme II - bovine >gi_639_emb_CAA68406_ (Y00301) phosphatidylinositol-specific phospholipase C. [Bos taurus] >gi_225974_prf__1404383A phospholipase C [Bos taurus]

Seq. No.	230340
Seq. ID	LIB3196-056-P1-M1-F6
Method	BLASTX
NCBI GI	g4193388
BLAST score	306
E value	3.0e-28
Match length	61
% identity	93
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	230341
Seq. ID	LIB3196-056-P1-M1-F7
Method	BLASTX
NCBI GI	g137578
BLAST score	446
E value	7.0e-50
Match length	115
% identity	94
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230342
Seq. ID	LIB3196-056-P1-M1-G10
Method	BLASTX
NCBI GI	g2088662
BLAST score	211
E value	6.0e-17
Match length	102
% identity	48
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	230343
Seq. ID	LIB3196-056-P1-M1-G12
Method	BLASTX
NCBI GI	g2507222
BLAST score	152
E value	5.0e-10
Match length	60
% identity	47
NCBI Description	KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi_1709236 (U09505) kinase associated protein phosphatase [Arabidopsis thaliana]

Seq. No.	230344
Seq. ID	LIB3196-056-P1-M1-H1
Method	BLASTX
NCBI GI	g2213425
BLAST score	150
E value	5.0e-10
Match length	76
% identity	28
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]

Seq. No.	230345
Seq. ID	LIB3196-057-P1-M1-A10
Method	BLASTX
NCBI GI	g113001
BLAST score	585
E value	9.0e-61
Match length	120
% identity	5
NCBI Description	ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1) >gi_106081_pir__A37098 gelation factor ABP-280, long form - human >gi_28243_emb_CAA37495_ (X53416) actin-binding protein [Homo sapiens] >gi_4503745_ref_NP_001447.1_pFLNA_ filamin 1 (actin-binding protein-280)

Seq. No.	230346
Seq. ID	LIB3196-057-P1-M1-A11
Method	BLASTX
NCBI GI	g137578
BLAST score	362
E value	3.0e-37
Match length	115
% identity	82
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230347
Seq. ID	LIB3196-057-P1-M1-A2
Method	BLASTX
NCBI GI	g595768
BLAST score	160
E value	2.0e-11
Match length	51
% identity	59
NCBI Description	(U13866) non-functional lacZ alpha peptide [Cloning vector]

Seq. No.	230348
Seq. ID	LIB3196-057-P1-M1-A5
Method	BLASTX
NCBI GI	g1864017
BLAST score	591
E value	2.0e-61
Match length	114
% identity	99
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	230349
Seq. ID	LIB3196-057-P1-M1-A6
Method	BLASTX
NCBI GI	g1070465
BLAST score	678
E value	1.0e-71

Match length	136
% identity	99
NCBI Description	protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13), epidermal - human >gi_186790 (M55183) protein-glutamine gamma-glutamyltransferase [Homo sapiens] >gi_219632_dbj_BAA14329_ (D90287) transglutaminase [Homo sapiens] >gi_1256959 (M98447) keratinocyte transglutaminase [Homo sapiens] >gi_3868760_dbj_BAA34203_ (D10353) transglutaminase 1 [Homo sapiens] >gi_4507475_ref_NP_000350.1_pTGM1_ transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)
Seq. No.	230350
Seq. ID	LIB3196-057-P1-M1-B1
Method	BLASTX
NCBI GI	g3183031
BLAST score	238
E value	4.0e-20
Match length	122
% identity	48
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4H (EIF-4H) (KIAA0038) >gi_2914759 (AF045555) wbscr1 [Homo sapiens]
Seq. No.	230351
Seq. ID	LIB3196-057-P1-M1-B11
Method	BLASTX
NCBI GI	g2117743
BLAST score	525
E value	1.0e-53
Match length	121
% identity	85
NCBI Description	glutathione transferase (EC 2.5.1.18) A3 - human (fragment) >gi_951352 (L13275) glutathione S-transferase A3 [Homo sapiens]
Seq. No.	230352
Seq. ID	LIB3196-057-P1-M1-B12
Method	BLASTX
NCBI GI	g1769895
BLAST score	471
E value	2.0e-47
Match length	127
% identity	69
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]
Seq. No.	230353
Seq. ID	LIB3196-057-P1-M1-B4
Method	BLASTX
NCBI GI	g4191344
BLAST score	541
E value	1.0e-55
Match length	131
% identity	83
NCBI Description	(AF085199) golgin-84 [Homo sapiens]
Seq. No.	230354

Seq. ID	LIB3196-057-P1-M1-B5
Method	BLASTX
NCBI GI	g3319958
BLAST score	335
E value	2.0e-31
Match length	250
% identity	10
NCBI Description	(AJ228139) VAKTI precursor [Homo sapiens]

Seq. No.	230355
Seq. ID	LIB3196-057-P1-M1-B7
Method	BLASTX
NCBI GI	g3122072
BLAST score	531
E value	2.0e-54
Match length	105
% identity	96
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]

Seq. No.	230356
Seq. ID	LIB3196-057-P1-M1-C10
Method	BLASTX
NCBI GI	g485514
BLAST score	441
E value	7.0e-44
Match length	93
% identity	88
NCBI Description	ADR11-2 protein - soybean (fragment) >gi_296443_emb_CAA49341_ (X69640) auxin down regulated [Glycine max]

Seq. No.	230357
Seq. ID	LIB3196-057-P1-M1-C2
Method	BLASTX
NCBI GI	g3876865
BLAST score	142
E value	7.0e-09
Match length	91
% identity	34
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	230358
Seq. ID	LIB3196-057-P1-M1-C3
Method	BLASTX
NCBI GI	g2979551
BLAST score	139
E value	7.0e-09
Match length	67
% identity	52
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	230359
Seq. ID	LIB3196-057-P1-M1-D1
Method	BLASTX
NCBI GI	g167367
BLAST score	282
E value	1.0e-25
Match length	74
% identity	74
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230360
Seq. ID	LIB3196-057-P1-M1-D12
Method	BLASTX
NCBI GI	g3758821
BLAST score	554
E value	4.0e-57
Match length	128
% identity	88
NCBI Description	(AJ011896) Naf1 beta protein [Homo sapiens]

Seq. No.	230361
Seq. ID	LIB3196-057-P1-M1-D3
Method	BLASTX
NCBI GI	g2119533
BLAST score	584
E value	1.0e-60
Match length	116
% identity	98
NCBI Description	giantin - human >gi_808869_dbj_BAA05025_ (D25542) human gcp372 [Homo sapiens]

Seq. No.	230362
Seq. ID	LIB3196-057-P1-M1-D4
Method	BLASTX
NCBI GI	g1049084
BLAST score	282
E value	3.0e-25
Match length	54
% identity	89
NCBI Description	(U30828) SRp55-2 [Homo sapiens]

Seq. No.	230363
Seq. ID	LIB3196-057-P1-M1-D5
Method	BLASTX
NCBI GI	g996057
BLAST score	505
E value	3.0e-51
Match length	97
% identity	97
NCBI Description	(X90872) associated to Golgi apparatus [Homo sapiens]

Seq. No.	230364
Seq. ID	LIB3196-057-P1-M1-D6
Method	BLASTX
NCBI GI	g2951931
BLAST score	543

E value	9.0e-56
Match length	129
% identity	84
NCBI Description	(U55206) human gamma-glutamyl hydrolase [Homo sapiens] >gi_4503987_ref_NP_003869.1_pGGH_ UNKNOWN

Seq. No.	230365
Seq. ID	LIB3196-057-P1-M1-D7
Method	BLASTX
NCBI GI	g167367
BLAST score	384
E value	3.0e-37
Match length	88
% identity	84
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230366
Seq. ID	LIB3196-057-P1-M1-E11
Method	BLASTX
NCBI GI	g464986
BLAST score	526
E value	8.0e-54
Match length	99
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	230367
Seq. ID	LIB3196-057-P1-M1-E12
Method	BLASTX
NCBI GI	g2459928
BLAST score	285
E value	2.0e-25
Match length	71
% identity	77
NCBI Description	(AF007189) claudin 3 [Homo sapiens] >gi_2570129_dbj_BAA22986_ (AB000714) RVP1 [Homo sapiens] >gi_4502875_ref_NP_001297.1_pCLDN3_ Clostridium perfringens enterotoxin receptor

Seq. No.	230368
Seq. ID	LIB3196-057-P1-M1-E2
Method	BLASTX
NCBI GI	g3023847
BLAST score	465
E value	1.0e-46
Match length	97
% identity	49

NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]
Seq. No.	230369
Seq. ID	LIB3196-057-P1-M1-E3
Method	BLASTX
NCBI GI	g2652938
BLAST score	567
E value	1.0e-58
Match length	116
% identity	54
NCBI Description	(Z47554) orf [Zea mays]
Seq. No.	230370
Seq. ID	LIB3196-057-P1-M1-E7
Method	BLASTX
NCBI GI	g4557067
BLAST score	329
E value	1.0e-30
Match length	127
% identity	47
NCBI Description	(AC007045) putative pol polyprotein [Arabidopsis thaliana]
Seq. No.	230371
Seq. ID	LIB3196-057-P1-M1-E8
Method	BLASTX
NCBI GI	g306926
BLAST score	190
E value	1.0e-14
Match length	57
% identity	61
NCBI Description	(M69241) insulin-like growth factor binding protein 2 [Homo sapiens]
Seq. No.	230372
Seq. ID	LIB3196-057-P1-M1-E9
Method	BLASTX
NCBI GI	g1083762
BLAST score	356
E value	7.0e-34
Match length	106
% identity	69
NCBI Description	prolactin-induced T cell protein c15 - rat >gi_619907_emb_CAA57825_ (X82445) RnudC [Rattus norvegicus]
Seq. No.	230373
Seq. ID	LIB3196-057-P1-M1-F1
Method	BLASTX
NCBI GI	g2605714
BLAST score	345
E value	1.0e-32
Match length	87
% identity	79
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	230374
Seq. ID	LIB3196-057-P1-M1-F10
Method	BLASTX
NCBI GI	g136471
BLAST score	249
E value	2.0e-21
Match length	112
% identity	53
NCBI Description	TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR-INDUCIBLE NUCLEAR PROTEIN NUP475) >gi_423132_pir__S34427 tristetraproline protein - human >gi_183443 (M92843) zinc finger transcriptional regulator [Homo sapiens] >gi_183445 (M92844) zinc finger transcriptional regulator [Homo sapiens] >gi_340013 (M63625) tristetraproline [Homo sapiens] >gi_4507961_ref_NP_003398.1_pZFP36_ zinc finger protein homologous to Zfp-36 in mouse

Seq. No.	230375
Seq. ID	LIB3196-057-P1-M1-F12
Method	BLASTX
NCBI GI	g266690
BLAST score	378
E value	2.0e-36
Match length	106
% identity	74
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	230376
Seq. ID	LIB3196-057-P1-M1-F3
Method	BLASTX
NCBI GI	g3914962
BLAST score	600
E value	2.0e-62
Match length	130
% identity	88
NCBI Description	SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 >gi_2232241 (AF005038) secretory carrier membrane protein [Homo sapiens]

Seq. No.	230377
Seq. ID	LIB3196-057-P1-M1-F4
Method	BLASTX
NCBI GI	g3123515
BLAST score	608
E value	2.0e-63
Match length	125
% identity	94
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	230378
Seq. ID	LIB3196-057-P1-M1-F6
Method	BLASTX
NCBI GI	g1083308
BLAST score	207

E value	2.0e-16
Match length	42
% identity	95
NCBI Description	enhancer-trap-locus-1 protein - mouse (fragment) >gi_50866_emb_CAA49560_ (X69942) enhancer-trap-locus-1 [Mus musculus]

Seq. No.	230379
Seq. ID	LIB3196-057-P1-M1-F7
Method	BLASTX
NCBI GI	g266691
BLAST score	201
E value	7.0e-16
Match length	80
% identity	56
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	230380
Seq. ID	LIB3196-057-P1-M1-F8
Method	BLASTX
NCBI GI	g2114014
BLAST score	149
E value	1.0e-09
Match length	99
% identity	42
NCBI Description	(Z95558) hypothetical protein Rv0552 [Mycobacterium tuberculosis]

Seq. No.	230381
Seq. ID	LIB3196-057-P1-M1-F9
Method	BLASTX
NCBI GI	g88052
BLAST score	190
E value	2.0e-14
Match length	99
% identity	45
NCBI Description	keratin K5, 58K type II, epidermal (version 2) - human (fragment)

Seq. No.	230382
Seq. ID	LIB3196-057-P1-M1-G1
Method	BLASTX
NCBI GI	g3283166
BLAST score	287
E value	9.0e-26
Match length	110
% identity	54
NCBI Description	(AF057526) erythrocyte membrane protein Rh50 [Mus musculus] >gi_3329467 (AF065395) Rh50-like protein [Mus musculus] >gi_3445508_dbj_BAA32441_ (AB015192) 50 kD glycoprotein (Rh50) [Mus musculus]

Seq. No.	230383
Seq. ID	LIB3196-057-P1-M1-G11
Method	BLASTX
NCBI GI	g1363944

BLAST score	671
E value	8.0e-71
Match length	133
% identity	99
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230384
Seq. ID	LIB3196-057-P1-M1-G2
Method	BLASTX
NCBI GI	g226120
BLAST score	557
E value	2.0e-57
Match length	108
% identity	100
NCBI Description	vicilin gene B [Saguinus oedipus]

Seq. No.	230385
Seq. ID	LIB3196-057-P1-M1-G3
Method	BLASTX
NCBI GI	g2623297
BLAST score	229
E value	5.0e-19
Match length	99
% identity	43
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana]

Seq. No.	230386
Seq. ID	LIB3196-057-P1-M1-G4
Method	BLASTX
NCBI GI	g2136462
BLAST score	698
E value	6.0e-74
Match length	136
% identity	99
NCBI Description	ribosomal protein S3a - cat (fragment) >gi_950113 (U22231) ribosomal protein S3a [Felis catus]

Seq. No.	230387
Seq. ID	LIB3196-057-P1-M1-G9
Method	BLASTX
NCBI GI	g2245077
BLAST score	358
E value	4.0e-34
Match length	118
% identity	54
NCBI Description	(Z97343) glucanase homolog [Arabidopsis thaliana]

Seq. No.	230388
Seq. ID	LIB3196-057-P1-M1-H11
Method	BLASTX
NCBI GI	g1856971
BLAST score	396
E value	1.0e-38

Match length	83
% identity	90
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	230389
Seq. ID	LIB3196-057-P1-M1-H12
Method	BLASTX
NCBI GI	g1171978
BLAST score	513
E value	3.0e-52
Match length	129
% identity	24
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	230390
Seq. ID	LIB3196-057-P1-M1-H5
Method	BLASTX
NCBI GI	g3941736
BLAST score	165
E value	2.0e-11
Match length	77
% identity	48
NCBI Description	(AF109719) BAT3 [Mus musculus]

Seq. No.	230391
Seq. ID	LIB3196-057-P1-M1-H6
Method	BLASTX
NCBI GI	g4104976
BLAST score	281
E value	3.0e-25
Match length	55
% identity	100
NCBI Description	(AF043117) ubiquitin-fusion degradation protein 2 [Homo sapiens]

Seq. No.	230392
Seq. ID	LIB3196-057-P1-M1-H9
Method	BLASTX
NCBI GI	g2137308
BLAST score	529
E value	4.0e-54
Match length	105
% identity	38
NCBI Description	G protein beta subuit like - mouse >gi_475012_dbj_BAA06185_ (D29802) G protein beta subuit like [Mus musculus]

Seq. No.	230393
Seq. ID	LIB3196-058-P1-M1-A1
Method	BLASTX
NCBI GI	g1350680
BLAST score	185
E value	8.0e-14

Match length	40
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	230394
Seq. ID	LIB3196-058-P1-M1-A10
Method	BLASTX
NCBI GI	g399940
BLAST score	533
E value	9.0e-55
Match length	111
% identity	95
NCBI Description	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	230395
Seq. ID	LIB3196-058-P1-M1-A11
Method	BLASTX
NCBI GI	g2505876
BLAST score	341
E value	4.0e-32
Match length	94
% identity	72
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	230396
Seq. ID	LIB3196-058-P1-M1-A12
Method	BLASTX
NCBI GI	g228316
BLAST score	189
E value	7.0e-15
Match length	61
% identity	64
NCBI Description	albumin [Theobroma cacao]

Seq. No.	230397
Seq. ID	LIB3196-058-P1-M1-A3
Method	BLASTX
NCBI GI	g1518540
BLAST score	592
E value	1.0e-61
Match length	125
% identity	89
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	230398
Seq. ID	LIB3196-058-P1-M1-A7
Method	BLASTX
NCBI GI	g3650030
BLAST score	252
E value	1.0e-21
Match length	105
% identity	55
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	230399
Seq. ID	LIB3196-058-P1-M1-A8
Method	BLASTX
NCBI GI	g266691
BLAST score	314
E value	5.0e-29
Match length	100
% identity	67
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	230400
Seq. ID	LIB3196-058-P1-M1-A9
Method	BLASTX
NCBI GI	g3273089
BLAST score	639
E value	5.0e-67
Match length	129
% identity	99
NCBI Description	(Y16610) paraplegin [Homo sapiens] >gi_4507173_ref_NP_003110.1_pSPG7_ spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)

Seq. No.	230401
Seq. ID	LIB3196-058-P1-M1-B1
Method	BLASTX
NCBI GI	g2995405
BLAST score	459
E value	6.0e-46
Match length	127
% identity	66
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	230402
Seq. ID	LIB3196-058-P1-M1-B10
Method	BLASTX
NCBI GI	g3885884
BLAST score	459
E value	5.0e-46
Match length	114
% identity	78
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	230403
Seq. ID	LIB3196-058-P1-M1-B11
Method	BLASTX
NCBI GI	g1346347
BLAST score	606
E value	3.0e-63
Match length	123
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	230404

Seq. ID	LIB3196-058-P1-M1-B2
Method	BLASTX
NCBI GI	g2662343
BLAST score	553
E value	4.0e-57
Match length	105
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	230405
Seq. ID	LIB3196-058-P1-M1-B3
Method	BLASTX
NCBI GI	g136479
BLAST score	217
E value	6.0e-18
Match length	48
% identity	88
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23) >gi_88948_pir__S06590 IgE-dependent histamine-releasing factor - human >gi_37496_emb_CAA34200_ (X16064) tumor protein (AA 1 - 172) [Homo sapiens] >gi_4507669_ref_NP_003286.1_pTPT1_ tumor protein, translationally-controlled

Seq. No.	230406
Seq. ID	LIB3196-058-P1-M1-B5
Method	BLASTX
NCBI GI	g1346349
BLAST score	318
E value	1.0e-42
Match length	114
% identity	83
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II - human >gi_908805 (L42612) keratin type II [Homo sapiens]

Seq. No.	230407
Seq. ID	LIB3196-058-P1-M1-C1
Method	BLASTX
NCBI GI	g3183316
BLAST score	190
E value	2.0e-14
Match length	88
% identity	44
NCBI Description	HYPOTHETICAL 24.4 KD PROTEIN C16E8.14C IN CHROMOSOME I >gi_2330702_emb_CAB11042_ (Z98529) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	230408
Seq. ID	LIB3196-058-P1-M1-C3
Method	BLASTX
NCBI GI	g207905
BLAST score	537
E value	4.0e-55
Match length	123
% identity	89
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	230409
Seq. ID	LIB3196-058-P1-M1-C6
Method	BLASTX
NCBI GI	g1351867
BLAST score	692
E value	3.0e-73
Match length	129
% identity	100
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi_761724 (U20114) beta-actin [Cricetulus griseus]

Seq. No.	230410
Seq. ID	LIB3196-058-P1-M1-C7
Method	BLASTX
NCBI GI	g2244734
BLAST score	484
E value	6.0e-49
Match length	93
% identity	100
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	230411
Seq. ID	LIB3196-058-P1-M1-D10
Method	BLASTX
NCBI GI	g126156
BLAST score	444
E value	3.0e-44
Match length	123
% identity	72
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	230412
Seq. ID	LIB3196-058-P1-M1-D11
Method	BLASTX
NCBI GI	g225581
BLAST score	269
E value	1.0e-23
Match length	67
% identity	84
NCBI Description	storage protein C94 [Saguinus oedipus]

Seq. No.	230413
Seq. ID	LIB3196-058-P1-M1-D3
Method	BLASTX
NCBI GI	g2118403
BLAST score	308
E value	3.0e-28
Match length	130
% identity	46
NCBI Description	alpha-2-macroglobulin - human (fragment) >gi_177872 (M36501) alpha-2-macroglobulin [Homo sapiens]

Seq. No.	230414
Seq. ID	LIB3196-058-P1-M1-D4
Method	BLASTX
NCBI GI	g732207
BLAST score	159
E value	7.0e-11
Match length	87
% identity	37
NCBI Description	HYPOTHETICAL 75.4 KD PROTEIN IN AUT1-CSE2 INTERGENIC REGION >gi_626466_pir__S45131 probable membrane protein YNR008w - yeast (Saccharomyces cerevisiae) >gi_496725_emb_CAA54576_ (X77395) N2042 [Saccharomyces cerevisiae] >gi_1302482_emb_CAA96285_ (Z71623) ORF YNR008w [Saccharomyces cerevisiae]

Seq. No.	230415
Seq. ID	LIB3196-058-P1-M1-D6
Method	BLASTX
NCBI GI	g3892051
BLAST score	504
E value	3.0e-51
Match length	110
% identity	84
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	230416
Seq. ID	LIB3196-058-P1-M1-E1
Method	BLASTX
NCBI GI	g2317905
BLAST score	178
E value	5.0e-13
Match length	115
% identity	41
NCBI Description	(U89959) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	230417
Seq. ID	LIB3196-058-P1-M1-E10
Method	BLASTX
NCBI GI	g225581
BLAST score	656
E value	4.0e-69
Match length	122
% identity	100
NCBI Description	storage protein C94 [Saguinus oedipus]

Seq. No.	230418
Seq. ID	LIB3196-058-P1-M1-E11
Method	BLASTX
NCBI GI	g167367
BLAST score	395
E value	2.0e-38
Match length	106
% identity	73
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230419
Seq. ID	LIB3196-058-P1-M1-E6
Method	BLASTX
NCBI GI	g135098
BLAST score	597
E value	3.0e-62
Match length	117
% identity	97
NCBI Description	ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) >gi_68530_pir__SYHUDT aspartate--tRNA ligase (EC 6.1.1.12) - human >gi_179102 (J05032) aspartyl-tRNA synthetase [Homo sapiens] >gi_4557513_ref_NP_001340.1_pDARS_ aspartyl-tRNA synthetase

Seq. No.	230420
Seq. ID	LIB3196-058-P1-M1-E7
Method	BLASTX
NCBI GI	g1373125
BLAST score	285
E value	1.0e-25
Match length	103
% identity	59
NCBI Description	(U43709) similar to the metB gene product of Escherichia coli; cloned by functional complementation of a metB mutant strain of Escherichia coli LE392 [Arabidopsis thaliana]

Seq. No.	230421
Seq. ID	LIB3196-058-P1-M1-E8
Method	BLASTX
NCBI GI	g1076389
BLAST score	217
E value	1.0e-17
Match length	48
% identity	48
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	230422
Seq. ID	LIB3196-058-P1-M1-F4
Method	BLASTX
NCBI GI	g4510363
BLAST score	289
E value	4.0e-26
Match length	68
% identity	81
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	230423
Seq. ID	LIB3196-058-P1-M1-F6
Method	BLASTX
NCBI GI	g167359
BLAST score	161
E value	4.0e-11
Match length	100
% identity	39

NCBI Description	(M86213) 2S albumin storage protein [Gossypium hirsutum] >gi_444334_prf__1906383A 2S albumin [Gossypium hirsutum]
Seq. No.	230424
Seq. ID	LIB3196-058-P1-M1-F7
Method	BLASTX
NCBI GI	g3746127
BLAST score	428
E value	2.0e-42
Match length	106
% identity	76
NCBI Description	(U76253) E25B protein [Mus musculus]
Seq. No.	230425
Seq. ID	LIB3196-058-P1-M1-F9
Method	BLASTX
NCBI GI	g1703108
BLAST score	586
E value	7.0e-61
Match length	120
% identity	95
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307_(U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]
Seq. No.	230426
Seq. ID	LIB3196-058-P1-M1-G4
Method	BLASTX
NCBI GI	g3063643
BLAST score	605
E value	4.0e-63
Match length	121
% identity	92
NCBI Description	(AF056622) putative Cu/Zn superoxide dismutase precursor [Vitis vinifera]
Seq. No.	230427
Seq. ID	LIB3196-058-P1-M1-G7
Method	BLASTX
NCBI GI	g1169228
BLAST score	169
E value	3.0e-12
Match length	43
% identity	81
NCBI Description	RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639 helicase-like protein - Wood tobacco >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris]
Seq. No.	230428
Seq. ID	LIB3196-058-P1-M1-G9
Method	BLASTX
NCBI GI	g585922
BLAST score	348
E value	6.0e-33

Match length	85
% identity	78
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN

Seq. No.	230429
Seq. ID	LIB3196-058-P1-M1-H1
Method	BLASTX
NCBI GI	g747900
BLAST score	180
E value	2.0e-13
Match length	48
% identity	58
NCBI Description	(Z48758) unknown [Saccharomyces cerevisiae]

Seq. No.	230430
Seq. ID	LIB3196-058-P1-M1-H10
Method	BLASTX
NCBI GI	g3935151
BLAST score	497
E value	2.0e-50
Match length	118
% identity	73
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	230431
Seq. ID	LIB3196-058-P1-M1-H2
Method	BLASTX
NCBI GI	g137578
BLAST score	612
E value	6.0e-64
Match length	118
% identity	98
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230432
Seq. ID	LIB3196-058-P1-M1-H3
Method	BLASTX
NCBI GI	g585966
BLAST score	529
E value	4.0e-54
Match length	106
% identity	92
NCBI Description	AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) >gi_2135787_pir__A49585 Na+ channel protein, amiloride-sensitive - human >gi_452650_emb_CAA53773_ (X76180) Na+ channel protein [Homo sapiens] >gi_493605 (L29007) Na+ channel [Homo sapiens] >gi_2765702_emb_CAB07505_ (Z92978) amiloride-sensitive epithelial sodium channel alpha subunit [Homo sapiens] >gi_744560_prf__2015190A amiloride-sensitive Na channel

[Homo sapiens] >gi_4506815_ref_NP_001029.1_pSCNN1A_ sodium channel, nonvoltage-gated 1 alpha >gi_4507057_ref_NP_003038.1_pSLC9A1_ solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)

Seq. No.	230433
Seq. ID	LIB3196-058-P1-M1-H4
Method	BLASTX
NCBI GI	g207905
BLAST score	544
E value	6.0e-56
Match length	127
% identity	86
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	230434
Seq. ID	LIB3196-059-P1-M1-A1
Method	BLASTX
NCBI GI	g3184184
BLAST score	261
E value	5.0e-23
Match length	74
% identity	76
NCBI Description	(AB002134) airway trypsin-like protease [Homo sapiens]

Seq. No.	230435
Seq. ID	LIB3196-059-P1-M1-A10
Method	BLASTX
NCBI GI	g3063396
BLAST score	399
E value	5.0e-39
Match length	93
% identity	81
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	230436
Seq. ID	LIB3196-059-P1-M1-A5
Method	BLASTX
NCBI GI	g2506802
BLAST score	573
E value	2.0e-59
Match length	118
% identity	96
NCBI Description	THYMIDYLATE KINASE (DTMP KINASE)

Seq. No.	230437
Seq. ID	LIB3196-059-P1-M1-A6
Method	BLASTX
NCBI GI	g4432846
BLAST score	306
E value	4.0e-28
Match length	115
% identity	66
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 230438

09604060.960304

Seq. ID	LIB3196-059-P1-M1-A8
Method	BLASTX
NCBI GI	g117759
BLAST score	201
E value	3.0e-16
Match length	44
% identity	95
NCBI Description	CYTOCHROME C1, HEME PROTEIN PRECURSOR >gi_181240 (J04444) cytochrome c-1 [Homo sapiens]

Seq. No.	230439
Seq. ID	LIB3196-059-P1-M1-A9
Method	BLASTX
NCBI GI	g2443320
BLAST score	360
E value	1.0e-34
Match length	87
% identity	83
NCBI Description	(D85597) polyprotein [Oryza australiensis]

Seq. No.	230440
Seq. ID	LIB3196-059-P1-M1-B10
Method	BLASTX
NCBI GI	g1843527
BLAST score	404
E value	1.0e-39
Match length	110
% identity	75
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	230441
Seq. ID	LIB3196-059-P1-M1-B12
Method	BLASTX
NCBI GI	g167367
BLAST score	445
E value	2.0e-44
Match length	116
% identity	75
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230442
Seq. ID	LIB3196-059-P1-M1-B3
Method	BLASTX
NCBI GI	g2118384
BLAST score	584
E value	1.0e-60
Match length	127
% identity	91
NCBI Description	squamous cell carcinoma antigen 2 - human

Seq. No.	230443
Seq. ID	LIB3196-059-P1-M1-B8
Method	BLASTX
NCBI GI	g2118965
BLAST score	510
E value	6.0e-52
Match length	105

% identity	31
NCBI Description	polyubiquitin - bovine (fragment) >gi_163573 (M62428) polyubiquitin [Bos taurus]

Seq. No.	230444
Seq. ID	LIB3196-059-P1-M1-C10
Method	BLASTX
NCBI GI	g2213867
BLAST score	517
E value	7.0e-53
Match length	111
% identity	89
NCBI Description	(AF003124) fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Seq. No.	230445
Seq. ID	LIB3196-059-P1-M1-C11
Method	BLASTX
NCBI GI	g120668
BLAST score	351
E value	2.0e-33
Match length	84
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82399_pir__A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var. distichum]

Seq. No.	230446
Seq. ID	LIB3196-059-P1-M1-C12
Method	BLASTX
NCBI GI	g3850816
BLAST score	352
E value	2.0e-33
Match length	69
% identity	91
NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	230447
Seq. ID	LIB3196-059-P1-M1-C2
Method	BLASTX
NCBI GI	g2605714
BLAST score	382
E value	6.0e-37
Match length	99
% identity	77
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	230448
Seq. ID	LIB3196-059-P1-M1-C5
Method	BLASTX
NCBI GI	g602076

BLAST score	581
E value	2.0e-60
Match length	119
% identity	23
NCBI Description	(X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No.	230449
Seq. ID	LIB3196-059-P1-M1-C6
Method	BLASTX
NCBI GI	g137578
BLAST score	230
E value	1.0e-19
Match length	62
% identity	77
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230450
Seq. ID	LIB3196-059-P1-M1-C7
Method	BLASTX
NCBI GI	g1223926
BLAST score	144
E value	4.0e-09
Match length	110
% identity	34
NCBI Description	(U49741) Vigna radiata carboxypeptidase II mRNA, partial cds [Vigna radiata]

Seq. No.	230451
Seq. ID	LIB3196-059-P1-M1-D1
Method	BLASTX
NCBI GI	g1263291
BLAST score	496
E value	2.0e-50
Match length	95
% identity	99
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	230452
Seq. ID	LIB3196-059-P1-M1-D10
Method	BLASTX
NCBI GI	g1346344
BLAST score	602
E value	9.0e-63
Match length	123
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II - human >gi_908779 (L42583) keratin type II [Homo sapiens]

Seq. No.	230453
Seq. ID	LIB3196-059-P1-M1-D2
Method	BLASTX

NCBI GI	g2129727
BLAST score	163
E value	2.0e-11
Match length	97
% identity	42
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	230454
Seq. ID	LIB3196-059-P1-M1-D4
Method	BLASTX
NCBI GI	g416922
BLAST score	322
E value	6.0e-30
Match length	103
% identity	65
NCBI Description	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP pyrophosphatase (EC 3.6.1.23) - tomato >gi_251897_bbs_109276 (S40549) deoxyuridine triphosphatase, dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No.	230455
Seq. ID	LIB3196-059-P1-M1-D5
Method	BLASTX
NCBI GI	g2605714
BLAST score	309
E value	2.0e-28
Match length	79
% identity	78
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	230456
Seq. ID	LIB3196-059-P1-M1-D6
Method	BLASTX
NCBI GI	g2578033
BLAST score	630
E value	4.0e-66
Match length	120
% identity	98
NCBI Description	(X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No.	230457
Seq. ID	LIB3196-059-P1-M1-D8
Method	BLASTX
NCBI GI	g2781363
BLAST score	164
E value	2.0e-11
Match length	64
% identity	53
NCBI Description	(AC003113) F24O1.19 [Arabidopsis thaliana]

Seq. No.	230458
Seq. ID	LIB3196-059-P1-M1-D9
Method	BLASTX

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NCBI GI	g132659
BLAST score	147
E value	2.0e-09
Match length	80
% identity	45
NCBI Description	50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13) >gi_81483_pir__A32033 ribosomal protein L13 precursor, chloroplast - spinach >gi_170133 (J04461) ribosomal protein L13 [Spinacia oleracea]

Seq. No.	230459
Seq. ID	LIB3196-059-P1-M1-E1
Method	BLASTX
NCBI GI	g206440
BLAST score	539
E value	2.0e-55
Match length	103
% identity	99
NCBI Description	(M62752) statin-related protein [Rattus norvegicus]

Seq. No.	230460
Seq. ID	LIB3196-059-P1-M1-E10
Method	BLASTX
NCBI GI	g2982453
BLAST score	504
E value	3.0e-51
Match length	119
% identity	82
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	230461
Seq. ID	LIB3196-059-P1-M1-E11
Method	BLASTX
NCBI GI	g2498323
BLAST score	412
E value	2.0e-40
Match length	98
% identity	82
NCBI Description	EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) >gi_1488324 (U65932) extracellular matrix protein 1 [Homo sapiens] >gi_1488332 (U65938) extracellular matrix protein 1 [Homo sapiens] >gi_2654433 (U68186) extracellular matrix protein 1 [Homo sapiens]

Seq. No.	230462
Seq. ID	LIB3196-059-P1-M1-E4
Method	BLASTX
NCBI GI	g542184
BLAST score	219
E value	7.0e-18
Match length	117
% identity	41
NCBI Description	globulin-1S, GLB1S - maize

Seq. No.	230463
Seq. ID	LIB3196-059-P1-M1-E6

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Method	BLASTX
NCBI GI	g3915830
BLAST score	626
E value	1.0e-65
Match length	127
% identity	95
NCBI Description	REP-8 PROTEIN (D8S2298E) >gi_1913785_dbj_BAA18958_ (D83767) Rep-8 [Homo sapiens]

Seq. No.	230464
Seq. ID	LIB3196-059-P1-M1-E8
Method	BLASTX
NCBI GI	g2497938
BLAST score	571
E value	8.0e-60
Match length	123
% identity	97
NCBI Description	AQUAPORIN 3 >gi_1854374_dbj_BAA19237_ (AB001325) aquaporin 3 [Homo sapiens]

Seq. No.	230465
Seq. ID	LIB3196-059-P1-M1-E9
Method	BLASTX
NCBI GI	g283971
BLAST score	648
E value	4.0e-68
Match length	126
% identity	97
NCBI Description	aldehyde dehydrogenase (NAD(P)+) (EC 1.2.1.5) 3 - human >gi_178375 (M77477) aldehyde dehydrogenase [Homo sapiens] >gi_300402_bbs_132241 (S61044) aldehyde dehydrogenase isozyme 3, ALDH3 {EC 1.2.1.3} [human, stomach, Peptide, 453 aa] [Homo sapiens]

Seq. No.	230466
Seq. ID	LIB3196-059-P1-M1-F1
Method	BLASTX
NCBI GI	g1199772
BLAST score	218
E value	9.0e-18
Match length	45
% identity	87
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No.	230467
Seq. ID	LIB3196-059-P1-M1-F12
Method	BLASTX
NCBI GI	g4454026
BLAST score	326
E value	2.0e-30
Match length	94
% identity	69
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	230468

09604704.090698

Seq. ID	LIB3196-059-P1-M1-F2
Method	BLASTX
NCBI GI	g137578
BLAST score	509
E value	7.0e-52
Match length	100
% identity	96
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230469
Seq. ID	LIB3196-059-P1-M1-F3
Method	BLASTX
NCBI GI	g804996
BLAST score	297
E value	6.0e-27
Match length	61
% identity	90
NCBI Description	(Z49216) mitoxantrone-resistance associated gene [Homo sapiens]

Seq. No.	230470
Seq. ID	LIB3196-059-P1-M1-F5
Method	BLASTX
NCBI GI	g346219
BLAST score	214
E value	3.0e-17
Match length	77
% identity	62
NCBI Description	keratin K4a - human (fragment)

Seq. No.	230471
Seq. ID	LIB3196-059-P1-M1-F6
Method	BLASTX
NCBI GI	g3599491
BLAST score	234
E value	1.0e-19
Match length	55
% identity	78
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	230472
Seq. ID	LIB3196-059-P1-M1-F7
Method	BLASTX
NCBI GI	g3445210
BLAST score	342
E value	3.0e-32
Match length	108
% identity	57
NCBI Description	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 230473

Seq. ID	LIB3196-059-P1-M1-F9
Method	BLASTX
NCBI GI	g1083762
BLAST score	293
E value	2.0e-26
Match length	57
% identity	98
NCBI Description	prolactin-induced T cell protein c15 - rat >gi_619907_emb_CAA57825_ (X82445) RnudC [Rattus norvegicus]

Seq. No.	230474
Seq. ID	LIB3196-059-P1-M1-G1
Method	BLASTX
NCBI GI	g477138
BLAST score	365
E value	6.0e-35
Match length	71
% identity	94
NCBI Description	carcinoma-associated antigen GA733-1 precursor - human >gi_31591_emb_CAA31781_ (X13425) GA733-1 protein (AA 1-323) [Homo sapiens]

Seq. No.	230475
Seq. ID	LIB3196-059-P1-M1-G11
Method	BLASTX
NCBI GI	g4455287
BLAST score	284
E value	2.0e-25
Match length	97
% identity	56
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	230476
Seq. ID	LIB3196-059-P1-M1-G12
Method	BLASTX
NCBI GI	g137578
BLAST score	273
E value	2.0e-42
Match length	95
% identity	90
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230477
Seq. ID	LIB3196-059-P1-M1-G4
Method	BLASTX
NCBI GI	g3122072
BLAST score	522
E value	2.0e-53
Match length	104
% identity	96
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation

	factor 1 alpha - chicken >gi_488468 (L00677) elongation factor 1 alpha [Gallus gallus]
Seq. No.	230478
Seq. ID	LIB3196-059-P1-M1-G6
Method	BLASTX
NCBI GI	g126156
BLAST score	308
E value	2.0e-28
Match length	110
% identity	64
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]
Seq. No.	230479
Seq. ID	LIB3196-059-P1-M1-G7
Method	BLASTX
NCBI GI	g88044
BLAST score	589
E value	3.0e-61
Match length	125
% identity	96
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]
Seq. No.	230480
Seq. ID	LIB3196-059-P1-M1-G9
Method	BLASTX
NCBI GI	g3158376
BLAST score	234
E value	1.0e-19
Match length	90
% identity	53
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]
Seq. No.	230481
Seq. ID	LIB3196-059-P1-M1-H1
Method	BLASTX
NCBI GI	g1702983
BLAST score	356
E value	6.0e-34
Match length	111
% identity	59
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein [Fragaria ananassa]
Seq. No.	230482
Seq. ID	LIB3196-059-P1-M1-H12
Method	BLASTX

NCBI GI	g207905
BLAST score	543
E value	7.0e-56
Match length	121
% identity	89
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	230483
Seq. ID	LIB3196-059-P1-M1-H2
Method	BLASTX
NCBI GI	g547753
BLAST score	452
E value	4.0e-45
Match length	94
% identity	96
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	230484
Seq. ID	LIB3196-059-P1-M1-H3
Method	BLASTX
NCBI GI	g137578
BLAST score	494
E value	4.0e-50
Match length	116
% identity	84
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230485
Seq. ID	LIB3196-059-P1-M1-H4
Method	BLASTX
NCBI GI	g133041
BLAST score	519
E value	5.0e-53
Match length	101
% identity	99
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi_71137_pir__R5HUP0 acidic ribosomal protein P0 - human >gi_190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041) [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_ ribosomal protein, large, P0

Seq. No.	230486
Seq. ID	LIB3196-059-P1-M1-H9
Method	BLASTX
NCBI GI	g3851636
BLAST score	451
E value	4.0e-45
Match length	103
% identity	83
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206

	muscle - rabbit >gi_91852_pir__S03838 tropomyosin beta, skeletal muscle - mouse >gi_92922_pir__B25073 tropomyosin beta, skeletal muscle - rat >gi_54857_emb_CAA31181_ (X12650) beta-tropomyosin (AA 1-284) [Mus musculus] >gi_202163 (M81086) beta-tropomyosin [Mus musculus] >gi_207497 (L00382) skeletal muscle beta-tropomyosin [Rattus norvegicus] >gi_223122_prf__0510185A tropomyosin beta [Oryctolagus cuniculus]
Seq. No.	229522
Seq. ID	LIB3196-034-P1-M1-F6
Method	BLASTX
NCBI GI	g3859675
BLAST score	176
E value	8.0e-13
Match length	86
% identity	42
NCBI Description	(AL033503) nadh-ubiquinone oxidoreductase [Candida albicans]
Seq. No.	229523
Seq. ID	LIB3196-034-P1-M1-F7
Method	BLASTX
NCBI GI	g2262100
BLAST score	316
E value	1.0e-37
Match length	114
% identity	70
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.	229524
Seq. ID	LIB3196-034-P1-M1-F9
Method	BLASTX
NCBI GI	g3790587
BLAST score	236
E value	7.0e-20
Match length	50
% identity	84
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]
Seq. No.	229525
Seq. ID	LIB3196-034-P1-M1-G1
Method	BLASTX
NCBI GI	g225581
BLAST score	536
E value	5.0e-55
Match length	117
% identity	87
NCBI Description	storage protein C94 [Saguinus oedipus]
Seq. No.	229526
Seq. ID	LIB3196-034-P1-M1-G10
Method	BLASTX
NCBI GI	g3347848
BLAST score	158
E value	1.0e-10

Match length	81
% identity	46
NCBI Description	(AF055666) kinesin light chain 2 [Mus musculus]

Seq. No.	229527
Seq. ID	LIB3196-034-P1-M1-G11
Method	BLASTX
NCBI GI	g267131
BLAST score	178
E value	4.0e-13
Match length	81
% identity	14
NCBI Description	NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN) >gi_423120_pir__A46174 RNA-binding protein TIAR - human >gi_189310 (M96954) nucleolysin TIAR [Homo sapiens] >gi_4507499_ref_NP_003243.1_pTIAL1_ TIA1 cytotoxic granule-associated RNA-binding protein-like

Seq. No.	229528
Seq. ID	LIB3196-034-P1-M1-G12
Method	BLASTX
NCBI GI	g1220196
BLAST score	447
E value	1.0e-44
Match length	90
% identity	94
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	229529
Seq. ID	LIB3196-034-P1-M1-G3
Method	BLASTX
NCBI GI	g547753
BLAST score	420
E value	2.0e-41
Match length	120
% identity	72
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	229530
Seq. ID	LIB3196-034-P1-M1-G4
Method	BLASTX
NCBI GI	g4378765
BLAST score	517
E value	8.0e-53
Match length	102
% identity	97
NCBI Description	(AF115516) orphan G protein-coupled receptor GPR54 [Rattus norvegicus]

Seq. No.	229531
Seq. ID	LIB3196-034-P1-M1-G5
Method	BLASTX
NCBI GI	g4378765
BLAST score	239
E value	2.0e-20
Match length	57
% identity	82

NCBI Description	(AF115516) orphan G protein-coupled receptor GPR54 [Rattus norvegicus]
Seq. No.	229532
Seq. ID	LIB3196-034-P1-M1-G6
Method	BLASTX
NCBI GI	g3211975
BLAST score	190
E value	2.0e-14
Match length	40
% identity	97
NCBI Description	(AF068195) putative glialblastoma cell differentiation-related protein [Homo sapiens]
Seq. No.	229533
Seq. ID	LIB3196-034-P1-M1-G7
Method	BLASTX
NCBI GI	g1842140
BLAST score	209
E value	7.0e-17
Match length	92
% identity	40
NCBI Description	(AB001024) similar to Saccharomyces cerevisiae ORM1 gene: EMBL Accession Number Y08687 [Schizosaccharomyces pombe]
Seq. No.	229534
Seq. ID	LIB3196-034-P1-M1-G9
Method	BLASTX
NCBI GI	g280816
BLAST score	297
E value	4.0e-27
Match length	66
% identity	88
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin
Seq. No.	229535
Seq. ID	LIB3196-034-P1-M1-H12
Method	BLASTX
NCBI GI	g2765366
BLAST score	217
E value	1.0e-17
Match length	81
% identity	47
NCBI Description	(Y14038) putative Ole e 1 protein [Betula pendula]
Seq. No.	229536
Seq. ID	LIB3196-034-P1-M1-H2
Method	BLASTX
NCBI GI	g1399321
BLAST score	478
E value	3.0e-48
Match length	118
% identity	78
NCBI Description	(U41830) MHC class I antigen Mamu B*08 [Macaca mulatta]

Seq. No.	229537
Seq. ID	LIB3196-034-P1-M1-H7
Method	BLASTX
NCBI GI	g464707
BLAST score	246
E value	3.0e-21
Match length	51
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	229538
Seq. ID	LIB3196-034-P1-M1-H8
Method	BLASTX
NCBI GI	g4104681
BLAST score	219
E value	7.0e-18
Match length	45
% identity	98
NCBI Description	(AF038844) MKP-1 like protein tyrosine phosphatase [Homo sapiens]

Seq. No.	229539
Seq. ID	LIB3196-035-P1-M1-A1
Method	BLASTX
NCBI GI	g1351901
BLAST score	390
E value	6.0e-38
Match length	112
% identity	6
NCBI Description	[Segment 2 of 2] NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK (DESMOYOKIN) >gi_897824 (M80899) AHNAK gene product [Homo sapiens]

Seq. No.	229540
Seq. ID	LIB3196-035-P1-M1-A2
Method	BLASTX
NCBI GI	g2497938
BLAST score	467
E value	5.0e-47
Match length	96
% identity	95
NCBI Description	AQUAPORIN 3 >gi_1854374_dbj_BAA19237_ (AB001325) aquaporin

3 [Homo sapiens]

Seq. No.	229541
Seq. ID	LIB3196-035-P1-M1-A3
Method	BLASTX
NCBI GI	g2072023
BLAST score	276
E value	2.0e-24
Match length	83
% identity	71
NCBI Description	(U93506) symbiosis-related protein [Laccaria bicolor]

Seq. No.	229542
Seq. ID	LIB3196-035-P1-M1-A4
Method	BLASTX
NCBI GI	g2497487
BLAST score	415
E value	9.0e-41
Match length	89
% identity	90
NCBI Description	UMP-CMP KINASE (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) >gi_1085437_pir__JC4181 cytidylate kinase (EC 2.7.4.14) - pig >gi_893400_dbj_BAA06130_ (D29655) UMP-CMP kinase [Sus scrofa] >gi_1096714_prf__2112267A UMP-CMP kinase [Sus scrofa domestica]

Seq. No.	229543
Seq. ID	LIB3196-035-P1-M1-A6
Method	BLASTX
NCBI GI	g728835
BLAST score	157
E value	3.0e-14
Match length	88
% identity	9
NCBI Description	ALU SUBFAMILY SC WARNING ENTRY !!!!

Seq. No.	229544
Seq. ID	LIB3196-035-P1-M1-A7
Method	BLASTX
NCBI GI	g137578
BLAST score	342
E value	2.0e-32
Match length	102
% identity	72
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229545
Seq. ID	LIB3196-035-P1-M1-C10
Method	BLASTX
NCBI GI	g1706379
BLAST score	338
E value	9.0e-32

Match length	69
% identity	94
NCBI Description	FATTY ALDEHYDE DEHYDROGENASE (ALDEHYDE DEHYDROGENASE, MICROSOMAL) (CLASS 3) >gi_1082036 (L47162) fatty aldehyde dehydrogenase [Homo sapiens] >gi_1666530 (U75297) fatty aldehyde dehydrogenase [Homo sapiens] >gi_1870244 (U46689) aldehyde dehydrogenase [Homo sapiens] >gi_1586822_prf__2204389A fatty aldehyde dehydrogenase [Homo sapiens] >gi_4557303_ref_NP_000373.1_pALDH10_ aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)
Seq. No.	229546
Seq. ID	LIB3196-035-P1-M1-C11
Method	BLASTX
NCBI GI	g1173027
BLAST score	298
E value	4.0e-27
Match length	101
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]
Seq. No.	229547
Seq. ID	LIB3196-035-P1-M1-C12
Method	BLASTX
NCBI GI	g3402711
BLAST score	376
E value	3.0e-36
Match length	127
% identity	38
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]
Seq. No.	229548
Seq. ID	LIB3196-035-P1-M1-C8
Method	BLASTX
NCBI GI	g2498323
BLAST score	265
E value	2.0e-23
Match length	61
% identity	84
NCBI Description	EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) >gi_1488324 (U65932) extracellular matrix protein 1 [Homo sapiens] >gi_1488332 (U65938) extracellular matrix protein 1 [Homo sapiens] >gi_2654433 (U68186) extracellular matrix protein 1 [Homo sapiens]
Seq. No.	229549
Seq. ID	LIB3196-035-P1-M1-D1
Method	BLASTX
NCBI GI	g2765097
BLAST score	192
E value	6.0e-15
Match length	81
% identity	48
NCBI Description	(Y11207) P54 protein [Pisum sativum]

Seq. No.	229550
Seq. ID	LIB3196-035-P1-M1-D2
Method	BLASTX
NCBI GI	g4235430
BLAST score	392
E value	3.0e-38
Match length	92
% identity	82
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	229551
Seq. ID	LIB3196-035-P1-M1-D4
Method	BLASTX
NCBI GI	g1524121
BLAST score	534
E value	1.0e-54
Match length	133
% identity	76
NCBI Description	(X96539) malate dehydrogenase [Mesembryanthemum crystallinum]

Seq. No.	229552
Seq. ID	LIB3196-035-P1-M1-D7
Method	BLASTX
NCBI GI	g3522925
BLAST score	260
E value	3.0e-23
Match length	53
% identity	96
NCBI Description	(AC005545) AP-3 complex delta subunit, partial CDS [Homo sapiens]

Seq. No.	229553
Seq. ID	LIB3196-035-P1-M1-E10
Method	BLASTX
NCBI GI	g1076669
BLAST score	366
E value	5.0e-35
Match length	100
% identity	76
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_668987_emb_CAA59063_ (X84320) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	229554
Seq. ID	LIB3196-035-P1-M1-E11
Method	BLASTX
NCBI GI	g3947448
BLAST score	212
E value	4.0e-17
Match length	106
% identity	39
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST

yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

Seq. No.	229555
Seq. ID	LIB3196-035-P1-M1-E12
Method	BLASTX
NCBI GI	g88044
BLAST score	628
E value	1.0e-65
Match length	137
% identity	94
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	229556
Seq. ID	LIB3196-035-P1-M1-E2
Method	BLASTX
NCBI GI	g3913018
BLAST score	460
E value	3.0e-46
Match length	109
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	229557
Seq. ID	LIB3196-035-P1-M1-E4
Method	BLASTX
NCBI GI	g445613
BLAST score	325
E value	3.0e-30
Match length	95
% identity	69
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	229558
Seq. ID	LIB3196-035-P1-M1-E7
Method	BLASTX
NCBI GI	g2894306
BLAST score	372
E value	5.0e-36
Match length	105
% identity	74
NCBI Description	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]

Seq. No.	229559
Seq. ID	LIB3196-035-P1-M1-E9
Method	BLASTX
NCBI GI	g2738520
BLAST score	407
E value	5.0e-40
Match length	80
% identity	99

NCBI Description	(AF010187) FGF-1 intracellular binding protein [Homo sapiens] >gi_2738522 (AF010188) FGF-1 intracellular binding protein [Chlorocebus aethiops]

Seq. No.	229560
Seq. ID	LIB3196-035-P1-M1-F1
Method	BLASTX
NCBI GI	g2499819
BLAST score	494
E value	5.0e-50
Match length	131
% identity	68
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	229561
Seq. ID	LIB3196-035-P1-M1-F2
Method	BLASTX
NCBI GI	g683553
BLAST score	270
E value	9.0e-24
Match length	121
% identity	50
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	229562
Seq. ID	LIB3196-035-P1-M1-F3
Method	BLASTX
NCBI GI	g124224
BLAST score	578
E value	7.0e-60
Match length	124
% identity	90
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	229563
Seq. ID	LIB3196-035-P1-M1-F4
Method	BLASTX
NCBI GI	g124224
BLAST score	206
E value	1.0e-16
Match length	82
% identity	56
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	229564
Seq. ID	LIB3196-035-P1-M1-F8

Method	BLASTX
NCBI GI	g4218034
BLAST score	169
E value	3.0e-12
Match length	43
% identity	81
NCBI Description	(U73169) GTP-binding regulatory protein Gi alpha-2 chain [Homo sapiens]

Seq. No.	229565
Seq. ID	LIB3196-035-P1-M1-F9
Method	BLASTX
NCBI GI	g3413165
BLAST score	161
E value	1.0e-17
Match length	103
% identity	54
NCBI Description	(AJ010224) glyceraldehyde 3-phosphate dehydrogenase, cytosolic [Cicer arietinum]

Seq. No.	229566
Seq. ID	LIB3196-035-P1-M1-G12
Method	BLASTX
NCBI GI	g416917
BLAST score	227
E value	1.0e-18
Match length	91
% identity	54
NCBI Description	DESMOGLEIN 1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN 1) (DG1) >gi_319948_pir__IJHUG1 desmoglein 1 precursor - human >gi_30506_emb_CAA39976_ (X56654) desmoglein type 1 [Homo sapiens] >gi_3983129 (AF097935) desmoglein 1 [Homo sapiens] >gi_4503401_ref_NP_001933.1_pDSG1_ desmoglein

Seq. No.	229567
Seq. ID	LIB3196-035-P1-M1-G2
Method	BLASTX
NCBI GI	g137578
BLAST score	472
E value	1.0e-47
Match length	115
% identity	82
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229568
Seq. ID	LIB3196-035-P1-M1-G4
Method	BLASTX
NCBI GI	g2286153
BLAST score	533
E value	1.0e-54
Match length	110
% identity	97

NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	229569
Seq. ID	LIB3196-035-P1-M1-G5
Method	BLASTX
NCBI GI	g609342
BLAST score	471
E value	2.0e-47
Match length	94
% identity	98
NCBI Description	(U04946) nucleophosmin-anaplastic lymphoma kinase fusion protein [Homo sapiens]

Seq. No.	229570
Seq. ID	LIB3196-035-P1-M1-G6
Method	BLASTX
NCBI GI	g4530585
BLAST score	332
E value	5.0e-31
Match length	80
% identity	75
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	229571
Seq. ID	LIB3196-035-P1-M1-G8
Method	BLASTX
NCBI GI	g3024812
BLAST score	359
E value	3.0e-34
Match length	80
% identity	95
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_2599050 (AF027705) vacuolar ATPase 16kDa subunit c [Ovis aries]

Seq. No.	229572
Seq. ID	LIB3196-035-P1-M1-H2
Method	BLASTX
NCBI GI	g207905
BLAST score	435
E value	3.0e-43
Match length	101
% identity	82
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	229573
Seq. ID	LIB3196-035-P1-M1-H3
Method	BLASTX
NCBI GI	g130348
BLAST score	227
E value	1.0e-18
Match length	45
% identity	100
NCBI Description	PHOSPHOGLYCERATE MUTASE, BRAIN FORM (PGAM-B) (BPG-DEPENDENT PGAM) >gi_68469_pir__PMHUYB phosphoglycerate mutase (EC 5.4.2.1) B - human >gi_551174 (J04173) phosphoglycerate mutase 2 [Homo sapiens] >gi_4505753_ref_NP_002620.1_pPGAM1_ phosphoglycerate mutase 1 (brain)

Seq. No.	229574
Seq. ID	LIB3196-035-P1-M1-H9
Method	BLASTX
NCBI GI	g2723393
BLAST score	172
E value	3.0e-12
Match length	120
% identity	38
NCBI Description	(AB009284) EXTR2 [Homo sapiens] >gi_2895062 (AF000416) EXT-like protein 2 [Homo sapiens]

Seq. No.	229575
Seq. ID	LIB3196-036-P1-M1-A10
Method	BLASTX
NCBI GI	g2735857
BLAST score	317
E value	2.0e-29
Match length	80
% identity	79
NCBI Description	(AF012073) cAMP-specific phosphodiesterase PDE4D5 [Homo sapiens]

Seq. No.	229576
Seq. ID	LIB3196-036-P1-M1-A12
Method	BLASTX
NCBI GI	g2435512
BLAST score	237
E value	2.0e-20
Match length	59
% identity	78
NCBI Description	(AF024504) No definition line found [Arabidopsis thaliana]

Seq. No.	229577
Seq. ID	LIB3196-036-P1-M1-A5
Method	BLASTX
NCBI GI	g1706326
BLAST score	397
E value	1.0e-38
Match length	84
% identity	83
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_2146786_pir__S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_ (Z66543) pyruvate decarboxylase [Pisum sativum]

Seq. No.	229578
Seq. ID	LIB3196-036-P1-M1-B1
Method	BLASTX
NCBI GI	g114682
BLAST score	289
E value	4.0e-26
Match length	99
% identity	64
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_100471_pir__A35227 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No.	229579
Seq. ID	LIB3196-036-P1-M1-B10
Method	BLASTX
NCBI GI	g4335751
BLAST score	207
E value	2.0e-16
Match length	120
% identity	42
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	229580
Seq. ID	LIB3196-036-P1-M1-B11
Method	BLASTX
NCBI GI	g137580
BLAST score	246
E value	5.0e-21
Match length	118
% identity	47
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No.	229581
Seq. ID	LIB3196-036-P1-M1-B12
Method	BLASTX
NCBI GI	g464981
BLAST score	391
E value	5.0e-38
Match length	74
% identity	96
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	229582
Seq. ID	LIB3196-036-P1-M1-B3
Method	BLASTX
NCBI GI	g167311
BLAST score	311
E value	7.0e-29
Match length	79
% identity	78
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	229583
Seq. ID	LIB3196-036-P1-M1-B6
Method	BLASTX
NCBI GI	g126156
BLAST score	372
E value	8.0e-43
Match length	128

% identity	73
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229584
Seq. ID	LIB3196-036-P1-M1-B8
Method	BLASTX
NCBI GI	g3212868
BLAST score	512
E value	3.0e-52
Match length	107
% identity	86
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	229585
Seq. ID	LIB3196-036-P1-M1-C10
Method	BLASTX
NCBI GI	g128378
BLAST score	274
E value	3.0e-24
Match length	91
% identity	56
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP) >gi_82031_pir__S07142 nonspecific lipid transfer protein - castor bean >gi_224909_prf__1204170A protein,nonspecific lipid transfer [Ricinus communis]

Seq. No.	229586
Seq. ID	LIB3196-036-P1-M1-C11
Method	BLASTX
NCBI GI	g126156
BLAST score	482
E value	1.0e-48
Match length	121
% identity	76
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229587
Seq. ID	LIB3196-036-P1-M1-C12
Method	BLASTX
NCBI GI	g1170505
BLAST score	185
E value	5.0e-14
Match length	39
% identity	92
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor

eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana]

Seq. No.	229588
Seq. ID	LIB3196-036-P1-M1-C4
Method	BLASTX
NCBI GI	g2407800
BLAST score	349
E value	4.0e-33
Match length	78
% identity	90
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	229589
Seq. ID	LIB3196-036-P1-M1-C8
Method	BLASTX
NCBI GI	g3582332
BLAST score	316
E value	2.0e-29
Match length	82
% identity	73
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	229590
Seq. ID	LIB3196-036-P1-M1-D12
Method	BLASTX
NCBI GI	g2765837
BLAST score	256
E value	3.0e-22
Match length	110
% identity	55
NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No.	229591
Seq. ID	LIB3196-036-P1-M1-D3
Method	BLASTX
NCBI GI	g1771780
BLAST score	435
E value	3.0e-43
Match length	112
% identity	79
NCBI Description	(Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No.	229592
Seq. ID	LIB3196-036-P1-M1-D5
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	3.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	229593
Seq. ID	LIB3196-036-P1-M1-D7
Method	BLASTX

NCBI GI	g423053
BLAST score	200
E value	1.0e-15
Match length	40
% identity	97
NCBI Description	protransglutaminase E, TGase3 - human

Seq. No.	229594
Seq. ID	LIB3196-036-P1-M1-D8
Method	BLASTX
NCBI GI	g2497542
BLAST score	467
E value	4.0e-47
Match length	99
% identity	92
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi_629696_pir__S44287 pyruvate kinase, plastid - common tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	229595
Seq. ID	LIB3196-036-P1-M1-D9
Method	BLASTX
NCBI GI	g125351
BLAST score	315
E value	1.0e-37
Match length	104
% identity	84
NCBI Description	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FER (P94-FER) (C-FER) >gi_66833_pir__TVHUFE protein-tyrosine kinase (EC 2.7.1.112) fer - human >gi_339715 (J03358) tyrosine kinase (FER) [Homo sapiens]

Seq. No.	229596
Seq. ID	LIB3196-036-P1-M1-E10
Method	BLASTX
NCBI GI	g177207
BLAST score	561
E value	6.0e-58
Match length	130
% identity	86
NCBI Description	(J02769) 4F2 antigen heavy chain [Homo sapiens]

Seq. No.	229597
Seq. ID	LIB3196-036-P1-M1-E11
Method	BLASTX
NCBI GI	g266691
BLAST score	351
E value	3.0e-33
Match length	106
% identity	70
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	229598
Seq. ID	LIB3196-036-P1-M1-E7
Method	BLASTX

NCBI GI	g416563
BLAST score	512
E value	4.0e-52
Match length	98
% identity	99
NCBI Description	INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4) >gi_422742_pir__S32567 A4 protein - human >gi_177900 (L09604) A4 protein [Homo sapiens] >gi_2707599 (U93305) A4 differentiation-dependent protein [Homo sapiens] >gi_4505893_ref_NP_002659.1_pPLP2_ proteolipid protein 2 (colonic epithelium-enriched)

Seq. No.	229599
Seq. ID	LIB3196-036-P1-M1-E9
Method	BLASTX
NCBI GI	g267069
BLAST score	525
E value	1.0e-53
Match length	97
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	229600
Seq. ID	LIB3196-036-P1-M1-F10
Method	BLASTX
NCBI GI	g3493660
BLAST score	669
E value	1.0e-70
Match length	132
% identity	99
NCBI Description	(AF084530) cyclin-D binding Myb-like protein [Homo sapiens]

Seq. No.	229601
Seq. ID	LIB3196-036-P1-M1-F2
Method	BLASTX
NCBI GI	g3033391
BLAST score	223
E value	2.0e-18
Match length	95
% identity	58
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	229602
Seq. ID	LIB3196-036-P1-M1-F3
Method	BLASTX
NCBI GI	g3915031
BLAST score	638
E value	6.0e-67
Match length	126
% identity	95
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No.	229603
Seq. ID	LIB3196-036-P1-M1-F4
Method	BLASTX
NCBI GI	g398953
BLAST score	659
E value	2.0e-69
Match length	133
% identity	98
NCBI Description	14-3-3 PROTEIN SIGMA (STRATIFIN) (EPITHELIAL CELL MARKER PROTEIN 1) >gi_486666_pir__S34753 stratifin - human >gi_23940_emb_CAA40623_ (X57348) 9112 [Homo sapiens] >gi_2702353 (AF029081) 14-3-3 sigma protein [Homo sapiens] >gi_2702355 (AF029082) 14-3-3 sigma protein [Homo sapiens]

Seq. No.	229604
Seq. ID	LIB3196-036-P1-M1-F5
Method	BLASTX
NCBI GI	g3915742
BLAST score	618
E value	1.0e-64
Match length	127
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229605
Seq. ID	LIB3196-036-P1-M1-F6
Method	BLASTX
NCBI GI	g4006867
BLAST score	183
E value	1.0e-13
Match length	126
% identity	45
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	229606
Seq. ID	LIB3196-036-P1-M1-F7
Method	BLASTX
NCBI GI	g4567181
BLAST score	170
E value	4.0e-12
Match length	64
% identity	5
NCBI Description	(AC007228) BC37295_3 [Homo sapiens]

Seq. No.	229607
Seq. ID	LIB3196-036-P1-M1-G10
Method	BLASTX
NCBI GI	g167367
BLAST score	533
E value	1.0e-54
Match length	117
% identity	90

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No.	229608
Seq. ID	LIB3196-036-P1-M1-G12
Method	BLASTX
NCBI GI	g1730288
BLAST score	370
E value	2.0e-35
Match length	89
% identity	83
NCBI Description	(U61263) acetolactate synthase homolog [Homo sapiens]

Seq. No.	229609
Seq. ID	LIB3196-036-P1-M1-G4
Method	BLASTX
NCBI GI	g477138
BLAST score	179
E value	3.0e-23
Match length	63
% identity	92
NCBI Description	carcinoma-associated antigen GA733-1 precursor - human >gi_31591_emb_CAA31781_ (X13425) GA733-1 protein (AA 1-323) [Homo sapiens]

Seq. No.	229610
Seq. ID	LIB3196-036-P1-M1-G6
Method	BLASTX
NCBI GI	g631131
BLAST score	424
E value	5.0e-42
Match length	97
% identity	89
NCBI Description	epithelial cell marker protein 1 - human >gi_187302 (M93010) epithelial cell marker protein 1 [Homo sapiens]

Seq. No.	229611
Seq. ID	LIB3196-036-P1-M1-G8
Method	BLASTX
NCBI GI	g479532
BLAST score	469
E value	4.0e-47
Match length	96
% identity	99
NCBI Description	GTP-binding regulatory protein Gs alpha chain - human >gi_1335091_emb_CAA39484_ (X56009) alpha subunit of GsGTP binding protein [Homo sapiens]

Seq. No.	229612
Seq. ID	LIB3196-036-P1-M1-G9
Method	BLASTX
NCBI GI	g1346347
BLAST score	431
E value	1.0e-42
Match length	90
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II -

	human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]
Seq. No.	229613
Seq. ID	LIB3196-036-P1-M1-H1
Method	BLASTX
NCBI GI	g3915742
BLAST score	427
E value	8.0e-46
Match length	119
% identity	80
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]
Seq. No.	229614
Seq. ID	LIB3196-036-P1-M1-H11
Method	BLASTX
NCBI GI	g3834322
BLAST score	169
E value	5.0e-12
Match length	39
% identity	82
NCBI Description	(AC005679) EST gb_R30300 comes from this gene. [Arabidopsis thaliana]
Seq. No.	229615
Seq. ID	LIB3196-036-P1-M1-H3
Method	BLASTX
NCBI GI	g3297823
BLAST score	300
E value	3.0e-27
Match length	82
% identity	66
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]
Seq. No.	229616
Seq. ID	LIB3196-036-P1-M1-H4
Method	BLASTX
NCBI GI	g2120082
BLAST score	355
E value	9.0e-34
Match length	94
% identity	69
NCBI Description	hypothetical protein II (retroposon LINE-1) - human
Seq. No.	229617
Seq. ID	LIB3196-036-P1-M1-H9
Method	BLASTX
NCBI GI	g120649
BLAST score	686
E value	1.0e-72
Match length	135
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate

	dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_182863 (J02642) glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_224880_prf__1203217A dehydrogenase,glyceraldehydephosphate [Homo sapiens]
Seq. No.	229618
Seq. ID	LIB3196-037-P1-M1-A11
Method	BLASTX
NCBI GI	g1916290
BLAST score	147
E value	2.0e-09
Match length	72
% identity	49
NCBI Description	(U89876) ALY [Mus musculus]
Seq. No.	229619
Seq. ID	LIB3196-037-P1-M1-A3
Method	BLASTX
NCBI GI	g1346349
BLAST score	217
E value	1.0e-17
Match length	43
% identity	100
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II - human >gi_908805 (L42612) keratin type II [Homo sapiens]
Seq. No.	229620
Seq. ID	LIB3196-037-P1-M1-A5
Method	BLASTX
NCBI GI	g2813965
BLAST score	329
E value	9.0e-31
Match length	119
% identity	59
NCBI Description	(Z97053) adenosine deaminase (ADA) [Homo sapiens]
Seq. No.	229621
Seq. ID	LIB3196-037-P1-M1-A6
Method	BLASTX
NCBI GI	g4539395
BLAST score	142
E value	7.0e-09
Match length	51
% identity	53
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]
Seq. No.	229622
Seq. ID	LIB3196-037-P1-M1-B11
Method	BLASTX
NCBI GI	g464707
BLAST score	516

E value	1.0e-52
Match length	105
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	229623
Seq. ID	LIB3196-037-P1-M1-B12
Method	BLASTX
NCBI GI	g3005063
BLAST score	529
E value	3.0e-54
Match length	125
% identity	83
NCBI Description	(AF043324) N-myristoyltransferase 1 [Homo sapiens]

Seq. No.	229624
Seq. ID	LIB3196-037-P1-M1-B4
Method	BLASTX
NCBI GI	g4056499
BLAST score	139
E value	1.0e-08
Match length	43
% identity	58
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	229625
Seq. ID	LIB3196-037-P1-M1-B8
Method	BLASTX
NCBI GI	g1363944
BLAST score	598
E value	2.0e-62
Match length	124
% identity	97
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	229626
Seq. ID	LIB3196-037-P1-M1-C1
Method	BLASTX
NCBI GI	g4249382
BLAST score	439
E value	1.0e-43

Match length	98
% identity	84
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	229627
Seq. ID	LIB3196-037-P1-M1-C11
Method	BLASTX
NCBI GI	g81546
BLAST score	477
E value	3.0e-48
Match length	103
% identity	89
NCBI Description	alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No.	229628
Seq. ID	LIB3196-037-P1-M1-C12
Method	BLASTX
NCBI GI	g762939
BLAST score	614
E value	4.0e-64
Match length	127
% identity	92
NCBI Description	(Y00057) precursor polypeptide (AA -14 to 747) [Homo sapiens]

Seq. No.	229629
Seq. ID	LIB3196-037-P1-M1-C4
Method	BLASTX
NCBI GI	g1843527
BLAST score	447
E value	1.0e-44
Match length	116
% identity	78
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	229630
Seq. ID	LIB3196-037-P1-M1-D1
Method	BLASTX
NCBI GI	g125080
BLAST score	533
E value	1.0e-54
Match length	106
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	229631
Seq. ID	LIB3196-037-P1-M1-D10
Method	BLASTX
NCBI GI	g3845568
BLAST score	200

E value 1.0e-15
Match length 78
% identity 51
NCBI Description (AB012042) keratin 6 beta [Mus musculus]

Seq. No. 229632
Seq. ID LIB3196-037-P1-M1-D11
Method BLASTX
NCBI GI g1498225
BLAST score 309
E value 2.0e-28
Match length 62
% identity 100
NCBI Description (Y07569) PHAPI2a protein [Homo sapiens] >gi_1698783 (U70439) silver-stainable protein SSP29 [Homo sapiens]

Seq. No. 229633
Seq. ID LIB3196-037-P1-M1-D2
Method BLASTX
NCBI GI g167311
BLAST score 496
E value 2.0e-50
Match length 113
% identity 86
NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No. 229634
Seq. ID LIB3196-037-P1-M1-D3
Method BLASTX
NCBI GI g119339
BLAST score 457
E value 1.0e-45
Match length 92
% identity 99
NCBI Description ALPHA ENOLASE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE) >gi_87368_pir__A29170 phosphopyruvate hydratase (EC 4.2.1.11) alpha - human >gi_182114 (M14328) alpha enolase (EC 4.2.1.11) [Homo sapiens] >gi_1167843_emb_CAA34360_ (X16288) alpha-enolase [Homo sapiens] >gi_4503571_ref_NP_001419.1_pENO1_ enolase 1, (alpha)

Seq. No. 229635
Seq. ID LIB3196-037-P1-M1-D5
Method BLASTX
NCBI GI g1000704
BLAST score 465
E value 1.0e-46
Match length 93
% identity 95
NCBI Description (Z50101) NAD(P) transhydrogenase [Homo sapiens] >gi_1589396_prf__2211247B nicotinamide nucleotide transhydrogenase [Homo sapiens]

Seq. No. 229636
Seq. ID LIB3196-037-P1-M1-D6
Method BLASTX

NCBI GI g421953
BLAST score 272
E value 2.0e-29
Match length 108
% identity 69
NCBI Description hypothetical protein 2 - potato transposon Tst1 >gi_21432_emb_CAA36614_ (X52387) ORF2 [Solanum tuberosum]

Seq. No. 229637
Seq. ID LIB3196-037-P1-M1-D8
Method BLASTX
NCBI GI g2944446
BLAST score 548
E value 2.0e-56
Match length 122
% identity 80
NCBI Description (AF050756) cysteine endopeptidase precursor [Ricinus communis]

Seq. No. 229638
Seq. ID LIB3196-037-P1-M1-E11
Method BLASTX
NCBI GI g3041738
BLAST score 618
E value 1.0e-64
Match length 122
% identity 97
NCBI Description T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]

Seq. No. 229639
Seq. ID LIB3196-037-P1-M1-E2
Method BLASTX
NCBI GI g901998
BLAST score 143
E value 7.0e-09
Match length 97
% identity 35
NCBI Description (U23731) TAR DNA-binding protein-43 [Homo sapiens]

Seq. No. 229640
Seq. ID LIB3196-037-P1-M1-E3
Method BLASTX
NCBI GI g2119228
BLAST score 227
E value 9.0e-19
Match length 111
% identity 51
NCBI Description keratin K4a - human (fragment) >gi_313159_emb_CAA47914_ (X67683) keratin K4a [Homo sapiens]

Seq. No. 229641
Seq. ID LIB3196-037-P1-M1-E6
Method BLASTX
NCBI GI g293119

BLAST score	500
E value	9.0e-51
Match length	121
% identity	83
NCBI Description	(L13307) immunoglobulin gamma [Macaca fascicularis]

Seq. No.	229642
Seq. ID	LIB3196-037-P1-M1-E9
Method	BLASTX
NCBI GI	g1694976
BLAST score	307
E value	3.0e-28
Match length	91
% identity	64
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	229643
Seq. ID	LIB3196-037-P1-M1-F2
Method	BLASTX
NCBI GI	g112440
BLAST score	358
E value	4.0e-34
Match length	93
% identity	52
NCBI Description	tropomyosin 1 alpha, brain - rat

Seq. No.	229644
Seq. ID	LIB3196-037-P1-M1-F4
Method	BLASTX
NCBI GI	g4063760
BLAST score	331
E value	5.0e-44
Match length	118
% identity	73
NCBI Description	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq. No.	229645
Seq. ID	LIB3196-037-P1-M1-F6
Method	BLASTX
NCBI GI	g3929617
BLAST score	658
E value	3.0e-69
Match length	128
% identity	99
NCBI Description	(U39412) alpha SNAP [Homo sapiens] >gi_4505329_ref_NP_003818.1_pNAPA_ UNKNOWN

Seq. No.	229646
Seq. ID	LIB3196-037-P1-M1-F8
Method	BLASTX
NCBI GI	g125080
BLAST score	517
E value	5.0e-53
Match length	104
% identity	100

NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	229647
Seq. ID	LIB3196-037-P1-M1-G10
Method	BLASTX
NCBI GI	g3882321
BLAST score	147
E value	2.0e-09
Match length	100
% identity	38
NCBI Description	(AB018343) KIAA0800 protein [Homo sapiens]

Seq. No.	229648
Seq. ID	LIB3196-037-P1-M1-G11
Method	BLASTX
NCBI GI	g2494911
BLAST score	617
E value	2.0e-64
Match length	119
% identity	97
NCBI Description	HYPOTHETICAL PROTEIN KIAA0124 >gi_1469171_dbj_BAA09473_ (D50914) The KIAA0124 gene product is novel. [Homo sapiens]

Seq. No.	229649
Seq. ID	LIB3196-037-P1-M1-G3
Method	BLASTX
NCBI GI	g729032
BLAST score	281
E value	4.0e-25
Match length	54
% identity	100
NCBI Description	ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1 (CAP 1) >gi_2137125_pir__I49572 adenylyl cyclase-associated protein - mouse >gi_293317 (L12367) adenylyl cyclase-associated protein [Mus musculus] >gi_744841_prf__2015321A adenylate cyclase-associated protein [Mus musculus]

Seq. No.	229650
Seq. ID	LIB3196-037-P1-M1-G8
Method	BLASTX
NCBI GI	g2500587
BLAST score	611
E value	8.0e-64
Match length	117
% identity	72
NCBI Description	SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53) >gi_1082799_pir__A54964 spliceosome-associated protein SAP-49 - human >gi_556217 (L35013) spliceosomal protein [Homo sapiens]

Seq. No.	229651
Seq. ID	LIB3196-037-P1-M1-G9
Method	BLASTX

NCBI GI	g2500587
BLAST score	585
E value	9.0e-61
Match length	117
% identity	64
NCBI Description	SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53) >gi_1082799_pir__A54964 spliceosome-associated protein SAP-49 - human >gi_556217 (L35013) spliceosomal protein [Homo sapiens]

Seq. No.	229652
Seq. ID	LIB3196-037-P1-M1-H11
Method	BLASTX
NCBI GI	g3643608
BLAST score	195
E value	5.0e-15
Match length	98
% identity	39
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229653
Seq. ID	LIB3196-037-P1-M1-H3
Method	BLASTX
NCBI GI	g4417310
BLAST score	161
E value	4.0e-11
Match length	86
% identity	41
NCBI Description	(AC006446) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]

Seq. No.	229654
Seq. ID	LIB3196-037-P1-M1-H4
Method	BLASTX
NCBI GI	g119172
BLAST score	464
E value	2.0e-51
Match length	108
% identity	96
NCBI Description	ELONGATION FACTOR 2 (EF-2) >gi_2144947_pir__EFHU2 translation elongation factor eEF-2 - human >gi_31106_emb_CAA35829_ (X51466) elongation factor 2 [Homo sapiens] >gi_31108_emb_CAA77750_ (Z11692) human elongation factor 2 [Homo sapiens] >gi_4503483_ref_NP_001952.1_pEEF2_ eukaryotic translation elongation factor

Seq. No.	229655
Seq. ID	LIB3196-037-P1-M1-H5
Method	BLASTX
NCBI GI	g1730015
BLAST score	311
E value	1.0e-28
Match length	82
% identity	72
NCBI Description	TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN) (APO-2 LIGAND) >gi_1149558 (U37518) TNF-related apoptosis inducing ligand TRAIL [Homo sapiens]

	>gi_1336208_gb_AAB01233_ (U57059) Apo-2 ligand [Homo sapiens] >gi_4507593_ref_NP_003801.1_pTNFSF10_ UNKNOWN
Seq. No.	229656
Seq. ID	LIB3196-037-P1-M1-H6
Method	BLASTX
NCBI GI	g2058282
BLAST score	190
E value	2.0e-14
Match length	51
% identity	69
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]
Seq. No.	229657
Seq. ID	LIB3196-037-P1-M1-H7
Method	BLASTX
NCBI GI	g3643607
BLAST score	531
E value	2.0e-54
Match length	119
% identity	81
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.	229658
Seq. ID	LIB3196-038-P1-M1-A2
Method	BLASTX
NCBI GI	g126682
BLAST score	386
E value	2.0e-37
Match length	74
% identity	97
NCBI Description	MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN MAD3 >gi_106956_pir__A39935 major histocompatibility complex enhance-binding protein MAD3 - human >gi_187291 (M69043) MAD3 [Homo sapiens]
Seq. No.	229659
Seq. ID	LIB3196-038-P1-M1-A4
Method	BLASTX
NCBI GI	g3033397
BLAST score	427
E value	2.0e-42
Match length	104
% identity	80
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.	229660
Seq. ID	LIB3196-038-P1-M1-A5
Method	BLASTX
NCBI GI	g137578
BLAST score	539
E value	2.0e-55
Match length	105
% identity	100
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor

[Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229661
Seq. ID	LIB3196-038-P1-M1-A6
Method	BLASTX
NCBI GI	g124204
BLAST score	391
E value	5.0e-38
Match length	87
% identity	87
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi_87941_pir__A31226 translation initiation factor eIF-2 beta chain - human >gi_109365_pir__S13147 protein synthesis factor - rabbit >gi_182067 (M29536) translational initiation factor beta subunit [Homo sapiens] >gi_227237_prf__1617105A initiation factor 2beta [Oryctolagus cuniculus] >gi_4503505_ref_NP_003899.1_pEIF2S2_ UNKNOWN

Seq. No.	229662
Seq. ID	LIB3196-038-P1-M1-A9
Method	BLASTX
NCBI GI	g3334245
BLAST score	228
E value	2.0e-19
Match length	53
% identity	85
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer arietinum]

Seq. No.	229663
Seq. ID	LIB3196-038-P1-M1-B10
Method	BLASTX
NCBI GI	g3885334
BLAST score	370
E value	9.0e-36
Match length	94
% identity	79
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	229664
Seq. ID	LIB3196-038-P1-M1-B12
Method	BLASTX
NCBI GI	g3334138
BLAST score	238
E value	2.0e-20
Match length	84
% identity	55
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	229665
Seq. ID	LIB3196-038-P1-M1-B3
Method	BLASTX
NCBI GI	g3875300
BLAST score	144
E value	3.0e-09
Match length	47
% identity	62
NCBI Description	(Z68160) Similarity to Yeast putative mitochondrial carrier protein PET8 (SW:PET8_YEAST); cDNA EST CEMSH22F comes from this gene; cDNA EST CEMSH22R comes from this gene; cDNA EST yk331b9.5 comes from this gene [Caenorhabditis e

Seq. No.	229666
Seq. ID	LIB3196-038-P1-M1-B5
Method	BLASTX
NCBI GI	g2465923
BLAST score	175
E value	9.0e-13
Match length	50
% identity	64
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	229667
Seq. ID	LIB3196-038-P1-M1-B6
Method	BLASTX
NCBI GI	g3834310
BLAST score	500
E value	7.0e-51
Match length	96
% identity	100
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	229668
Seq. ID	LIB3196-038-P1-M1-B8
Method	BLASTX
NCBI GI	g2887441
BLAST score	467
E value	3.0e-47
Match length	84
% identity	98
NCBI Description	(AB007891) KIAA0431 [Homo sapiens]

Seq. No.	229669
Seq. ID	LIB3196-038-P1-M1-C4
Method	BLASTX
NCBI GI	g4325382
BLAST score	465
E value	9.0e-47
Match length	92
% identity	99
NCBI Description	(AF129075) T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) [Homo sapiens]

Seq. No.	229670
Seq. ID	LIB3196-038-P1-M1-C6
Method	BLASTX
NCBI GI	g284314
BLAST score	673
E value	5.0e-71
Match length	122
% identity	100
NCBI Description	modulator recognition factor 1 - human (fragment) >gi_188684 (M62324) modulator recognition factor I [Homo sapiens]

Seq. No.	229671
Seq. ID	LIB3196-038-P1-M1-C8
Method	BLASTX
NCBI GI	g131162
BLAST score	209
E value	7.0e-17
Match length	42
% identity	90
NCBI Description	PHOTOSYSTEM I IRON-SULFUR CENTER 1 (PHOTOSYSTEM I SUBUNIT VII-1) (9 KD POLYPEPTIDE 1) (PSI-C-1) >gi_131163_sp_P07136_PSAC_TOBAC PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C) >gi_97657_pir__S14967 photosystem I iron-sulfur protein psaC - Synechocystis sp. (PCC 6803) >gi_100391_pir__S07170 photosystem I iron-sulfur protein psaC - common tobacco chloroplast >gi_11792_emb_CAA29304_ (X05881) 9kd polypeptide (psaC gene product, AA 1 - 81) [Nicotiana tabacum] >gi_47596_emb_CAA37836_ (X53842) 8.9kDa iron-sulfur containing subunit of Photosystem I [Synechocystis sp.] >gi_2924280_emb_CAA77433_ (Z00044) PSI 9kD protein [Nicotiana tabacum]

Seq. No.	229672
Seq. ID	LIB3196-038-P1-M1-D12
Method	BLASTX
NCBI GI	g224877
BLAST score	453
E value	2.0e-45
Match length	89
% identity	96
NCBI Description	deaminase a,adenosine [Homo sapiens]

Seq. No.	229673
Seq. ID	LIB3196-038-P1-M1-D3
Method	BLASTX
NCBI GI	g3170190
BLAST score	257
E value	8.0e-23
Match length	70
% identity	76
NCBI Description	(AF039695) antigen NY-CO-25 [Homo sapiens]

Seq. No.	229674
Seq. ID	LIB3196-038-P1-M1-E10

Method	BLASTX
NCBI GI	g1703446
BLAST score	385
E value	2.0e-37
Match length	119
% identity	66
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	229675
Seq. ID	LIB3196-038-P1-M1-E12
Method	BLASTX
NCBI GI	g3915742
BLAST score	448
E value	7.0e-45
Match length	98
% identity	88
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229676
Seq. ID	LIB3196-038-P1-M1-E3
Method	BLASTX
NCBI GI	g72287
BLAST score	474
E value	7.0e-48
Match length	107
% identity	88
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	229677
Seq. ID	LIB3196-038-P1-M1-E4
Method	BLASTX
NCBI GI	g284314
BLAST score	606
E value	3.0e-63
Match length	110
% identity	100
NCBI Description	modulator recognition factor 1 - human (fragment) >gi_188684 (M62324) modulator recognition factor I [Homo sapiens]

Seq. No.	229678
Seq. ID	LIB3196-038-P1-M1-E6
Method	BLASTX
NCBI GI	g2529678
BLAST score	187
E value	3.0e-14
Match length	75
% identity	55
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	229679
Seq. ID	LIB3196-038-P1-M1-E7
Method	BLASTX
NCBI GI	g137578
BLAST score	413
E value	9.0e-41
Match length	98
% identity	47
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229680
Seq. ID	LIB3196-038-P1-M1-E8
Method	BLASTX
NCBI GI	g3641838
BLAST score	409
E value	4.0e-40
Match length	89
% identity	88
NCBI Description	(AL023094) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	229681
Seq. ID	LIB3196-038-P1-M1-F12
Method	BLASTX
NCBI GI	g1346348
BLAST score	464
E value	6.0e-47
Match length	93
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E) (K6E KERATIN) >gi_2119223_pir__I61770 keratin type II - human >gi_908803 (L42611) keratin type II [Homo sapiens]

Seq. No.	229682
Seq. ID	LIB3196-038-P1-M1-F3
Method	BLASTX
NCBI GI	g167311
BLAST score	513
E value	2.0e-52
Match length	97
% identity	100
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No.	229683
Seq. ID	LIB3196-038-P1-M1-F4
Method	BLASTX
NCBI GI	g113944
BLAST score	563
E value	3.0e-58
Match length	121
% identity	93

NCBI Description	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi_71756_pir__LUHU annexin I - human >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I (lipocortin I)

Seq. No.	229684
Seq. ID	LIB3196-038-P1-M1-F7
Method	BLASTX
NCBI GI	g2827715
BLAST score	279
E value	6.0e-25
Match length	102
% identity	60
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	229685
Seq. ID	LIB3196-038-P1-M1-F8
Method	BLASTX
NCBI GI	g2055295
BLAST score	553
E value	5.0e-57
Match length	117
% identity	93
NCBI Description	(D87438) Similar to a C.elegans protein in cosmid C14H10 [Homo sapiens]

Seq. No.	229686
Seq. ID	LIB3196-038-P1-M1-F9
Method	BLASTX
NCBI GI	g4467804
BLAST score	513
E value	2.0e-52
Match length	100
% identity	95
NCBI Description	(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens]

Seq. No.	229687
Seq. ID	LIB3196-038-P1-M1-G1
Method	BLASTX
NCBI GI	g4406814
BLAST score	352
E value	9.0e-34
Match length	83
% identity	81
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	229688
Seq. ID	LIB3196-038-P1-M1-G11
Method	BLASTX
NCBI GI	g1169178

BLAST score	153
E value	2.0e-12
Match length	51
% identity	84
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (PPIASE) (ROTAMASE) (CYCLOPHILIN C) >gi_627417_pir__A54204 peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human >gi_547304_bbs_149388 (S71018) cyclophilin C, Cyp-C [human, kidney, Peptide, 212 aa] [Homo sapiens] >gi_4505991_ref_NP_000934.1_pPPIC_ peptidylprolyl isomerase C (cyclophilin C); Cyp-C

Seq. No.	229689
Seq. ID	LIB3196-038-P1-M1-G12
Method	BLASTX
NCBI GI	g2828290
BLAST score	216
E value	2.0e-17
Match length	90
% identity	47
NCBI Description	(AL021687) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	229690
Seq. ID	LIB3196-038-P1-M1-G2
Method	BLASTX
NCBI GI	g2554653
BLAST score	486
E value	2.0e-49
Match length	96
% identity	57
NCBI Description	Up1, The Two Rna-Recognition Motif Domain Of Hnrnp A1

Seq. No.	229691
Seq. ID	LIB3196-038-P1-M1-G6
Method	BLASTX
NCBI GI	g4090247
BLAST score	261
E value	1.0e-24
Match length	133
% identity	53
NCBI Description	(AJ006130) rer [Mus musculus]

Seq. No.	229692
Seq. ID	LIB3196-038-P1-M1-G7
Method	BLASTX
NCBI GI	g125080
BLAST score	463
E value	9.0e-47
Match length	94
% identity	100
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	229693

Seq. ID	LIB3196-038-P1-M1-G8
Method	BLASTX
NCBI GI	g2582665
BLAST score	434
E value	3.0e-43
Match length	94
% identity	89
NCBI Description	(Z82983) thi [Citrus sinensis]

Seq. No.	229694
Seq. ID	LIB3196-038-P1-M1-H2
Method	BLASTX
NCBI GI	g1438567
BLAST score	543
E value	6.0e-56
Match length	104
% identity	100
NCBI Description	(U61266) Rho-associated kinase beta [Rattus norvegicus]

Seq. No.	229695
Seq. ID	LIB3196-038-P1-M1-H3
Method	BLASTX
NCBI GI	g683553
BLAST score	155
E value	1.0e-10
Match length	72
% identity	51
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	229696
Seq. ID	LIB3196-038-P1-M1-H6
Method	BLASTX
NCBI GI	g3264767
BLAST score	379
E value	1.0e-36
Match length	115
% identity	62
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	229697
Seq. ID	LIB3196-039-P1-M1-A1
Method	BLASTX
NCBI GI	g2995405
BLAST score	345
E value	8.0e-33
Match length	96
% identity	73
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	229698
Seq. ID	LIB3196-039-P1-M1-A10
Method	BLASTX
NCBI GI	g131773
BLAST score	412
E value	2.0e-40
Match length	88

% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) - maize
Seq. No.	229699
Seq. ID	LIB3196-039-P1-M1-A11
Method	BLASTX
NCBI GI	g548774
BLAST score	257
E value	2.0e-22
Match length	69
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]
Seq. No.	229700
Seq. ID	LIB3196-039-P1-M1-A3
Method	BLASTX
NCBI GI	g71533
BLAST score	522
E value	2.0e-53
Match length	106
% identity	100
NCBI Description	keratin, 56K type II cytoskeletal - human
Seq. No.	229701
Seq. ID	LIB3196-039-P1-M1-A5
Method	BLASTX
NCBI GI	g119172
BLAST score	666
E value	3.0e-70
Match length	127
% identity	99
NCBI Description	ELONGATION FACTOR 2 (EF-2) >gi_2144947_pir__EFHU2 translation elongation factor eEF-2 - human >gi_31106_emb_CAA35829_ (X51466) elongation factor 2 [Homo sapiens] >gi_31108_emb_CAA77750_ (Z11692) human elongation factor 2 [Homo sapiens] >gi_4503483_ref_NP_001952.1_pEEF2_ eukaryotic translation elongation factor
Seq. No.	229702
Seq. ID	LIB3196-039-P1-M1-A6
Method	BLASTX
NCBI GI	g4379025
BLAST score	212
E value	5.0e-17
Match length	60
% identity	72
NCBI Description	(X03145) pot. ORF VI [Homo sapiens]
Seq. No.	229703
Seq. ID	LIB3196-039-P1-M1-A9
Method	BLASTX
NCBI GI	g547753
BLAST score	323

E value	3.0e-30
Match length	67
% identity	96
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	229704
Seq. ID	LIB3196-039-P1-M1-B11
Method	BLASTX
NCBI GI	g2879867
BLAST score	317
E value	2.0e-29
Match length	90
% identity	67
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	229705
Seq. ID	LIB3196-039-P1-M1-B3
Method	BLASTX
NCBI GI	g2499087
BLAST score	470
E value	3.0e-47
Match length	122
% identity	67
NCBI Description	UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) >gi_1085170_pir__S54723 UDP-glucose--glycoprotein glucosyltransferase - fruit fly (Drosophila sp.) >gi_790585 (U20554) UDP-glucose:glycoprotein glucosyltransferase precursor [Drosophila melanogaster]

Seq. No.	229706
Seq. ID	LIB3196-039-P1-M1-B4
Method	BLASTX
NCBI GI	g4164033
BLAST score	284
E value	2.0e-25
Match length	127
% identity	44
NCBI Description	(AF111075) latrophilin 2 splice variant babbe [Bos taurus]

Seq. No.	229707
Seq. ID	LIB3196-039-P1-M1-B6
Method	BLASTX
NCBI GI	g1130684
BLAST score	621
E value	5.0e-65
Match length	120
% identity	100
NCBI Description	(Z46960) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No.	229708
Seq. ID	LIB3196-039-P1-M1-B9
Method	BLASTX
NCBI GI	g4406225
BLAST score	491
E value	9.0e-50
Match length	99

% identity	97
NCBI Description	(AF104412) proliferating cell nuclear antigen II [Nicotiana tabacum]

Seq. No.	229709
Seq. ID	LIB3196-039-P1-M1-C1
Method	BLASTX
NCBI GI	g729978
BLAST score	171
E value	2.0e-12
Match length	50
% identity	70
NCBI Description	MAD PROTEIN (MAX DIMERIZER) >gi_346245_pir__A45181 Max-binding bHLH-Zip protein Mad - human >gi_187289 (L06895) antagonizer of myc transcriptional activity [Homo sapiens] >gi_4505069_ref_NP_002348.1_pMAD_ MAD protein (MAX-binding protein)

Seq. No.	229710
Seq. ID	LIB3196-039-P1-M1-C11
Method	BLASTX
NCBI GI	g2827550
BLAST score	154
E value	3.0e-10
Match length	51
% identity	59
NCBI Description	(AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	229711
Seq. ID	LIB3196-039-P1-M1-C2
Method	BLASTX
NCBI GI	g975290
BLAST score	268
E value	7.0e-24
Match length	79
% identity	72
NCBI Description	(U24183) phosphofructokinase [Homo sapiens]

Seq. No.	229712
Seq. ID	LIB3196-039-P1-M1-C3
Method	BLASTX
NCBI GI	g3860797
BLAST score	201
E value	7.0e-16
Match length	97
% identity	41
NCBI Description	(AJ235271) 30S RIBOSOMAL PROTEIN S9 (rpsI) [Rickettsia prowazekii]

Seq. No.	229713
Seq. ID	LIB3196-039-P1-M1-C4
Method	BLASTX
NCBI GI	g4138581
BLAST score	292
E value	2.0e-26
Match length	96

% identity	23
NCBI Description	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No.	229714
Seq. ID	LIB3196-039-P1-M1-C5
Method	BLASTX
NCBI GI	g2352492
BLAST score	339
E value	3.0e-32
Match length	78
% identity	81
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	229715
Seq. ID	LIB3196-039-P1-M1-C6
Method	BLASTX
NCBI GI	g1070474
BLAST score	587
E value	5.0e-61
Match length	119
% identity	92
NCBI Description	protein-tyrosine kinase (EC 2.7.1.112) fgr - feline sarcoma virus (strain Gardner-Rasheed) >gi_61543_emb_CAA25063_ (X00255) P70 gag gene [Feline sarcoma virus]

Seq. No.	229716
Seq. ID	LIB3196-039-P1-M1-C7
Method	BLASTX
NCBI GI	g4455211
BLAST score	200
E value	1.0e-15
Match length	85
% identity	39
NCBI Description	(AL035440) STIG1 like protein [Arabidopsis thaliana]

Seq. No.	229717
Seq. ID	LIB3196-039-P1-M1-D1
Method	BLASTX
NCBI GI	g2134892
BLAST score	472
E value	2.0e-47
Match length	92
% identity	100
NCBI Description	cell surface glycoprotein - human >gi_188256 (M60334) cell surface glycoprotein [Homo sapiens] >gi_1834460_emb_CAB06609_ (Z84814) HLA-DRA*0102 [Homo sapiens]

Seq. No.	229718
Seq. ID	LIB3196-039-P1-M1-D10
Method	BLASTX
NCBI GI	g2191127
BLAST score	475
E value	7.0e-48

Match length	101
% identity	89
NCBI Description	(AF007269) A_IG002N01.1 gene product [Arabidopsis thaliana]

Seq. No.	229719
Seq. ID	LIB3196-039-P1-M1-D3
Method	BLASTX
NCBI GI	g2252866
BLAST score	162
E value	3.0e-11
Match length	43
% identity	74
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	229720
Seq. ID	LIB3196-039-P1-M1-D8
Method	BLASTX
NCBI GI	g2832411
BLAST score	463
E value	2.0e-46
Match length	109
% identity	81
NCBI Description	(AJ002211) CXC chemokine [Homo sapiens] >gi_2911376 (AF044197) B lymphocyte chemoattractant BLC; B-cell homing chemokine [Homo sapiens] >gi_3169814 (AF029894) Angie [Homo sapiens]

Seq. No.	229721
Seq. ID	LIB3196-039-P1-M1-D9
Method	BLASTX
NCBI GI	g3600031
BLAST score	228
E value	7.0e-19
Match length	95
% identity	60
NCBI Description	(AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No.	229722
Seq. ID	LIB3196-039-P1-M1-E11
Method	BLASTX
NCBI GI	g1363944
BLAST score	607
E value	2.0e-63
Match length	121
% identity	100
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	229723
Seq. ID	LIB3196-039-P1-M1-E12
Method	BLASTX
NCBI GI	g2191150
BLAST score	384
E value	3.0e-37

Match length	82
% identity	36
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No.	229724
Seq. ID	LIB3196-039-P1-M1-E5
Method	BLASTX
NCBI GI	g1350945
BLAST score	255
E value	4.0e-22
Match length	64
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S17 >gi_1076596_pir__S51665 ribosomal protein S17 - tomato (fragment) >gi_603570_emb_CAA58444_ (X83421) ribosomal protein S17 [Lycopersicon esculentum]

Seq. No.	229725
Seq. ID	LIB3196-039-P1-M1-E9
Method	BLASTX
NCBI GI	g730456
BLAST score	416
E value	6.0e-41
Match length	98
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	229726
Seq. ID	LIB3196-039-P1-M1-F1
Method	BLASTX
NCBI GI	g3914916
BLAST score	637
E value	7.0e-67
Match length	121
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S4, Y ISOFORM >gi_4432937_dbj_BAA21076_ (D50105) Y-chromosome linked ribosomal protein S4 [Macaca fuscata]

Seq. No.	229727
Seq. ID	LIB3196-039-P1-M1-F11
Method	BLASTX
NCBI GI	g3947719
BLAST score	249
E value	2.0e-21
Match length	53
% identity	92
NCBI Description	(AJ012653) ribosomal protein S28 [Prunus persica] >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28 [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655) ribosomal protein S28 [Prunus persica]

Seq. No.	229728
Seq. ID	LIB3196-039-P1-M1-F12
Method	BLASTX
NCBI GI	g280816
BLAST score	138

E value	9.0e-09
Match length	60
% identity	50
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin

Seq. No.	229729
Seq. ID	LIB3196-039-P1-M1-F5
Method	BLASTX
NCBI GI	g1705996
BLAST score	653
E value	1.0e-68
Match length	127
% identity	99
NCBI Description	COATOMER ALPHA SUBUNIT (ALPHA-COAT PROTEIN) (ALPHA-COP) (HEP-COP) >gi_2144979_pir__ERHUAH coatomer complex alpha chain homolog - human >gi_1002369 (U24105) coatomer protein [Homo sapiens]

Seq. No.	229730
Seq. ID	LIB3196-039-P1-M1-F7
Method	BLASTX
NCBI GI	g137578
BLAST score	478
E value	2.0e-48
Match length	110
% identity	87
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229731
Seq. ID	LIB3196-039-P1-M1-F9
Method	BLASTX
NCBI GI	g266392
BLAST score	594
E value	8.0e-62
Match length	118
% identity	97
NCBI Description	TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) >gi_346215_pir__A45017 transcription factor ISGF3 gamma chain - human >gi_184653 (M87503) IFN-alpha responsive transcription factor [Homo sapiens]

Seq. No.	229732
Seq. ID	LIB3196-039-P1-M1-G2
Method	BLASTX
NCBI GI	g4105412
BLAST score	309
E value	2.0e-28

Match length	67
% identity	87
NCBI Description	(AF045564) development-related protein [Rattus norvegicus]

Seq. No.	229733
Seq. ID	LIB3196-039-P1-M1-G3
Method	BLASTX
NCBI GI	g3777617
BLAST score	291
E value	2.0e-26
Match length	73
% identity	84
NCBI Description	(AF097709) serine protease [Homo sapiens]

Seq. No.	229734
Seq. ID	LIB3196-039-P1-M1-G5
Method	BLASTX
NCBI GI	g137580
BLAST score	604
E value	5.0e-63
Match length	119
% identity	98
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No.	229735
Seq. ID	LIB3196-039-P1-M1-G6
Method	BLASTX
NCBI GI	g123101
BLAST score	330
E value	7.0e-31
Match length	100
% identity	72
NCBI Description	NONHISTONE CHROMOSOMAL PROTEIN HMG-14 >gi_107207_pir__A33310 nonhistone chromosomal protein HMG-14 - human >gi_306863 (J02621) high mobility group protein 14 [Homo sapiens] >gi_386779 (M21339) high mobility group protein 14 [Homo sapiens] >gi_3171155 (AF064861) HMG-14 [Homo sapiens]

Seq. No.	229736
Seq. ID	LIB3196-039-P1-M1-G9
Method	BLASTX
NCBI GI	g2995405
BLAST score	345
E value	1.0e-32
Match length	109
% identity	63
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	229737
Seq. ID	LIB3196-039-P1-M1-H10
Method	BLASTX
NCBI GI	g280816
BLAST score	624

E value	3.0e-65
Match length	127
% identity	98
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens] >gi_4504911_ref_NP_002265.1_pKRT13_ keratin

Seq. No.	229738
Seq. ID	LIB3196-039-P1-M1-H11
Method	BLASTX
NCBI GI	g3717946
BLAST score	172
E value	2.0e-15
Match length	81
% identity	62
NCBI Description	(AJ005901) vag1 [Arabidopsis thaliana]

Seq. No.	229739
Seq. ID	LIB3196-039-P1-M1-H4
Method	BLASTX
NCBI GI	g3121828
BLAST score	596
E value	5.0e-62
Match length	124
% identity	92
NCBI Description	BENE PROTEIN >gi_2135423_pir__I38891 hypothetical protein - human (fragment) >gi_1000712 (U17077) unknown [Homo sapiens]

Seq. No.	229740
Seq. ID	LIB3196-039-P1-M1-H7
Method	BLASTX
NCBI GI	g631009
BLAST score	355
E value	9.0e-34
Match length	67
% identity	99
NCBI Description	G-protein - chicken >gi_2119466_pir__I50230 G protein alpha subunit - chicken >gi_454411 (L24550) G protein alpha subunit [Gallus gallus]

Seq. No.	229741
Seq. ID	LIB3196-039-P1-M1-H8
Method	BLASTX
NCBI GI	g3396079
BLAST score	250
E value	1.0e-21
Match length	97
% identity	47
NCBI Description	(AF080173) inositol 1,3,4-trisphosphate 5/6-kinase [Arabidopsis thaliana]

Seq. No.	229742
Seq. ID	LIB3196-040-P1-M1-A6
Method	BLASTX
NCBI GI	g3745821

BLAST score	660
E value	2.0e-69
Match length	124
% identity	99
NCBI Description	Chain A, Tubulin Alpha-Beta Dimer, Electron Diffraction

Seq. No.	229743
Seq. ID	LIB3196-040-P1-M1-A8
Method	BLASTX
NCBI GI	g119172
BLAST score	604
E value	5.0e-63
Match length	117
% identity	99
NCBI Description	ELONGATION FACTOR 2 (EF-2) >gi_2144947_pir__EFHU2 translation elongation factor eEF-2 - human >gi_31106_emb_CAA35829_ (X51466) elongation factor 2 [Homo sapiens] >gi_31108_emb_CAA77750_ (Z11692) human elongation factor 2 [Homo sapiens] >gi_4503483_ref_NP_001952.1_pEEF2_ eukaryotic translation elongation factor

Seq. No.	229744
Seq. ID	LIB3196-040-P1-M1-B10
Method	BLASTX
NCBI GI	g126156
BLAST score	655
E value	6.0e-69
Match length	128
% identity	98
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229745
Seq. ID	LIB3196-040-P1-M1-B7
Method	BLASTX
NCBI GI	g3122673
BLAST score	407
E value	7.0e-40
Match length	108
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	229746
Seq. ID	LIB3196-040-P1-M1-C10
Method	BLASTX
NCBI GI	g2244979
BLAST score	422
E value	1.0e-41
Match length	122
% identity	68
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	229747
Seq. ID	LIB3196-040-P1-M1-C11
Method	BLASTX
NCBI GI	g125105
BLAST score	416
E value	3.0e-41
Match length	83
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	229748
Seq. ID	LIB3196-040-P1-M1-C2
Method	BLASTX
NCBI GI	g544939
BLAST score	469
E value	4.0e-47
Match length	138
% identity	70
NCBI Description	(S68736) myosin heavy chain, MHC [rats, CCl4-cirrhotic liver, fat-storing cell line, Peptide, 882 aa] [Rattus sp.]

Seq. No.	229749
Seq. ID	LIB3196-040-P1-M1-C4
Method	BLASTX
NCBI GI	g417103
BLAST score	591
E value	2.0e-61
Match length	120
% identity	99
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	229750
Seq. ID	LIB3196-040-P1-M1-C6
Method	BLASTX

NCBI GI	g728838
BLAST score	147
E value	2.0e-09
Match length	47
% identity	14
NCBI Description	ALU SUBFAMILY SX WARNING ENTRY !!!!

Seq. No.	229751
Seq. ID	LIB3196-040-P1-M1-D1
Method	BLASTX
NCBI GI	g2414156
BLAST score	652
E value	1.0e-68
Match length	124
% identity	100
NCBI Description	(Y09787) delta-endotoxin [Bacillus thuringiensis]

Seq. No.	229752
Seq. ID	LIB3196-040-P1-M1-D10
Method	BLASTX
NCBI GI	g3915742
BLAST score	582
E value	2.0e-60
Match length	122
% identity	90
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229753
Seq. ID	LIB3196-040-P1-M1-D11
Method	BLASTX
NCBI GI	g3860274
BLAST score	204
E value	5.0e-16
Match length	53
% identity	70
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	229754
Seq. ID	LIB3196-040-P1-M1-D12
Method	BLASTX
NCBI GI	g1363944
BLAST score	649
E value	3.0e-68
Match length	129
% identity	100
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	229755
Seq. ID	LIB3196-040-P1-M1-D5
Method	BLASTX

NCBI GI	g1173055
BLAST score	606
E value	3.0e-63
Match length	121
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No.	229756
Seq. ID	LIB3196-040-P1-M1-D7
Method	BLASTX
NCBI GI	g2911060
BLAST score	236
E value	8.0e-20
Match length	95
% identity	36
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana] >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	229757
Seq. ID	LIB3196-040-P1-M1-D8
Method	BLASTX
NCBI GI	g106322
BLAST score	578
E value	5.0e-60
Match length	113
% identity	90
NCBI Description	hypothetical protein (L1H 3' region) - human

Seq. No.	229758
Seq. ID	LIB3196-040-P1-M1-E10
Method	BLASTX
NCBI GI	g2062154
BLAST score	283
E value	3.0e-25
Match length	101
% identity	61
NCBI Description	(AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229759
Seq. ID	LIB3196-040-P1-M1-E2
Method	BLASTX
NCBI GI	g3820648
BLAST score	305
E value	5.0e-37
Match length	121
% identity	70
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	229760
Seq. ID	LIB3196-040-P1-M1-E8
Method	BLASTX
NCBI GI	g400205
BLAST score	646

E value	6.0e-68
Match length	124
% identity	95
NCBI Description	PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE) >gi_420086_pir__A38206 procollagen-lysine 5-dioxygenase (EC 1.14.11.4) precursor - human >gi_190074 (L06419) lysyl hydroxylase [Homo sapiens] >gi_4557837_ref_NP_000293.1_pPLOD_ procollagen-lysine 5-dioxygenase; lysine hydroxylase; procollagen-lysine, 2-oxoglutarate 5-dioxygenase; lysine, 2-oxoglutarate 5-dioxygenase

Seq. No.	229761
Seq. ID	LIB3196-040-P1-M1-F10
Method	BLASTX
NCBI GI	g1724114
BLAST score	305
E value	7.0e-28
Match length	68
% identity	85
NCBI Description	(U80041) Af10-protein [Avena fatua]

Seq. No.	229762
Seq. ID	LIB3196-040-P1-M1-F12
Method	BLASTX
NCBI GI	g4126405
BLAST score	525
E value	1.0e-53
Match length	117
% identity	91
NCBI Description	(AB011798) homolog to defender against apoptotic death 1 [Citrus unshiu]

Seq. No.	229763
Seq. ID	LIB3196-040-P1-M1-F2
Method	BLASTX
NCBI GI	g1362819
BLAST score	211
E value	7.0e-17
Match length	114
% identity	40
NCBI Description	HPBRII-7 protein - human >gi_871299_emb_CAA47752_ (X67337) Human pre-mRNA cleavage factor I 68 kDa subunit [Homo sapiens] >gi_871301_emb_CAA47751_ (X67336) HPBRII-7 [Homo sapiens]

Seq. No.	229764
Seq. ID	LIB3196-040-P1-M1-F4
Method	BLASTX
NCBI GI	g1363944
BLAST score	678
E value	1.0e-71
Match length	136
% identity	100
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	229765
Seq. ID	LIB3196-040-P1-M1-F5
Method	BLASTX
NCBI GI	g3184184
BLAST score	544
E value	7.0e-56
Match length	137
% identity	80
NCBI Description	(AB002134) airway trypsin-like protease [Homo sapiens]

Seq. No.	229766
Seq. ID	LIB3196-040-P1-M1-F8
Method	BLASTX
NCBI GI	g1209756
BLAST score	498
E value	1.0e-50
Match length	126
% identity	79
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	229767
Seq. ID	LIB3196-040-P1-M1-F9
Method	BLASTX
NCBI GI	g72287
BLAST score	575
E value	1.0e-59
Match length	109
% identity	100
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	229768
Seq. ID	LIB3196-040-P1-M1-G10
Method	BLASTX
NCBI GI	g586120
BLAST score	231
E value	3.0e-19
Match length	102
% identity	49
NCBI Description	TRICHOHYALIN >gi_539701_pir__A45973 trichohyalin - human >gi_292836 (L09190) trichohyalin [Homo sapiens]

Seq. No.	229769
Seq. ID	LIB3196-040-P1-M1-G11
Method	BLASTX
NCBI GI	g1101029
BLAST score	476
E value	5.0e-48
Match length	110
% identity	85
NCBI Description	(U30891) pyruvate carboxylase precursor [Homo sapiens] >gi_4505627_ref_NP_000911.1_pPC_ pyruvate carboxylase

Seq. No.	229770
Seq. ID	LIB3196-040-P1-M1-G2

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Method	BLASTX
NCBI GI	g3122232
BLAST score	178
E value	5.0e-13
Match length	99
% identity	51
NCBI Description	MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana]

Seq. No.	229771
Seq. ID	LIB3196-040-P1-M1-G5
Method	BLASTX
NCBI GI	g544184
BLAST score	646
E value	7.0e-68
Match length	133
% identity	81
NCBI Description	4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No.	229772
Seq. ID	LIB3196-040-P1-M1-G7
Method	BLASTX
NCBI GI	g3115204
BLAST score	149
E value	1.0e-09
Match length	82
% identity	46
NCBI Description	(Y12059) strong homology to human RING3 sequence [Homo sapiens]

Seq. No.	229773
Seq. ID	LIB3196-040-P1-M1-G9
Method	BLASTX
NCBI GI	g2118965
BLAST score	631
E value	4.0e-66
Match length	125
% identity	32
NCBI Description	polyubiquitin - bovine (fragment) >gi_163573 (M62428) polyubiquitin [Bos taurus]

Seq. No.	229774
Seq. ID	LIB3196-040-P1-M1-H1
Method	BLASTX
NCBI GI	g4455253
BLAST score	389
E value	9.0e-38
Match length	110
% identity	64
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1)

(Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	229775
Seq. ID	LIB3196-040-P1-M1-H10
Method	BLASTX
NCBI GI	g126156
BLAST score	428
E value	2.0e-42
Match length	120
% identity	71
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229776
Seq. ID	LIB3196-040-P1-M1-H6
Method	BLASTX
NCBI GI	g3395938
BLAST score	318
E value	2.0e-29
Match length	107
% identity	34
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	229777
Seq. ID	LIB3196-040-P1-M1-H7
Method	BLASTX
NCBI GI	g2791834
BLAST score	407
E value	6.0e-50
Match length	103
% identity	99
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	229778
Seq. ID	LIB3196-041-P1-M1-A10
Method	BLASTX
NCBI GI	g3874039
BLAST score	211
E value	7.0e-17
Match length	109
% identity	37
NCBI Description	(Z75526) Weak similarity to Staphyloccus autolysin gene (TR:G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	229779
Seq. ID	LIB3196-041-P1-M1-A5
Method	BLASTX
NCBI GI	g4490331
BLAST score	373
E value	7.0e-36

Match length	97
% identity	73
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229780
Seq. ID	LIB3196-041-P1-M1-A7
Method	BLASTX
NCBI GI	g167367
BLAST score	468
E value	5.0e-47
Match length	112
% identity	82
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	229781
Seq. ID	LIB3196-041-P1-M1-A8
Method	BLASTX
NCBI GI	g2911247
BLAST score	289
E value	4.0e-26
Match length	70
% identity	83
NCBI Description	(AF047863) PNS specific microtubule-associated protein tau, adult isoform [Homo sapiens]

Seq. No.	229782
Seq. ID	LIB3196-041-P1-M1-B12
Method	BLASTX
NCBI GI	g3914477
BLAST score	317
E value	3.0e-29
Match length	56
% identity	100
NCBI Description	PROTEASE SERINE-LIKE 1 PRECURSOR (NORMAL EPITHELIAL CELL-SPECIFIC 1) >gi_1835925_bbs_178917 (S82666) serine protease homolog=NES1 [human, mammary epithelial cells, 76N, Peptide, 276 aa] [Homo sapiens] >gi_2558912 (AF024605) serine protease-like protease [Homo sapiens] >gi_3065711 (AF055481) normal epithelial cell-specific 1 [Homo sapiens] >gi_4506157_ref_NP_002767.1_pPRSSL1_ protease, serine-like,

Seq. No.	229783
Seq. ID	LIB3196-041-P1-M1-B2
Method	BLASTX
NCBI GI	g2459421
BLAST score	410
E value	3.0e-40
Match length	110
% identity	68
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	229784
Seq. ID	LIB3196-041-P1-M1-B3
Method	BLASTX
NCBI GI	g2995990
BLAST score	209

E value	8.0e-17
Match length	79
% identity	59
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	229785
Seq. ID	LIB3196-041-P1-M1-B4
Method	BLASTX
NCBI GI	g3044212
BLAST score	134
E value	6.0e-13
Match length	87
% identity	48
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	229786
Seq. ID	LIB3196-041-P1-M1-B7
Method	BLASTX
NCBI GI	g3127127
BLAST score	424
E value	8.0e-42
Match length	101
% identity	88
NCBI Description	(AF061016) UDP-glucose dehydrogenase [Homo sapiens] >gi_3452405_emb_CAA07609_ (AJ007702) UDPglucose dehydrogenase [Homo sapiens] >gi_4507813_ref_NP_003350.1_pUGDH_ UDP-glucose dehydrogenase

Seq. No.	229787
Seq. ID	LIB3196-041-P1-M1-C10
Method	BLASTX
NCBI GI	g2832661
BLAST score	154
E value	3.0e-16
Match length	105
% identity	46
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	229788
Seq. ID	LIB3196-041-P1-M1-C11
Method	BLASTX
NCBI GI	g2522230
BLAST score	238
E value	4.0e-20
Match length	125
% identity	39
NCBI Description	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq. No.	229789
Seq. ID	LIB3196-041-P1-M1-C5
Method	BLASTX
NCBI GI	g3452507

BLAST score	598
E value	3.0e-62
Match length	132
% identity	86
NCBI Description	(AJ010483) CtBP1 protein [Mus musculus]

Seq. No.	229790
Seq. ID	LIB3196-041-P1-M1-C6
Method	BLASTX
NCBI GI	g1350762
BLAST score	348
E value	2.0e-33
Match length	68
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT BINDING PROTEIN 107) (TAXREB107) (NEOPLASM-RELATED PROTEIN C140) >gi_2136251_pir__I51803 TAXREB107 - human >gi_433416_dbj_BAA04491_ (D17554) TAXREB107 [Homo sapiens]

Seq. No.	229791
Seq. ID	LIB3196-041-P1-M1-C7
Method	BLASTX
NCBI GI	g3738257
BLAST score	448
E value	1.0e-44
Match length	94
% identity	94
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	229792
Seq. ID	LIB3196-041-P1-M1-C9
Method	BLASTX
NCBI GI	g1350681
BLAST score	649
E value	3.0e-68
Match length	130
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L1 (L4)

Seq. No.	229793
Seq. ID	LIB3196-041-P1-M1-D1
Method	BLASTX
NCBI GI	g322750
BLAST score	535
E value	6.0e-55
Match length	105
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	229794
Seq. ID	LIB3196-041-P1-M1-D10
Method	BLASTX
NCBI GI	g2443887
BLAST score	490

E value	1.0e-49
Match length	120
% identity	78
NCBI Description	(AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No.	229795
Seq. ID	LIB3196-041-P1-M1-D11
Method	BLASTX
NCBI GI	g2129604
BLAST score	184
E value	1.0e-13
Match length	50
% identity	76
NCBI Description	GTP-binding protein 1 - Arabidopsis thaliana >gi_2129607_pir__S71584 GTP-binding protein ATBG1 - Arabidopsis thaliana >gi_1184981 (U46924) ATGB1 [Arabidopsis thaliana]

Seq. No.	229796
Seq. ID	LIB3196-041-P1-M1-D12
Method	BLASTX
NCBI GI	g140551
BLAST score	564
E value	3.0e-58
Match length	124
% identity	88
NCBI Description	HYPOTHETICAL 250 KD PROTEIN (ORF 2131) >gi_81505_pir__S01446 hypothetical protein 2131 - spinach chloroplast >gi_12246_emb_CAA30743_ (X07908) ORF 2131 (AA 1-2131) [Spinacia oleracea]

Seq. No.	229797
Seq. ID	LIB3196-041-P1-M1-D3
Method	BLASTX
NCBI GI	g2660676
BLAST score	155
E value	2.0e-10
Match length	32
% identity	91
NCBI Description	(AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No.	229798
Seq. ID	LIB3196-041-P1-M1-D5
Method	BLASTX
NCBI GI	g125101
BLAST score	175
E value	1.0e-12
Match length	38
% identity	89
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (CYTOSKELETAL 57 KD KERATIN) >gi_91010_pir__A23518 keratin, 57K type II cytoskeletal - mouse >gi_52785_emb_CAA27207_ (X03491) 57 kd keratin (aa 1-524) [Mus musculus]

Seq. No.	229799
Seq. ID	LIB3196-041-P1-M1-D9

Method	BLASTX
NCBI GI	g2317908
BLAST score	471
E value	2.0e-47
Match length	114
% identity	41
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	229800
Seq. ID	LIB3196-041-P1-M1-E10
Method	BLASTX
NCBI GI	g1350786
BLAST score	298
E value	4.0e-27
Match length	96
% identity	64
NCBI Description	PUTATIVE 60S RIBOSOMAL PROTEIN >gi_285945_dbj_BAA03494_ (D14660) KIAA00104 [Homo sapiens] >gi_3947438 (AC005034) ribosomal protein-like [Homo sapiens]

Seq. No.	229801
Seq. ID	LIB3196-041-P1-M1-E11
Method	BLASTX
NCBI GI	g4467153
BLAST score	524
E value	1.0e-53
Match length	118
% identity	82
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	229802
Seq. ID	LIB3196-041-P1-M1-E5
Method	BLASTX
NCBI GI	g184226
BLAST score	536
E value	6.0e-55
Match length	109
% identity	49
NCBI Description	(M83205) HLF2 [Homo sapiens]

Seq. No.	229803
Seq. ID	LIB3196-041-P1-M1-E9
Method	BLASTX
NCBI GI	g547753
BLAST score	466
E value	5.0e-47
Match length	98
% identity	97
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	229804
Seq. ID	LIB3196-041-P1-M1-F1
Method	BLASTX
NCBI GI	g122085
BLAST score	432
E value	6.0e-43

Match length	105
% identity	84
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	229805
Seq. ID	LIB3196-041-P1-M1-F4
Method	BLASTX
NCBI GI	g1652434
BLAST score	303
E value	1.0e-27
Match length	126
% identity	51
NCBI Description	(D90905) N-acetylglutamate kinase [Synechocystis sp.]

Seq. No.	229806
Seq. ID	LIB3196-041-P1-M1-G12
Method	BLASTX
NCBI GI	g2804273
BLAST score	679
E value	9.0e-72
Match length	131
% identity	35
NCBI Description	(D89980) alpha actinin 4 [Homo sapiens]

Seq. No.	229807
Seq. ID	LIB3196-041-P1-M1-G2
Method	BLASTX
NCBI GI	g3127127
BLAST score	190
E value	8.0e-15
Match length	46
% identity	83
NCBI Description	(AF061016) UDP-glucose dehydrogenase [Homo sapiens] >gi_3452405_emb_CAA07609_ (AJ007702) UDPglucose

	dehydrogenase [Homo sapiens] >gi_4507813_ref_NP_003350.1_pUGDH_ UDP-glucose dehydrogenase
Seq. No.	229808
Seq. ID	LIB3196-041-P1-M1-G3
Method	BLASTX
NCBI GI	g167311
BLAST score	496
E value	2.0e-50
Match length	113
% identity	86
NCBI Description	(M83301) 2S albumin storage protein [Gossypium hirsutum]
Seq. No.	229809
Seq. ID	LIB3196-041-P1-M1-G4
Method	BLASTX
NCBI GI	g114549
BLAST score	491
E value	1.0e-49
Match length	128
% identity	81
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_106207_pir__A33370 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - human >gi_179281 (M27132) ATP synthase beta subunit precursor [Homo sapiens]
Seq. No.	229810
Seq. ID	LIB3196-041-P1-M1-G5
Method	BLASTX
NCBI GI	g167367
BLAST score	464
E value	1.0e-46
Match length	120
% identity	76
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	229811
Seq. ID	LIB3196-041-P1-M1-G6
Method	BLASTX
NCBI GI	g2765244
BLAST score	282
E value	3.0e-25
Match length	118
% identity	49
NCBI Description	(Y12807) invertase inhibitor homolog [Arabidopsis thaliana]
Seq. No.	229812
Seq. ID	LIB3196-041-P1-M1-G7
Method	BLASTX
NCBI GI	g266691
BLAST score	243
E value	8.0e-21
Match length	88
% identity	61
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin

[redacted] [redacted]

[Gossypium hirsutum]

Seq. No.	229813
Seq. ID	LIB3196-041-P1-M1-G8
Method	BLASTX
NCBI GI	g3650032
BLAST score	279
E value	7.0e-25
Match length	60
% identity	70
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	229814
Seq. ID	LIB3196-041-P1-M1-G9
Method	BLASTX
NCBI GI	g386850
BLAST score	572
E value	3.0e-59
Match length	115
% identity	99
NCBI Description	(M19723) keratin K5 [Homo sapiens]

Seq. No.	229815
Seq. ID	LIB3196-041-P1-M1-H12
Method	BLASTX
NCBI GI	g3337356
BLAST score	364
E value	6.0e-35
Match length	70
% identity	97
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	229816
Seq. ID	LIB3196-041-P1-M1-H3
Method	BLASTX
NCBI GI	g544939
BLAST score	465
E value	1.0e-46
Match length	131
% identity	73
NCBI Description	(S68736) myosin heavy chain, MHC [rats, CCl4-cirrhotic liver fat-storing cell line, Peptide, 882 aa] [Rattus sp.]

Seq. No.	229817
Seq. ID	LIB3196-041-P1-M1-H4
Method	BLASTX
NCBI GI	g3702327
BLAST score	150
E value	9.0e-10
Match length	92
% identity	41
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	229818
Seq. ID	LIB3196-041-P1-M1-H6

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Method	BLASTX
NCBI GI	g4105683
BLAST score	429
E value	2.0e-42
Match length	119
% identity	63
NCBI Description	(AF049892) unknown [Oryza sativa] >gi_4105692 (AF050155) embryo-specific protein [Oryza sativa subsp. indica]

Seq. No.	229819
Seq. ID	LIB3196-041-P1-M1-H7
Method	BLASTX
NCBI GI	g3115374
BLAST score	174
E value	9.0e-13
Match length	90
% identity	46
NCBI Description	(AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

Seq. No.	229820
Seq. ID	LIB3196-041-P1-M1-H9
Method	BLASTX
NCBI GI	g1694976
BLAST score	352
E value	2.0e-33
Match length	99
% identity	68
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	229821
Seq. ID	LIB3196-042-P1-M1-A10
Method	BLASTX
NCBI GI	g1199772
BLAST score	201
E value	9.0e-16
Match length	43
% identity	84
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No.	229822
Seq. ID	LIB3196-042-P1-M1-A3
Method	BLASTX
NCBI GI	g3746652
BLAST score	571
E value	4.0e-59
Match length	127
% identity	88
NCBI Description	(AF070523) JWA protein [Homo sapiens]

Seq. No.	229823
Seq. ID	LIB3196-042-P1-M1-A9
Method	BLASTX
NCBI GI	g3334138

BLAST score 535
E value 6.0e-55
Match length 119
% identity 82
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No. 229824
Seq. ID LIB3196-042-P1-M1-B11
Method BLASTX
NCBI GI g137578
BLAST score 396
E value 1.0e-38
Match length 108
% identity 75
NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No. 229825
Seq. ID LIB3196-042-P1-M1-B3
Method BLASTX
NCBI GI g2498829
BLAST score 134
E value 3.0e-12
Match length 43
% identity 88
NCBI Description RETINA-SPECIFIC 15.7 KD PROTEIN >gi_2136811_pir__I45978 retina-specific 15.7 kDa protein - bovine >gi_163673 (M34915) retina-specific 15.7 kDa protein [Bos taurus] >gi_356830_prf__1211339A protein,retina specific [Bos taurus]

Seq. No. 229826
Seq. ID LIB3196-042-P1-M1-B8
Method BLASTX
NCBI GI g2351035
BLAST score 600
E value 2.0e-62
Match length 126
% identity 90
NCBI Description (AB004930) Smad 3 [Homo sapiens]

Seq. No. 229827
Seq. ID LIB3196-042-P1-M1-C1
Method BLASTX
NCBI GI g2497367
BLAST score 372
E value 4.0e-68
Match length 127
% identity 96
NCBI Description HYPOTHETICAL PROTEIN KIAA0274 >gi_1665813_dbj_BAA13403_ (D87464) Similar to S.cerevisiae hypothetical protein N0330 (S55864) [Homo sapiens]

Seq. No.	229828
Seq. ID	LIB3196-042-P1-M1-C4
Method	BLASTX
NCBI GI	g3176726
BLAST score	294
E value	1.0e-26
Match length	93
% identity	60
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	229829
Seq. ID	LIB3196-042-P1-M1-C6
Method	BLASTX
NCBI GI	g1705678
BLAST score	580
E value	3.0e-60
Match length	120
% identity	49
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No.	229830
Seq. ID	LIB3196-042-P1-M1-C7
Method	BLASTX
NCBI GI	g2833388
BLAST score	436
E value	2.0e-43
Match length	113
% identity	75
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	229831
Seq. ID	LIB3196-042-P1-M1-C8
Method	BLASTX
NCBI GI	g2648442
BLAST score	179
E value	3.0e-13
Match length	110
% identity	21
NCBI Description	(AE000959) cell division control protein 48, AAA family (cdc48-2) [Archaeoglobus fulgidus]

Seq. No.	229832
Seq. ID	LIB3196-042-P1-M1-C9
Method	BLASTX
NCBI GI	g266690
BLAST score	338
E value	7.0e-32
Match length	94
% identity	73

NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]
Seq. No.	229833
Seq. ID	LIB3196-042-P1-M1-D1
Method	BLASTX
NCBI GI	g1514614
BLAST score	141
E value	2.0e-11
Match length	119
% identity	40
NCBI Description	(X92842) nuclear protein [Mus musculus]
Seq. No.	229834
Seq. ID	LIB3196-042-P1-M1-D5
Method	BLASTX
NCBI GI	g339743
BLAST score	200
E value	1.0e-31
Match length	71
% identity	91
NCBI Description	(M55913) tumor necrosis factor-beta [Homo sapiens] >gi_4505031_ref_NP_000586.1_pLTA_ lymphotoxin alpha (formerly tumor necrosis factor beta)
Seq. No.	229835
Seq. ID	LIB3196-042-P1-M1-D8
Method	BLASTX
NCBI GI	g3901014
BLAST score	234
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	229836
Seq. ID	LIB3196-042-P1-M1-E11
Method	BLASTX
NCBI GI	g135858
BLAST score	231
E value	2.0e-21
Match length	88
% identity	68
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi_99760_pir__S22201 tonoplast intrinsic protein alpha - Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.	229837
Seq. ID	LIB3196-042-P1-M1-E6
Method	BLASTX
NCBI GI	g1707480

BLAST score	146
E value	3.0e-09
Match length	71
% identity	42
NCBI Description	(Y08614) CRM1 [Homo sapiens]

Seq. No.	229838
Seq. ID	LIB3196-042-P1-M1-E7
Method	BLASTX
NCBI GI	g729887
BLAST score	552
E value	4.0e-57
Match length	121
% identity	98
NCBI Description	TYROSINE-PROTEIN KINASE CSK (C-SRC KINASE) (PROTEIN-TYROSINE KINASE CYL) >gi_88519_pir__JH0559 protein-tyrosine kinase (EC 2.7.1.112) CSK - human >gi_30256_emb_CAA42556_ (X59932) c-src-kinase [Homo sapiens] >gi_30315_emb_CAA42713_ (X60114) put. cytoplasmic tyrosine kinase [Homo sapiens]

Seq. No.	229839
Seq. ID	LIB3196-042-P1-M1-F2
Method	BLASTX
NCBI GI	g852428
BLAST score	473
E value	1.0e-47
Match length	101
% identity	88
NCBI Description	(U09202) ornithine decarboxylase antizyme [Homo sapiens]

Seq. No.	229840
Seq. ID	LIB3196-042-P1-M1-F5
Method	BLASTX
NCBI GI	g3877201
BLAST score	323
E value	5.0e-30
Match length	123
% identity	48
NCBI Description	(Z70780) cDNA EST yk465d10.3 comes from this gene; cDNA EST yk465d10.5 comes from this gene; cDNA EST yk481d9.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	229841
Seq. ID	LIB3196-042-P1-M1-F7
Method	BLASTX
NCBI GI	g1304227
BLAST score	405
E value	1.0e-39
Match length	88
% identity	83
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	229842
Seq. ID	LIB3196-042-P1-M1-G1

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Method	BLASTX
NCBI GI	g996057
BLAST score	621
E value	6.0e-65
Match length	125
% identity	96
NCBI Description	(X90872) associated to Golgi apparatus [Homo sapiens]

Seq. No.	229843
Seq. ID	LIB3196-042-P1-M1-G2
Method	BLASTX
NCBI GI	g728831
BLAST score	139
E value	9.0e-18
Match length	172
% identity	15
NCBI Description	ALU SUBFAMILY J WARNING ENTRY !!!!

Seq. No.	229844
Seq. ID	LIB3196-042-P1-M1-G3
Method	BLASTX
NCBI GI	g1336807
BLAST score	310
E value	1.0e-28
Match length	112
% identity	56
NCBI Description	(S81193) CEN=GTP-binding protein homolog [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum] >gi_1587482_prf__2206476A CEN gene [Antirrhinum sp.]

Seq. No.	229845
Seq. ID	LIB3196-042-P1-M1-G7
Method	BLASTX
NCBI GI	g3024889
BLAST score	214
E value	2.0e-17
Match length	87
% identity	49
NCBI Description	HYPOTHETICAL PROTEIN KIAA0288 (HA6116) >gi_2564324_dbj_BAA22957_ (AB006626) KIAA0288 [Homo sapiens]

Seq. No.	229846
Seq. ID	LIB3196-042-P1-M1-H1
Method	BLASTX
NCBI GI	g266691
BLAST score	265
E value	2.0e-23
Match length	51
% identity	100
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	229847
Seq. ID	LIB3196-042-P1-M1-H10
Method	BLASTX
NCBI GI	g2749943

BLAST score	353
E value	9.0e-34
Match length	92
% identity	66
NCBI Description	(U71244) pathogenesis-related group 5 protein [Brassica rapa]

Seq. No.	229848
Seq. ID	LIB3196-042-P1-M1-H3
Method	BLASTX
NCBI GI	g2959872
BLAST score	176
E value	8.0e-27
Match length	73
% identity	88
NCBI Description	(AJ002308) synaptogyrin 2 [Homo sapiens]

Seq. No.	229849
Seq. ID	LIB3196-042-P1-M1-H7
Method	BLASTX
NCBI GI	g37848
BLAST score	216
E value	2.0e-17
Match length	65
% identity	69
NCBI Description	(X16478) vimentin N-terminal fragment (AA 1-135) [Homo sapiens]

Seq. No.	229850
Seq. ID	LIB3196-043-P1-M1-A1
Method	BLASTX
NCBI GI	g2496887
BLAST score	239
E value	4.0e-20
Match length	100
% identity	54
NCBI Description	HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III >gi_732538 (U22832) C09F5.2 gene product [Caenorhabditis elegans]

Seq. No.	229851
Seq. ID	LIB3196-043-P1-M1-A10
Method	BLASTX
NCBI GI	g123644
BLAST score	591
E value	2.0e-61
Match length	131
% identity	92
NCBI Description	HEAT SHOCK COGNATE 71 KD PROTEIN >gi_108737_pir__S11456 heat shock cognate protein, 79K - bovine >gi_428_emb_CAA37823_ (X53827) 79KDa heat shock cognate protein [Bos taurus]

Seq. No.	229852
Seq. ID	LIB3196-043-P1-M1-A2
Method	BLASTX
NCBI GI	g3738257

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BLAST score	483
E value	9.0e-49
Match length	100
% identity	94
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	229853
Seq. ID	LIB3196-043-P1-M1-A4
Method	BLASTX
NCBI GI	g417031
BLAST score	353
E value	2.0e-33
Match length	70
% identity	99
NCBI Description	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1) >gi_87609_pir__A41268 guanine nucleotide-binding protein 1 - human >gi_183002 (M55542) guanylate binding protein isoform I [Homo sapiens] >gi_4503939_ref_NP_002044.1_pGBP1_ guanylate binding protein 1, interferon-inducible, 67kD

Seq. No.	229854
Seq. ID	LIB3196-043-P1-M1-A5
Method	BLASTX
NCBI GI	g225580
BLAST score	568
E value	9.0e-59
Match length	126
% identity	88
NCBI Description	storage protein C72 [Saguinus oedipus]

Seq. No.	229855
Seq. ID	LIB3196-043-P1-M1-B10
Method	BLASTX
NCBI GI	g1732511
BLAST score	360
E value	2.0e-34
Match length	95
% identity	73
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	229856
Seq. ID	LIB3196-043-P1-M1-B12
Method	BLASTX
NCBI GI	g2494238
BLAST score	549
E value	2.0e-56
Match length	130
% identity	87
NCBI Description	PROBABLE PEROXISOMAL ENOYL-COA HYDRATASE >gi_2135896_pir__I38882 peroxisomal enoyl-CoA hydratase-like protein - human >gi_564065 (U16660) peroxisomal enoyl-CoA hydratase-like protein [Homo sapiens] >gi_2623168 (AF030249) putative dienoyl-CoA isomerase [Homo sapiens] >gi_4503447_ref_NP_001389.1_pECH1_ enoyl Coenzyme

A hydratase 1, peroxisomal

Seq. No.	229857
Seq. ID	LIB3196-043-P1-M1-B2
Method	BLASTX
NCBI GI	g1200256
BLAST score	507
E value	1.0e-51
Match length	127
% identity	77
NCBI Description	(X90990) stpk1 protein kinase [Solanum tuberosum]

Seq. No.	229858
Seq. ID	LIB3196-043-P1-M1-B8
Method	BLASTX
NCBI GI	g3281851
BLAST score	92
E value	1.0e-09
Match length	49
% identity	82
NCBI Description	(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]

Seq. No.	229859
Seq. ID	LIB3196-043-P1-M1-B9
Method	BLASTX
NCBI GI	g683553
BLAST score	247
E value	4.0e-21
Match length	112
% identity	50
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	229860
Seq. ID	LIB3196-043-P1-M1-C1
Method	BLASTX
NCBI GI	g2308997
BLAST score	224
E value	1.0e-18
Match length	44
% identity	100
NCBI Description	(AB004066) DEC1 [Homo sapiens] >gi_4503299_ref_NP_003661.1_pDEC1_ differentiated Embryo Chondrocyte expressed gene

Seq. No.	229861
Seq. ID	LIB3196-043-P1-M1-C3
Method	BLASTX
NCBI GI	g539602
BLAST score	691
E value	4.0e-73
Match length	136
% identity	99
NCBI Description	glycine hydroxymethyltransferase (EC 2.1.2.1) precursor, mitochondrial - human (fragment) >gi_703093 (L11932) serine hydroxymethyltransferase [Homo sapiens]

Seq. No.	229862
Seq. ID	LIB3196-043-P1-M1-C4
Method	BLASTX
NCBI GI	g2780365
BLAST score	157
E value	1.0e-10
Match length	58
% identity	55
NCBI Description	(AB007693) Elongin C [Drosophila melanogaster]

Seq. No.	229863
Seq. ID	LIB3196-043-P1-M1-C6
Method	BLASTX
NCBI GI	g2507222
BLAST score	403
E value	2.0e-39
Match length	113
% identity	64
NCBI Description	KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi_1709236 (U09505) kinase associated protein phosphatase [Arabidopsis thaliana]

Seq. No.	229864
Seq. ID	LIB3196-043-P1-M1-C7
Method	BLASTX
NCBI GI	g3851697
BLAST score	448
E value	1.0e-44
Match length	100
% identity	83
NCBI Description	(AF100204) putative chemokine receptor [Macaca mulatta]

Seq. No.	229865
Seq. ID	LIB3196-043-P1-M1-D1
Method	BLASTX
NCBI GI	g4490295
BLAST score	158
E value	1.0e-10
Match length	128
% identity	29
NCBI Description	(AL035678) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229866
Seq. ID	LIB3196-043-P1-M1-D5
Method	BLASTX
NCBI GI	g4455323
BLAST score	521
E value	3.0e-53
Match length	125
% identity	82
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	229867
Seq. ID	LIB3196-043-P1-M1-D6
Method	BLASTX

NCBI GI	g965470
BLAST score	658
E value	3.0e-69
Match length	134
% identity	98
NCBI Description	(L37033) FK-506 binding protein homologue [Homo sapiens] >gi_3395419 (AC005387) FK-506 binding protein homologue [Homo sapiens]

Seq. No.	229868
Seq. ID	LIB3196-043-P1-M1-D8
Method	BLASTX
NCBI GI	g3915742
BLAST score	597
E value	4.0e-62
Match length	124
% identity	91
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319 (M69188) legumin A [Gossypium hirsutum] >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	229869
Seq. ID	LIB3196-043-P1-M1-D9
Method	BLASTX
NCBI GI	g106322
BLAST score	120
E value	7.0e-10
Match length	113
% identity	42
NCBI Description	hypothetical protein (L1H 3' region) - human

Seq. No.	229870
Seq. ID	LIB3196-043-P1-M1-E10
Method	BLASTX
NCBI GI	g2982268
BLAST score	399
E value	5.0e-39
Match length	87
% identity	90
NCBI Description	(AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No.	229871
Seq. ID	LIB3196-043-P1-M1-E2
Method	BLASTX
NCBI GI	g2289003
BLAST score	466
E value	8.0e-47
Match length	127
% identity	73
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	229872
Seq. ID	LIB3196-043-P1-M1-E6
Method	BLASTX

NCBI GI	g129356
BLAST score	228
E value	2.0e-19
Match length	47
% identity	94
NCBI Description	P3 PROTEIN >gi_87501_pir__S01696 gene P3 protein - human >gi_35188_emb_CAA30998_ (X12458) P3 protein (AA 1-1382) [Homo sapiens] >gi_1203976 (L44140) P3 gene product [Homo sapiens]

Seq. No.	229873
Seq. ID	LIB3196-043-P1-M1-E7
Method	BLASTX
NCBI GI	g1399325
BLAST score	627
E value	1.0e-65
Match length	131
% identity	89
NCBI Description	(U41832) MHC class I antigen Mamu A*07 [Macaca mulatta]

Seq. No.	229874
Seq. ID	LIB3196-043-P1-M1-E8
Method	BLASTX
NCBI GI	g2736151
BLAST score	255
E value	5.0e-22
Match length	131
% identity	38
NCBI Description	(AF021935) mytonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]

Seq. No.	229875
Seq. ID	LIB3196-043-P1-M1-E9
Method	BLASTX
NCBI GI	g417103
BLAST score	533
E value	1.0e-54
Match length	107
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	229876
Seq. ID	LIB3196-043-P1-M1-F2
Method	BLASTX
NCBI GI	g4567253
BLAST score	166
E value	1.0e-11
Match length	67
% identity	54
NCBI Description	(AC007070) putative serpin protein [Arabidopsis thaliana]

Seq. No.	229877
Seq. ID	LIB3196-043-P1-M1-F7
Method	BLASTX
NCBI GI	g3786016
BLAST score	431
E value	1.0e-42
Match length	95
% identity	79
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	229878
Seq. ID	LIB3196-043-P1-M1-F8
Method	BLASTX
NCBI GI	g4033735
BLAST score	693
E value	2.0e-73
Match length	133
% identity	98
NCBI Description	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No.	229879
Seq. ID	LIB3196-043-P1-M1-F9
Method	BLASTX
NCBI GI	g2213610
BLAST score	216
E value	2.0e-17
Match length	111
% identity	41
NCBI Description	(AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No.	229880
Seq. ID	LIB3196-043-P1-M1-G1
Method	BLASTX
NCBI GI	g2493319
BLAST score	380
E value	1.0e-36
Match length	94
% identity	70
NCBI Description	MAVICYANIN >gi_1836088_bbs_179249 mavicyanin=12.752 kda small blue copper-containing stellacyanin-like glycoprotein/type I cupredoxin [Cucurbita pepo=green zucchini, peelings, Peptide, 108 aa]

Seq. No.	229881

Seq. ID	LIB3196-043-P1-M1-G11
Method	BLASTX
NCBI GI	g2864615
BLAST score	595
E value	6.0e-62
Match length	125
% identity	92
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	229882
Seq. ID	LIB3196-043-P1-M1-G12
Method	BLASTX
NCBI GI	g88044
BLAST score	395
E value	1.0e-38
Match length	108
% identity	77
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]

Seq. No.	229883
Seq. ID	LIB3196-043-P1-M1-G2
Method	BLASTX
NCBI GI	g1346347
BLAST score	650
E value	2.0e-68
Match length	132
% identity	99
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	229884
Seq. ID	LIB3196-043-P1-M1-G5
Method	BLASTX
NCBI GI	g2431771
BLAST score	157
E value	4.0e-11
Match length	42
% identity	71
NCBI Description	(U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No.	229885
Seq. ID	LIB3196-043-P1-M1-G8
Method	BLASTX
NCBI GI	g3249066
BLAST score	234
E value	1.0e-19
Match length	127
% identity	46
NCBI Description	(AC004473) Similar to S. cerevisiae SIK1P protein gb_984964. ESTs gb_F15433 and gb_AA395158 come from this gene. [Arabidopsis thaliana]

Seq. No.	229886

Seq. ID	LIB3196-043-P1-M1-H10
Method	BLASTX
NCBI GI	g2997591
BLAST score	522
E value	2.0e-53
Match length	104
% identity	95
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	229887
Seq. ID	LIB3196-043-P1-M1-H4
Method	BLASTX
NCBI GI	g2435514
BLAST score	325
E value	3.0e-30
Match length	108
% identity	64
NCBI Description	(AF024504) Similar to serine/threonine protein kinase; coded for by A. thaliana cDNA T20930; coded for by A. thaliana cDNA T43472 [Arabidopsis thaliana]

Seq. No.	229888
Seq. ID	LIB3196-043-P1-M1-H9
Method	BLASTX
NCBI GI	g266691
BLAST score	150
E value	4.0e-10
Match length	65
% identity	49
NCBI Description	OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	229889
Seq. ID	LIB3196-044-P1-M1-A3
Method	BLASTX
NCBI GI	g3342571
BLAST score	140
E value	1.0e-08
Match length	48
% identity	62
NCBI Description	(AF078817) high mobility group protein [Nannospalax ehrenbergi]

Seq. No.	229890
Seq. ID	LIB3196-044-P1-M1-B2
Method	BLASTX
NCBI GI	g416662
BLAST score	467
E value	6.0e-47
Match length	120
% identity	68
NCBI Description	21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin inhibitor homolog - soybean >gi_21909_emb_CAA39860_ (X56509) 21 kDa seed protein [Theobroma cacao]

Seq. No. 229891

Seq. ID	LIB3196-044-P1-M1-B3
Method	BLASTX
NCBI GI	g3080426
BLAST score	400
E value	4.0e-39
Match length	113
% identity	66
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	229892
Seq. ID	LIB3196-044-P1-M1-B7
Method	BLASTX
NCBI GI	g1199772
BLAST score	257
E value	3.0e-22
Match length	100
% identity	59
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No.	229893
Seq. ID	LIB3196-044-P1-M1-C1
Method	BLASTX
NCBI GI	g4008159
BLAST score	440
E value	8.0e-44
Match length	115
% identity	72
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	229894
Seq. ID	LIB3196-044-P1-M1-C11
Method	BLASTX
NCBI GI	g1061040
BLAST score	293
E value	1.0e-26
Match length	89
% identity	60
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	229895
Seq. ID	LIB3196-044-P1-M1-C12
Method	BLASTX
NCBI GI	g100196
BLAST score	462
E value	2.0e-46
Match length	109
% identity	80
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	229896
Seq. ID	LIB3196-044-P1-M1-C7
Method	BLASTX
NCBI GI	g82035

BLAST score	227
E value	6.0e-19
Match length	107
% identity	35
NCBI Description	ricin E - castor bean (fragment) >gi_169715 (M17631) ricin E beta chain [Ricinus communis] >gi_225896_prf__1402359A ricin E [Ricinus communis]

Seq. No.	229897
Seq. ID	LIB3196-044-P1-M1-D11
Method	BLASTX
NCBI GI	g2662341
BLAST score	650
E value	2.0e-68
Match length	124
% identity	100
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	229898
Seq. ID	LIB3196-044-P1-M1-D3
Method	BLASTX
NCBI GI	g2498323
BLAST score	388
E value	1.0e-37
Match length	93
% identity	81
NCBI Description	EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) >gi_1488324 (U65932) extracellular matrix protein 1 [Homo sapiens] >gi_1488332 (U65938) extracellular matrix protein 1 [Homo sapiens] >gi_2654433 (U68186) extracellular matrix protein 1 [Homo sapiens]

Seq. No.	229899
Seq. ID	LIB3196-044-P1-M1-D4
Method	BLASTX
NCBI GI	g1513059
BLAST score	275
E value	2.0e-24
Match length	68
% identity	75
NCBI Description	(D87258) serin protease with IGF-binding motif [Homo sapiens] >gi_1621244_emb_CAA69226_ (Y07921) novel serine protease, PRSS11 [Homo sapiens] >gi_4506141_ref_NP_002766.1_pPRSS11_ protease, serine, 11 (IGF binding)

Seq. No.	229900
Seq. ID	LIB3196-044-P1-M1-D6
Method	BLASTX
NCBI GI	g125077
BLAST score	496
E value	3.0e-50
Match length	128
% identity	81

NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]
Seq. No.	229901
Seq. ID	LIB3196-044-P1-M1-E1
Method	BLASTX
NCBI GI	g3643595
BLAST score	291
E value	2.0e-26
Match length	104
% identity	55
NCBI Description	(AC005395) putative oleosin protein [Arabidopsis thaliana]
Seq. No.	229902
Seq. ID	LIB3196-044-P1-M1-E6
Method	BLASTX
NCBI GI	g3649778
BLAST score	333
E value	2.0e-31
Match length	110
% identity	66
NCBI Description	(AJ011303) pepc2 [Vicia faba]
Seq. No.	229903
Seq. ID	LIB3196-044-P1-M1-F10
Method	BLASTX
NCBI GI	g1363944
BLAST score	385
E value	3.0e-37
Match length	80
% identity	96
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]
Seq. No.	229904
Seq. ID	LIB3196-044-P1-M1-F12
Method	BLASTX
NCBI GI	g116850
BLAST score	548
E value	2.0e-56
Match length	108
% identity	98
NCBI Description	COFILIN, NON-MUSCLE ISOFORM >gi_89176_pir__A29240 cofilin - pig >gi_164425 (M20866) cofilin [Sus scrofa]
Seq. No.	229905
Seq. ID	LIB3196-044-P1-M1-F3
Method	BLASTX
NCBI GI	g2131161
BLAST score	158
E value	1.0e-10
Match length	60
% identity	52
NCBI Description	4-nitrophenylphosphatase (EC 3.1.3.41) - yeast

09604745.000600

(Saccharomyces cerevisiae) >gi_1431400_emb_CAA98816_ (Z74284) ORF YDL236w [Saccharomyces cerevisiae]

Seq. No.	229906
Seq. ID	LIB3196-044-P1-M1-F9
Method	BLASTX
NCBI GI	g1707017
BLAST score	275
E value	2.0e-24
Match length	65
% identity	80
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	229907
Seq. ID	LIB3196-044-P1-M1-G3
Method	BLASTX
NCBI GI	g133041
BLAST score	614
E value	4.0e-64
Match length	128
% identity	95
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi_71137_pir__R5HUP0 acidic ribosomal protein P0 - human >gi_190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041) [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_ ribosomal protein, large, P0

Seq. No.	229908
Seq. ID	LIB3196-044-P1-M1-G4
Method	BLASTX
NCBI GI	g662366
BLAST score	341
E value	4.0e-32
Match length	107
% identity	58
NCBI Description	(L39786) conglutin gamma [Lupinus angustifolius] >gi_666056_emb_CAA46552_ (X65601) conglutin gamma [Lupinus angustifolius]

Seq. No.	229909
Seq. ID	LIB3196-044-P1-M1-G5
Method	BLASTX
NCBI GI	g131805
BLAST score	577
E value	8.0e-60
Match length	116
% identity	97
NCBI Description	RAS-RELATED PROTEIN RAB-11A (RAB-11) (24KG) (YL8) >gi_108105_pir__E36364 GTP-binding protein Rab11 - dog >gi_111292_pir__JN0056 GTP-binding protein rab11 - rat >gi_631186_pir__S47169 GTP-binding protein Rab11 - human >gi_917_emb_CAA39799_ (X56388) rab11 [Canis familiaris] >gi_35889_emb_CAA37300_ (X53143) ras-like protein (AA 1-216) [Homo sapiens] >gi_206567 (M75153) ras p21-like small GTP-binding protein [Rattus norvegicus] >gi_310067

	(L19260) tubulovesicle-associated protein [Oryctolagus cuniculus] >gi_505541_emb_CAA40064_ (X56740) H rab11 small GTP binding protein [Homo sapiens] >gi_2149975 (AF000231) rab11a [Homo sapiens] >gi_1089909_prf__2018147A GTP-binding protein rab11 [Oryctolagus cuniculus]
Seq. No.	229910
Seq. ID	LIB3196-044-P1-M1-G6
Method	BLASTX
NCBI GI	g407308
BLAST score	452
E value	2.0e-45
Match length	95
% identity	92
NCBI Description	(U02493) 54 kDa protein [Homo sapiens] >gi_2808511_emb_CAA72157_ (Y11289) p54nrb [Homo sapiens]
Seq. No.	229911
Seq. ID	LIB3196-044-P1-M1-G7
Method	BLASTX
NCBI GI	g505133
BLAST score	341
E value	3.0e-32
Match length	118
% identity	66
NCBI Description	(D28557) RYB-a [Rattus norvegicus]
Seq. No.	229912
Seq. ID	LIB3196-044-P1-M1-G8
Method	BLASTX
NCBI GI	g1399319
BLAST score	469
E value	3.0e-47
Match length	117
% identity	74
NCBI Description	(U41829) MHC class I antigen Mamu B*07 [Macaca mulatta]
Seq. No.	229913
Seq. ID	LIB3196-044-P1-M1-G9
Method	BLASTX
NCBI GI	g137578
BLAST score	513
E value	2.0e-52
Match length	118
% identity	87
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	229914
Seq. ID	LIB3196-044-P1-M1-H3
Method	BLASTX
NCBI GI	g3123274
BLAST score	333

E value	3.0e-31
Match length	90
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L32 (RP49) >gi_1928968 (U92431) ribosomal protein 49 [Drosophila melanogaster] >gi_2739301_emb_CAA74278_ (Y13939) ribosomal protein 49 [Drosophila melanogaster]

Seq. No.	229915
Seq. ID	LIB3196-044-P1-M1-H9
Method	BLASTX
NCBI GI	g3421090
BLAST score	141
E value	9.0e-09
Match length	31
% identity	87
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	229916
Seq. ID	LIB3196-045-P1-M1-A1
Method	BLASTX
NCBI GI	g4105275
BLAST score	230
E value	4.0e-19
Match length	52
% identity	83
NCBI Description	(AF044671) MM46 [Homo sapiens]

Seq. No.	229917
Seq. ID	LIB3196-045-P1-M1-A11
Method	BLASTX
NCBI GI	g2497542
BLAST score	230
E value	5.0e-22
Match length	88
% identity	65
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi_629696_pir__S44287 pyruvate kinase, plastid - common tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	229918
Seq. ID	LIB3196-045-P1-M1-A6
Method	BLASTX
NCBI GI	g3746069
BLAST score	147
E value	2.0e-09
Match length	100
% identity	34
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	229919
Seq. ID	LIB3196-045-P1-M1-A8
Method	BLASTX
NCBI GI	g3882267

BLAST score	281
E value	5.0e-25
Match length	105
% identity	60
NCBI Description	(AB018316) KIAA0773 protein [Homo sapiens]

Seq. No.	229920
Seq. ID	LIB3196-045-P1-M1-B4
Method	BLASTX
NCBI GI	g2623158
BLAST score	614
E value	3.0e-64
Match length	121
% identity	93
NCBI Description	(AF030177) N-acetylglucosaminyl transferase component Gpi1 [Homo sapiens] >gi_2911142_dbj_BAA24948_ (AB003723) GPI1 [Homo sapiens]

Seq. No.	229921
Seq. ID	LIB3196-045-P1-M1-B5
Method	BLASTX
NCBI GI	g137578
BLAST score	482
E value	1.0e-48
Match length	118
% identity	82
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229922
Seq. ID	LIB3196-045-P1-M1-B9
Method	BLASTX
NCBI GI	g1350956
BLAST score	448
E value	1.0e-44
Match length	94
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	229923
Seq. ID	LIB3196-045-P1-M1-C10
Method	BLASTX
NCBI GI	g137479
BLAST score	415
E value	8.0e-41
Match length	89
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_107394_pir__A39367 H+-transporting ATPase (EC 3.6.1.35) chain PKD1 - human >gi_189676 (M62762) vacuolar H+ ATPase proton channel subunit [Homo sapiens] >gi_4502313_ref_NP_001685.1_pATP6C_ ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD

Seq. No.	229924
Seq. ID	LIB3196-045-P1-M1-C11
Method	BLASTX
NCBI GI	g2981631
BLAST score	210
E value	6.0e-17
Match length	100
% identity	47
NCBI Description	(AB012223) ORF2 [Canis familiaris]

Seq. No.	229925
Seq. ID	LIB3196-045-P1-M1-C2
Method	BLASTX
NCBI GI	g125105
BLAST score	633
E value	2.0e-66
Match length	127
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389) keratin type II [Homo sapiens] >gi_4557890_ref_NP_000415.1_pKRT5_ keratin

Seq. No.	229926
Seq. ID	LIB3196-045-P1-M1-C3
Method	BLASTX
NCBI GI	g4314361
BLAST score	216
E value	2.0e-17
Match length	44
% identity	95
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	229927
Seq. ID	LIB3196-045-P1-M1-C4
Method	BLASTX
NCBI GI	g126156
BLAST score	400
E value	4.0e-39
Match length	117
% identity	68
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229928
Seq. ID	LIB3196-045-P1-M1-C5
Method	BLASTX
NCBI GI	g137578
BLAST score	408
E value	5.0e-40
Match length	122

% identity	72
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229929
Seq. ID	LIB3196-045-P1-M1-C8
Method	BLASTX
NCBI GI	g4325354
BLAST score	259
E value	2.0e-25
Match length	102
% identity	56
NCBI Description	(AF128395) contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No.	229930
Seq. ID	LIB3196-045-P1-M1-C9
Method	BLASTX
NCBI GI	g4457221
BLAST score	324
E value	3.0e-30
Match length	82
% identity	78
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No.	229931
Seq. ID	LIB3196-045-P1-M1-D1
Method	BLASTX
NCBI GI	g2961372
BLAST score	503
E value	4.0e-51
Match length	99
% identity	93
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	229932
Seq. ID	LIB3196-045-P1-M1-D3
Method	BLASTX
NCBI GI	g227448
BLAST score	643
E value	1.0e-67
Match length	125
% identity	64
NCBI Description	phosphofructokinase [Homo sapiens]

Seq. No.	229933
Seq. ID	LIB3196-045-P1-M1-D5
Method	BLASTX
NCBI GI	g547753

BLAST score	436
E value	2.0e-43
Match length	93
% identity	95
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	229934
Seq. ID	LIB3196-045-P1-M1-D7
Method	BLASTX
NCBI GI	g3641870
BLAST score	309
E value	2.0e-28
Match length	116
% identity	60
NCBI Description	(AJ011013) hypothetical protein [Cicer arietinum]

Seq. No.	229935
Seq. ID	LIB3196-045-P1-M1-D9
Method	BLASTX
NCBI GI	g4191793
BLAST score	406
E value	8.0e-40
Match length	119
% identity	71
NCBI Description	(AC005917) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	229936
Seq. ID	LIB3196-045-P1-M1-E1
Method	BLASTX
NCBI GI	g113950
BLAST score	557
E value	2.0e-57
Match length	112
% identity	59
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II - human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo sapiens]

Seq. No.	229937
Seq. ID	LIB3196-045-P1-M1-E2
Method	BLASTX
NCBI GI	g1174448
BLAST score	385
E value	2.0e-37
Match length	119
% identity	61
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	229938
Seq. ID	LIB3196-045-P1-M1-E7
Method	BLASTX

09604505.060204

NCBI GI	g2914700
BLAST score	315
E value	3.0e-29
Match length	97
% identity	68
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	229939
Seq. ID	LIB3196-045-P1-M1-F1
Method	BLASTX
NCBI GI	g207905
BLAST score	522
E value	2.0e-53
Match length	121
% identity	88
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	229940
Seq. ID	LIB3196-045-P1-M1-F10
Method	BLASTX
NCBI GI	g1362600
BLAST score	192
E value	1.0e-14
Match length	90
% identity	44
NCBI Description	anillin - fruit fly (Drosophila melanogaster)

Seq. No.	229941
Seq. ID	LIB3196-045-P1-M1-F11
Method	BLASTX
NCBI GI	g1429226
BLAST score	163
E value	2.0e-11
Match length	32
% identity	91
NCBI Description	(X98861) TFIIA [Arabidopsis thaliana]

Seq. No.	229942
Seq. ID	LIB3196-045-P1-M1-F3
Method	BLASTX
NCBI GI	g1170567
BLAST score	369
E value	1.0e-35
Match length	74
% identity	88
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	229943
Seq. ID	LIB3196-045-P1-M1-F4
Method	BLASTX
NCBI GI	g232081
BLAST score	572
E value	3.0e-59
Match length	114

0005450-0005950

% identity	96
NCBI Description	FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) >gi_2119438_pir__I56326 fatty acid binding protein homologue - human >gi_182354 (M94856) fatty acid binding protein homologue [Homo sapiens] >gi_4557581_ref_NP_001435.1_pFABP5_ fatty acid binding protein 5, psoriasis-associated

Seq. No.	229944
Seq. ID	LIB3196-045-P1-M1-F6
Method	BLASTX
NCBI GI	g3868758
BLAST score	431
E value	9.0e-43
Match length	106
% identity	75
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	229945
Seq. ID	LIB3196-045-P1-M1-F9
Method	BLASTX
NCBI GI	g461776
BLAST score	319
E value	1.0e-29
Match length	54
% identity	100
NCBI Description	CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) >gi_251369_bbs_108679 (S40060) spr1=small proline rich squamous cell marker [Rhesus monkeys, tracheobronchial epithelium, Peptide, 89 aa] [Rhesus monkeys] >gi_342297 (M83999) small proline-rich protein [Macaca mulatta]

Seq. No.	229946
Seq. ID	LIB3196-045-P1-M1-G1
Method	BLASTX
NCBI GI	g1346349
BLAST score	544
E value	5.0e-56
Match length	111
% identity	100
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II - human >gi_908805 (L42612) keratin type II [Homo sapiens]

Seq. No.	229947
Seq. ID	LIB3196-045-P1-M1-G12
Method	BLASTX
NCBI GI	g116850
BLAST score	400
E value	2.0e-39
Match length	89
% identity	88
NCBI Description	COFILIN, NON-MUSCLE ISOFORM >gi_89176_pir__A29240 cofilin - pig >gi_164425 (M20866) cofilin [Sus scrofa]

Seq. No.	229948
Seq. ID	LIB3196-045-P1-M1-G4
Method	BLASTX
NCBI GI	g2507421
BLAST score	340
E value	5.0e-32
Match length	70
% identity	90
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	229949
Seq. ID	LIB3196-045-P1-M1-G6
Method	BLASTX
NCBI GI	g1176668
BLAST score	191
E value	1.0e-14
Match length	101
% identity	25
NCBI Description	HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II >gi_3874172_emb_CAA86664_ (Z46676) similar to Poly(A) RNA binding protein; cDNA EST EMBL:D65752 comes from this gene; cDNA EST EMBL:D69301 comes from this gene; cDNA EST EMBL:C11188 comes from this gene; cDNA EST EMBL:C13204 comes from this gene; cDNA E

Seq. No.	229950
Seq. ID	LIB3196-045-P1-M1-G7
Method	BLASTX
NCBI GI	g4432855
BLAST score	472
E value	1.0e-47
Match length	114
% identity	82
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	229951
Seq. ID	LIB3196-045-P1-M1-H1
Method	BLASTX
NCBI GI	g3776005
BLAST score	589
E value	3.0e-61
Match length	121
% identity	93
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	229952
Seq. ID	LIB3196-045-P1-M1-H11
Method	BLASTX
NCBI GI	g232031
BLAST score	283
E value	2.0e-25
Match length	108
% identity	53
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224

translation elongation factor eEF-1 beta' chain - rice
>gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
[Oryza sativa]

Seq. No.	229953
Seq. ID	LIB3196-045-P1-M1-H4
Method	BLASTX
NCBI GI	g1709442
BLAST score	614
E value	4.0e-64
Match length	125
% identity	98
NCBI Description	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX PRECURSOR (E2) (E2K)

Seq. No.	229954
Seq. ID	LIB3196-045-P1-M1-H9
Method	BLASTX
NCBI GI	g1429226
BLAST score	163
E value	3.0e-11
Match length	32
% identity	91
NCBI Description	(X98861) TFIIA [Arabidopsis thaliana]

Seq. No.	229955
Seq. ID	LIB3196-046-P1-M1-A10
Method	BLASTX
NCBI GI	g2136744
BLAST score	182
E value	1.0e-13
Match length	42
% identity	86
NCBI Description	endothelin converting enzyme-2 - bovine (fragment)

Seq. No.	229956
Seq. ID	LIB3196-046-P1-M1-A12
Method	BLASTX
NCBI GI	g2651313
BLAST score	290
E value	2.0e-26
Match length	84
% identity	68
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229957
Seq. ID	LIB3196-046-P1-M1-A3
Method	BLASTX
NCBI GI	g2605714
BLAST score	239
E value	3.0e-20
Match length	66
% identity	76
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 229958

0007054-070404

Seq. ID	LIB3196-046-P1-M1-A4
Method	BLASTX
NCBI GI	g2224691
BLAST score	268
E value	1.0e-23
Match length	102
% identity	53
NCBI Description	(AB002373) KIAA0375 [Homo sapiens]

Seq. No.	229959
Seq. ID	LIB3196-046-P1-M1-A7
Method	BLASTX
NCBI GI	g3047318
BLAST score	236
E value	2.0e-20
Match length	71
% identity	16
NCBI Description	(AF056625) poly-ubiquitin [Magnaporthe grisea]

Seq. No.	229960
Seq. ID	LIB3196-046-P1-M1-A9
Method	BLASTX
NCBI GI	g4455335
BLAST score	409
E value	4.0e-40
Match length	118
% identity	69
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	229961
Seq. ID	LIB3196-046-P1-M1-B10
Method	BLASTX
NCBI GI	g1352077
BLAST score	328
E value	1.0e-38
Match length	103
% identity	80
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (EXO-(1-->4)-BETA-D-GALACTANASE) >gi_971485_emb_CAA58734_ (X83854) putative beta-galactosidase/galactanase [Lycopersicon esculentum] >gi_4138139_emb_CAA10174_ (AJ012797) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	229962
Seq. ID	LIB3196-046-P1-M1-B11
Method	BLASTX
NCBI GI	g122087
BLAST score	109
E value	6.0e-12
Match length	119
% identity	45
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459)

histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	229963
Seq. ID	LIB3196-046-P1-M1-B12
Method	BLASTX
NCBI GI	g126156
BLAST score	670
E value	1.0e-70
Match length	130
% identity	100
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229964
Seq. ID	LIB3196-046-P1-M1-B6
Method	BLASTX
NCBI GI	g122007
BLAST score	332
E value	4.0e-31
Match length	90
% identity	74
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	229965
Seq. ID	LIB3196-046-P1-M1-B7
Method	BLASTX
NCBI GI	g125077
BLAST score	412
E value	1.0e-50
Match length	116
% identity	96
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	229966
Seq. ID	LIB3196-046-P1-M1-B8
Method	BLASTX
NCBI GI	g4510346
BLAST score	514
E value	2.0e-52
Match length	124
% identity	79
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	229967
Seq. ID	LIB3196-046-P1-M1-B9
Method	BLASTX
NCBI GI	g132944

BLAST score	528
E value	4.0e-54
Match length	103
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	229968
Seq. ID	LIB3196-046-P1-M1-C1
Method	BLASTX
NCBI GI	g34228
BLAST score	317
E value	2.0e-29
Match length	67
% identity	99
NCBI Description	(X03444) put. lamin A precursor (aa 1-702) [Homo sapiens] >gi_224901_prf__1203377A lamin A [Homo sapiens]

Seq. No.	229969
Seq. ID	LIB3196-046-P1-M1-C2
Method	BLASTX
NCBI GI	g181967
BLAST score	555
E value	4.0e-57
Match length	131
% identity	82
NCBI Description	(M29548) elongation factor 1-alpha [Homo sapiens]

Seq. No.	229970
Seq. ID	LIB3196-046-P1-M1-C3
Method	BLASTX
NCBI GI	g2493130
BLAST score	660
E value	2.0e-69
Match length	128
% identity	100
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi_459200 (U07053) vacuolar H+-ATPase subunit B [Gossypium hirsutum]

Seq. No.	229971
Seq. ID	LIB3196-046-P1-M1-C4
Method	BLASTX
NCBI GI	g81546
BLAST score	216
E value	1.0e-17
Match length	86
% identity	62
NCBI Description	alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No.	229972
Seq. ID	LIB3196-046-P1-M1-C6
Method	BLASTX
NCBI GI	g3063698
BLAST score	377

E value	2.0e-36
Match length	130
% identity	60
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	229973
Seq. ID	LIB3196-046-P1-M1-C7
Method	BLASTX
NCBI GI	g1765899
BLAST score	561
E value	6.0e-58
Match length	120
% identity	82
NCBI Description	(Y07917) Spot 3 protein [Arabidopsis thaliana] >gi_1839244 (U86700) EGF receptor like protein [Arabidopsis thaliana]

Seq. No.	229974
Seq. ID	LIB3196-046-P1-M1-D1
Method	BLASTX
NCBI GI	g2668557
BLAST score	164
E value	2.0e-11
Match length	92
% identity	47
NCBI Description	(U73690) cytosolic IMP-GMP specific 5'-nucleotidase [Bos taurus]

Seq. No.	229975
Seq. ID	LIB3196-046-P1-M1-D10
Method	BLASTX
NCBI GI	g4090257
BLAST score	430
E value	1.0e-42
Match length	84
% identity	96
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No.	229976
Seq. ID	LIB3196-046-P1-M1-D4
Method	BLASTX
NCBI GI	g137578
BLAST score	620
E value	8.0e-65
Match length	128
% identity	94
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	229977
Seq. ID	LIB3196-046-P1-M1-D5
Method	BLASTX
NCBI GI	g1708239
BLAST score	619

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E value	1.0e-64
Match length	118
% identity	100
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_410028 (L25798) 3-hydroxy-3-methylglutaryl coenzyme A synthase [Homo sapiens] >gi_4504429_ref_NP_002121.1_pHMGCS1_ 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)

Seq. No.	229978
Seq. ID	LIB3196-046-P1-M1-D7
Method	BLASTX
NCBI GI	g3377797
BLAST score	440
E value	9.0e-44
Match length	117
% identity	74
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	229979
Seq. ID	LIB3196-046-P1-M1-D9
Method	BLASTX
NCBI GI	g3451473
BLAST score	218
E value	1.0e-17
Match length	93
% identity	46
NCBI Description	(AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]

Seq. No.	229980
Seq. ID	LIB3196-046-P1-M1-E4
Method	BLASTX
NCBI GI	g133027
BLAST score	706
E value	7.0e-75
Match length	134
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L8 >gi_71075_pir__R5RTL8 ribosomal protein L8 - rat >gi_478326_pir__JN0923 ribosomal protein L8 - human >gi_57704_emb_CAA44071_ (X62145) ribosomal protein L8 [Rattus rattus] >gi_433899_emb_CAA82248_ (Z28407) ribosomal protein L8 [Homo sapiens] >gi_1527178 (U67771) ribosomal protein L8 [Mus musculus] >gi_4506663_ref_NP_000964.1_pRPL8_ ribosomal protein L8

Seq. No.	229981
Seq. ID	LIB3196-046-P1-M1-E5
Method	BLASTX
NCBI GI	g4455335
BLAST score	392
E value	3.0e-38

Match length	87
% identity	82
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	229982
Seq. ID	LIB3196-046-P1-M1-E6
Method	BLASTX
NCBI GI	g2961390
BLAST score	644
E value	1.0e-67
Match length	127
% identity	90
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	229983
Seq. ID	LIB3196-046-P1-M1-E9
Method	BLASTX
NCBI GI	g1362916
BLAST score	560
E value	8.0e-58
Match length	127
% identity	87
NCBI Description	protein-tyrosine kinase (EC 2.7.1.112) trkE precursor - human >gi_400463_emb_CAA52915_ (X74979) TrkE [Homo sapiens] >gi_732800_emb_CAA82335_ (Z29093) receptor tyrosine kinase [Homo sapiens] >gi_1160925 (L57508) receptor kinase [Homo sapiens] >gi_4503451_ref_NP_001945.1_pEDDR1_ epithelial discoidin domain receptor

Seq. No.	229984
Seq. ID	LIB3196-046-P1-M1-F1
Method	BLASTX
NCBI GI	g2764974
BLAST score	427
E value	3.0e-42
Match length	96
% identity	88
NCBI Description	(X99906) alpha endosulfine [Homo sapiens]

Seq. No.	229985
Seq. ID	LIB3196-046-P1-M1-F10
Method	BLASTX
NCBI GI	g140282
BLAST score	140
E value	1.0e-08
Match length	28
% identity	93
NCBI Description	HYPOTHETICAL 19 KD PROTEIN (ORF 170) >gi_1363543_pir__S58553 hypothetical protein 170 - maize chloroplast >gi_12430_emb_CAA41108_ (X58080) ORF170 [Zea mays] >gi_902223_emb_CAA60287_ (X86563) ORF170 [Zea mays]

Seq. No.	229986
Seq. ID	LIB3196-046-P1-M1-F3
Method	BLASTX
NCBI GI	g2804273

09684046.040100

BLAST score 671
E value 8.0e-71
Match length 129
% identity 46
NCBI Description (D89980) alpha actinin 4 [Homo sapiens]

Seq. No. 229987
Seq. ID LIB3196-046-P1-M1-F6
Method BLASTX
NCBI GI g2997694
BLAST score 232
E value 2.0e-19
Match length 119
% identity 43
NCBI Description (AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]

Seq. No. 229988
Seq. ID LIB3196-046-P1-M1-F9
Method BLASTX
NCBI GI g1335862
BLAST score 554
E value 4.0e-57
Match length 119
% identity 89
NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 229989
Seq. ID LIB3196-046-P1-M1-G12
Method BLASTX
NCBI GI g1167523
BLAST score 319
E value 1.0e-30
Match length 124
% identity 60
NCBI Description (D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq. No. 229990
Seq. ID LIB3196-046-P1-M1-G2
Method BLASTX
NCBI GI g1171035
BLAST score 195
E value 4.0e-15
Match length 50
% identity 68
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504 >gi_1086021_pir__S48038 metallothionein-like protein - kiwi fruit >gi_450245 (L27813) metallothionein-like protein [Actinidia deliciosa]

Seq. No. 229991
Seq. ID LIB3196-046-P1-M1-G4
Method BLASTX
NCBI GI g126156
BLAST score 630
E value 5.0e-66
Match length 129

% identity	95
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	229992
Seq. ID	LIB3196-046-P1-M1-G7
Method	BLASTX
NCBI GI	g346219
BLAST score	220
E value	6.0e-18
Match length	77
% identity	62
NCBI Description	keratin K4a - human (fragment)

Seq. No.	229993
Seq. ID	LIB3196-046-P1-M1-H2
Method	BLASTX
NCBI GI	g2134781
BLAST score	201
E value	6.0e-16
Match length	41
% identity	95
NCBI Description	APR peptide - human >gi_2135471_pir__I84441 immediate early response gene - human >gi_219476_dbj_BAA14111_ (D90070) APR peptide [Homo sapiens]

Seq. No.	229994
Seq. ID	LIB3196-046-P1-M1-H8
Method	BLASTX
NCBI GI	g125080
BLAST score	470
E value	2.0e-47
Match length	98
% identity	98
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	229995
Seq. ID	LIB3196-047-P1-M1-A12
Method	BLASTX
NCBI GI	g2522230
BLAST score	276
E value	2.0e-24
Match length	123
% identity	42
NCBI Description	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq. No.	229996
Seq. ID	LIB3196-047-P1-M1-A4

Method	BLASTX
NCBI GI	g3121828
BLAST score	580
E value	3.0e-60
Match length	121
% identity	91
NCBI Description	BENE PROTEIN >gi_2135423_pir__I38891 hypothetical protein - human (fragment) >gi_1000712 (U17077) unknown [Homo sapiens]

Seq. No.	229997
Seq. ID	LIB3196-047-P1-M1-B10
Method	BLASTX
NCBI GI	g266344
BLAST score	475
E value	1.0e-47
Match length	115
% identity	83
NCBI Description	LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) >gi_284073_pir__S27383 elastase inhibitor - human >gi_2997692 (AF053630) monocyte/neutrophil elastase inhibitor [Homo sapiens]

Seq. No.	229998
Seq. ID	LIB3196-047-P1-M1-B12
Method	BLASTX
NCBI GI	g2224557
BLAST score	331
E value	6.0e-31
Match length	128
% identity	52
NCBI Description	(AB002306) KIAA0308 [Homo sapiens]

Seq. No.	229999
Seq. ID	LIB3196-047-P1-M1-B4
Method	BLASTX
NCBI GI	g2605714
BLAST score	229
E value	3.0e-19
Match length	59
% identity	68
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	230000
Seq. ID	LIB3196-047-P1-M1-B7
Method	BLASTX
NCBI GI	g207905
BLAST score	543
E value	7.0e-56
Match length	121
% identity	86
NCBI Description	(M18027) alpha globulin B [Artificial gene]

Seq. No.	230001
Seq. ID	LIB3196-047-P1-M1-B8
Method	BLASTX

(AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	230487
Seq. ID	LIB3196-064-P1-M1-A12
Method	BLASTX
NCBI GI	g1800147
BLAST score	174
E value	1.0e-12
Match length	100
% identity	43
NCBI Description	(U83655) membrane associated protein [Arabidopsis thaliana]

Seq. No.	230488
Seq. ID	LIB3196-064-P1-M1-A3
Method	BLASTX
NCBI GI	g4235430
BLAST score	361
E value	1.0e-34
Match length	115
% identity	63
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	230489
Seq. ID	LIB3196-064-P1-M1-A7
Method	BLASTX
NCBI GI	g3913961
BLAST score	650
E value	2.0e-68
Match length	125
% identity	99
NCBI Description	KINESIN-LIKE PROTEIN KIF1C >gi_2738149 (U91329) kinesin-like motor protein KIF1C [Homo sapiens]

Seq. No.	230490
Seq. ID	LIB3196-064-P1-M1-A9
Method	BLASTX
NCBI GI	g115492
BLAST score	296
E value	6.0e-27
Match length	80
% identity	39
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	230491
Seq. ID	LIB3196-064-P1-M1-B1
Method	BLASTX
NCBI GI	g1346347
BLAST score	517
E value	9.0e-53
Match length	109
% identity	96
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II - human (fragment) >gi_914833 (L42610) keratin type II [Homo sapiens]

Seq. No.	230492
Seq. ID	LIB3196-064-P1-M1-B10
Method	BLASTX
NCBI GI	g461994
BLAST score	379
E value	1.0e-36
Match length	84
% identity	88
NCBI Description	ELONGATION FACTOR 1-DELTA (EF-1-DELTA) >gi_1085404_pir__S34626 translation elongation factor eEF-1 delta chain - human >gi_38522_emb_CAA79716_ (Z21507) human elongation factor-1-delta [Homo sapiens] >gi_4503479_ref_NP_001951.1_pEEF1D_ eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)

Seq. No.	230493
Seq. ID	LIB3196-064-P1-M1-B11
Method	BLASTX
NCBI GI	g3395758
BLAST score	172
E value	2.0e-12
Match length	79
% identity	41
NCBI Description	(U76300) unknown [Arabidopsis thaliana]

Seq. No.	230494
Seq. ID	LIB3196-064-P1-M1-B3
Method	BLASTX
NCBI GI	g2832617
BLAST score	178
E value	2.0e-13
Match length	42
% identity	76
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	230495
Seq. ID	LIB3196-064-P1-M1-B4
Method	BLASTX
NCBI GI	g3335226
BLAST score	371
E value	1.0e-35
Match length	77
% identity	29
NCBI Description	(AF077374) small proline-rich protein [Homo sapiens]

Seq. No.	230496
Seq. ID	LIB3196-064-P1-M1-B8
Method	BLASTX
NCBI GI	g224877
BLAST score	448
E value	9.0e-45
Match length	87
% identity	97
NCBI Description	deaminase a,adenosine [Homo sapiens]

Seq. No. 230497

Seq. ID	LIB3196-064-P1-M1-C6
Method	BLASTX
NCBI GI	g3724114
BLAST score	647
E value	5.0e-68
Match length	128
% identity	97
NCBI Description	(Y16792) keratin, type I [Homo sapiens] >gi_4504927_ref_NP_003762.1_pKRTHA6_ UNKNOWN

Seq. No.	230498
Seq. ID	LIB3196-064-P1-M1-C7
Method	BLASTX
NCBI GI	g2119924
BLAST score	509
E value	5.0e-52
Match length	99
% identity	97
NCBI Description	oncogene PTI-1 - human >gi_927065_gb_AAC09385.1_ (L41490) eukaryotic translation elongation factor 1 alpha 1-like 14 [Homo sapiens] >gi_927067 (L41498) longation factor 1-alpha 1 [Homo sapiens] >gi_4503473_ref_NP_001394.1_pEEF1A1L14_ eukaryotic translation elongation factor 1 alpha 1-like

Seq. No.	230499
Seq. ID	LIB3196-064-P1-M1-D1
Method	BLASTX
NCBI GI	g2245136
BLAST score	403
E value	1.0e-39
Match length	103
% identity	67
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	230500
Seq. ID	LIB3196-064-P1-M1-D10
Method	BLASTX
NCBI GI	g2804273
BLAST score	617
E value	2.0e-64
Match length	123
% identity	98
NCBI Description	(D89980) alpha actinin 4 [Homo sapiens]

Seq. No.	230501
Seq. ID	LIB3196-064-P1-M1-D2
Method	BLASTX
NCBI GI	g1001309
BLAST score	177
E value	6.0e-13
Match length	103
% identity	36
NCBI Description	(D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No.	230502
Seq. ID	LIB3196-064-P1-M1-D3

Method	BLASTX
NCBI GI	g137578
BLAST score	524
E value	1.0e-53
Match length	102
% identity	100
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	230503
Seq. ID	LIB3196-064-P1-M1-D5
Method	BLASTX
NCBI GI	g1504008
BLAST score	315
E value	4.0e-29
Match length	94
% identity	64
NCBI Description	(D86967) Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [Homo sapiens]

Seq. No.	230504
Seq. ID	LIB3196-064-P1-M1-D6
Method	BLASTX
NCBI GI	g266690
BLAST score	335
E value	2.0e-31
Match length	96
% identity	72
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	230505
Seq. ID	LIB3196-064-P1-M1-D8
Method	BLASTX
NCBI GI	g81546
BLAST score	541
E value	1.0e-55
Match length	114
% identity	94
NCBI Description	alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)

Seq. No.	230506
Seq. ID	LIB3196-064-P1-M1-D9
Method	BLASTX
NCBI GI	g1223922
BLAST score	465
E value	1.0e-46
Match length	104
% identity	77
NCBI Description	(U49445) Vigna radiata vicilin peptidohydrolase [Vigna

radiata]

Seq. No.	230507
Seq. ID	LIB3196-064-P1-M1-E11
Method	BLASTX
NCBI GI	g2522228
BLAST score	455
E value	1.0e-45
Match length	115
% identity	68
NCBI Description	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq. No.	230508
Seq. ID	LIB3196-064-P1-M1-E6
Method	BLASTX
NCBI GI	g3415119
BLAST score	560
E value	8.0e-58
Match length	116
% identity	58
NCBI Description	(AF081672) calmodulin [Gallus gallus]

Seq. No.	230509
Seq. ID	LIB3196-064-P1-M1-E8
Method	BLASTX
NCBI GI	g547683
BLAST score	608
E value	2.0e-63
Match length	119
% identity	97
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	230510
Seq. ID	LIB3196-064-P1-M1-F1
Method	BLASTX
NCBI GI	g3123271
BLAST score	340
E value	1.0e-32
Match length	70
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	230511
Seq. ID	LIB3196-064-P1-M1-F10
Method	BLASTX
NCBI GI	g3023180
BLAST score	375
E value	3.0e-36
Match length	89
% identity	85
NCBI Description	14-3-3-LIKE PROTEIN 10 >gi_1771166_emb_CAA67374.1_ (X98866) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	230512
Seq. ID	LIB3196-064-P1-M1-F11
Method	BLASTX
NCBI GI	g940395
BLAST score	539
E value	2.0e-55
Match length	109
% identity	12
NCBI Description	(D63782) polyubiquitin [Cricetulus sp.]

Seq. No.	230513
Seq. ID	LIB3196-064-P1-M1-F3
Method	BLASTX
NCBI GI	g167367
BLAST score	598
E value	2.0e-62
Match length	112
% identity	98
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230514
Seq. ID	LIB3196-064-P1-M1-F4
Method	BLASTX
NCBI GI	g627584
BLAST score	613
E value	5.0e-64
Match length	129
% identity	89
NCBI Description	protein p84 - human >gi_550058 (L36529) protein p84 [Homo sapiens]

Seq. No.	230515
Seq. ID	LIB3196-064-P1-M1-G1
Method	BLASTX
NCBI GI	g136452
BLAST score	342
E value	3.0e-32
Match length	105
% identity	62
NCBI Description	STEM-SPECIFIC PROTEIN TSJT1 >gi_100383_pir__S13551 stem-specific protein - common tobacco >gi_20037_emb_CAA36525_ (X52283) stem specific, weakly expressed in other organs [Nicotiana tabacum]

Seq. No.	230516
Seq. ID	LIB3196-064-P1-M1-G10
Method	BLASTX
NCBI GI	g70753
BLAST score	408
E value	5.0e-40
Match length	99
% identity	83
NCBI Description	histone H3 - garden pea >gi_82610_pir__S00373 histone H3 - wheat

Seq. No.	230517
Seq. ID	LIB3196-064-P1-M1-G2

Method	BLASTX
NCBI GI	g1931647
BLAST score	434
E value	4.0e-43
Match length	117
% identity	68
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	230518
Seq. ID	LIB3196-064-P1-M1-G4
Method	BLASTX
NCBI GI	g3341695
BLAST score	306
E value	5.0e-28
Match length	88
% identity	67
NCBI Description	(AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	230519
Seq. ID	LIB3196-064-P1-M1-G5
Method	BLASTX
NCBI GI	g224877
BLAST score	493
E value	6.0e-50
Match length	97
% identity	96
NCBI Description	deaminase a,adenosine [Homo sapiens]

Seq. No.	230520
Seq. ID	LIB3196-064-P1-M1-G6
Method	BLASTX
NCBI GI	g3548818
BLAST score	260
E value	1.0e-22
Match length	128
% identity	45
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	230521
Seq. ID	LIB3196-064-P1-M1-G8
Method	BLASTX
NCBI GI	g1707889
BLAST score	531
E value	2.0e-54
Match length	103
% identity	100
NCBI Description	RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2) >gi_285975_dbj_BAA03095_ (D13988) human rab GDI [Homo sapiens] >gi_4503973_ref_NP_001485.1_pGDI2_ GDP dissociation inhibitor

Seq. No.	230522
Seq. ID	LIB3196-064-P1-M1-H11
Method	BLASTX
NCBI GI	g1346345

BLAST score	617
E value	2.0e-64
Match length	124
% identity	98
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6B (CYTOKERATIN 6B) (CK 6B) (K6B KERATIN) >gi_2119220_pir__I61767 keratin type II - human >gi_908790 (L42592) keratin type II [Homo sapiens]

Seq. No.	230523
Seq. ID	LIB3196-064-P1-M1-H12
Method	BLASTX
NCBI GI	g2880051
BLAST score	272
E value	4.0e-24
Match length	64
% identity	81
NCBI Description	(AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No.	230524
Seq. ID	LIB3196-064-P1-M1-H5
Method	BLASTX
NCBI GI	g2244979
BLAST score	501
E value	6.0e-51
Match length	118
% identity	81
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	230525
Seq. ID	LIB3196-064-P1-M1-H9
Method	BLASTX
NCBI GI	g2605714
BLAST score	285
E value	1.0e-25
Match length	75
% identity	77
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	230526
Seq. ID	LIB3196-065-P1-M1-A1
Method	BLASTX
NCBI GI	g809561
BLAST score	213
E value	1.0e-17
Match length	61
% identity	72
NCBI Description	(X13055) gamma-actin [Mus musculus]

Seq. No.	230527
Seq. ID	LIB3196-065-P1-M1-A11
Method	BLASTX
NCBI GI	g2497938
BLAST score	652
E value	1.0e-68
Match length	128

% identity	98
NCBI Description	AQUAPORIN 3 >gi_1854374_dbj_BAA19237_ (AB001325) aquaporin 3 [Homo sapiens]

Seq. No.	230528
Seq. ID	LIB3196-065-P1-M1-A2
Method	BLASTX
NCBI GI	g2144098
BLAST score	403
E value	2.0e-39
Match length	115
% identity	74
NCBI Description	SC2 - rat >gi_256994_bbs_115268 (S45663) SC2=synaptic glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]

Seq. No.	230529
Seq. ID	LIB3196-065-P1-M1-A7
Method	BLASTX
NCBI GI	g1346344
BLAST score	539
E value	2.0e-55
Match length	108
% identity	100
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II - human >gi_908779 (L42583) keratin type II [Homo sapiens]

Seq. No.	230530
Seq. ID	LIB3196-065-P1-M1-B10
Method	BLASTX
NCBI GI	g126156
BLAST score	369
E value	2.0e-40
Match length	117
% identity	79
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	230531
Seq. ID	LIB3196-065-P1-M1-B12
Method	BLASTX
NCBI GI	g1076316
BLAST score	342
E value	3.0e-32
Match length	90
% identity	61
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	230532
Seq. ID	LIB3196-065-P1-M1-B3
Method	BLASTX

NCBI GI	g3901014
BLAST score	214
E value	3.0e-17
Match length	55
% identity	71
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	230533
Seq. ID	LIB3196-065-P1-M1-B5
Method	BLASTX
NCBI GI	g167367
BLAST score	480
E value	2.0e-48
Match length	122
% identity	76
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230534
Seq. ID	LIB3196-065-P1-M1-B7
Method	BLASTX
NCBI GI	g3122380
BLAST score	647
E value	5.0e-68
Match length	131
% identity	95
NCBI Description	ALPHA-MANNOSIDASE II (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II) >gi_1117827 (U31520) alpha mannosidase II [Homo sapiens]

Seq. No.	230535
Seq. ID	LIB3196-065-P1-M1-B8
Method	BLASTX
NCBI GI	g266690
BLAST score	364
E value	8.0e-35
Match length	105
% identity	72
NCBI Description	OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	230536
Seq. ID	LIB3196-065-P1-M1-B9
Method	BLASTX
NCBI GI	g2827715
BLAST score	244
E value	9.0e-21
Match length	102
% identity	43
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	230537
Seq. ID	LIB3196-065-P1-M1-C10
Method	BLASTX

NCBI GI	g3687237
BLAST score	198
E value	2.0e-15
Match length	99
% identity	53
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	230538
Seq. ID	LIB3196-065-P1-M1-C11
Method	BLASTX
NCBI GI	g2262172
BLAST score	151
E value	7.0e-10
Match length	98
% identity	40
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	230539
Seq. ID	LIB3196-065-P1-M1-C12
Method	BLASTX
NCBI GI	g494415
BLAST score	326
E value	2.0e-30
Match length	66
% identity	100
NCBI Description	Homo sapiens >gi_494416_pdb_1NRC_B Homo sapiens

Seq. No.	230540
Seq. ID	LIB3196-065-P1-M1-C2
Method	BLASTX
NCBI GI	g4105683
BLAST score	547
E value	3.0e-56
Match length	126
% identity	76
NCBI Description	(AF049892) unknown [Oryza sativa] >gi_4105692 (AF050155) embryo-specific protein [Oryza sativa subsp. indica]

Seq. No.	230541
Seq. ID	LIB3196-065-P1-M1-C3
Method	BLASTX
NCBI GI	g72223
BLAST score	524
E value	1.0e-53
Match length	131
% identity	82
NCBI Description	heat shock protein 84 - mouse

Seq. No.	230542
Seq. ID	LIB3196-065-P1-M1-C4
Method	BLASTX
NCBI GI	g2134794
BLAST score	695
E value	1.0e-73
Match length	133

% identity	99
NCBI Description	autoantigen - human >gi_533202 (L26339) autoantigen [Homo sapiens]
Seq. No.	230543
Seq. ID	LIB3196-065-P1-M1-C5
Method	BLASTX
NCBI GI	g1917019
BLAST score	548
E value	2.0e-56
Match length	127
% identity	83
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]
Seq. No.	230544
Seq. ID	LIB3196-065-P1-M1-C6
Method	BLASTX
NCBI GI	g1565223
BLAST score	409
E value	4.0e-40
Match length	128
% identity	64
NCBI Description	(Y08301) MCM2-related protein [Arabidopsis thaliana]
Seq. No.	230545
Seq. ID	LIB3196-065-P1-M1-C7
Method	BLASTX
NCBI GI	g4529893
BLAST score	373
E value	8.0e-36
Match length	121
% identity	69
NCBI Description	(AF134726) HSP70-1 [Homo sapiens]
Seq. No.	230546
Seq. ID	LIB3196-065-P1-M1-C8
Method	BLASTX
NCBI GI	g88044
BLAST score	637
E value	8.0e-67
Match length	132
% identity	98
NCBI Description	keratin 4, type II, cytoskeletal - human (fragment) >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens]
Seq. No.	230547
Seq. ID	LIB3196-065-P1-M1-C9
Method	BLASTX
NCBI GI	g137578
BLAST score	611
E value	8.0e-64
Match length	123
% identity	95
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor

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	[Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	230548
Seq. ID	LIB3196-065-P1-M1-D1
Method	BLASTX
NCBI GI	g2293575
BLAST score	606
E value	3.0e-63
Match length	131
% identity	91
NCBI Description	(AF013213) elongation factor 1 alpha [Bos taurus]
Seq. No.	230549
Seq. ID	LIB3196-065-P1-M1-D10
Method	BLASTX
NCBI GI	g137578
BLAST score	531
E value	2.0e-54
Match length	125
% identity	86
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]
Seq. No.	230550
Seq. ID	LIB3196-065-P1-M1-D11
Method	BLASTX
NCBI GI	g1330343
BLAST score	327
E value	2.0e-30
Match length	104
% identity	60
NCBI Description	(U58755) C34D4.12 gene product [Caenorhabditis elegans]
Seq. No.	230551
Seq. ID	LIB3196-065-P1-M1-D2
Method	BLASTX
NCBI GI	g4529892
BLAST score	659
E value	2.0e-69
Match length	132
% identity	100
NCBI Description	(AF134726) HSP70-2 [Homo sapiens]
Seq. No.	230552
Seq. ID	LIB3196-065-P1-M1-D3
Method	BLASTX
NCBI GI	g2842648
BLAST score	256
E value	4.0e-22
Match length	120
% identity	42

NCBI Description	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KD SUBUNIT RELATED-PROTEIN 2 >gi_2137782_pir__A57120 small nuclear ribonucleoprotein auxiliary factor U2 - mouse >gi_927659_dbj_BAA08143_ (D45205) U2af1-rs2 [Mus musculus]
Seq. No.	230553
Seq. ID	LIB3196-065-P1-M1-D4
Method	BLASTX
NCBI GI	g2662415
BLAST score	214
E value	3.0e-17
Match length	53
% identity	64
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]
Seq. No.	230554
Seq. ID	LIB3196-065-P1-M1-D6
Method	BLASTX
NCBI GI	g2129538
BLAST score	644
E value	1.0e-67
Match length	128
% identity	98
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]
Seq. No.	230555
Seq. ID	LIB3196-065-P1-M1-D9
Method	BLASTX
NCBI GI	g2464914
BLAST score	155
E value	2.0e-10
Match length	59
% identity	54
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.	230556
Seq. ID	LIB3196-065-P1-M1-E1
Method	BLASTX
NCBI GI	g113950
BLAST score	661
E value	1.0e-69
Match length	133
% identity	55
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II - human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo sapiens]
Seq. No.	230557
Seq. ID	LIB3196-065-P1-M1-E10
Method	BLASTX
NCBI GI	g2735010
BLAST score	195
E value	5.0e-15
Match length	76

% identity	59
NCBI Description	(U82166) CD99 type II-COS7 [Cercopithecus aethiops]

Seq. No.	230558
Seq. ID	LIB3196-065-P1-M1-E2
Method	BLASTX
NCBI GI	g1843527
BLAST score	301
E value	5.0e-33
Match length	106
% identity	75
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	230559
Seq. ID	LIB3196-065-P1-M1-E3
Method	BLASTX
NCBI GI	g3184283
BLAST score	270
E value	8.0e-24
Match length	77
% identity	70
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	230560
Seq. ID	LIB3196-065-P1-M1-E5
Method	BLASTX
NCBI GI	g1890152
BLAST score	480
E value	2.0e-48
Match length	128
% identity	69
NCBI Description	(X92510) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	230561
Seq. ID	LIB3196-065-P1-M1-E7
Method	BLASTX
NCBI GI	g2062167
BLAST score	410
E value	3.0e-40
Match length	85
% identity	89
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	230562
Seq. ID	LIB3196-065-P1-M1-F1
Method	BLASTX
NCBI GI	g1854035
BLAST score	697
E value	8.0e-74
Match length	134
% identity	99
NCBI Description	(U86753) pombe Cdc5-related protein [Homo sapiens]

Seq. No.	230563
Seq. ID	LIB3196-065-P1-M1-F4

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Method	BLASTX
NCBI GI	g3738283
BLAST score	402
E value	3.0e-39
Match length	82
% identity	85
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	230564
Seq. ID	LIB3196-065-P1-M1-G10
Method	BLASTX
NCBI GI	g2894599
BLAST score	290
E value	3.0e-26
Match length	72
% identity	69
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	230565
Seq. ID	LIB3196-065-P1-M1-G11
Method	BLASTX
NCBI GI	g1351867
BLAST score	670
E value	1.0e-70
Match length	131
% identity	99
NCBI Description	ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi_761724 (U20114) beta-actin [Cricetulus griseus]

Seq. No.	230566
Seq. ID	LIB3196-065-P1-M1-G12
Method	BLASTX
NCBI GI	g167367
BLAST score	438
E value	1.0e-43
Match length	117
% identity	74
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	230567
Seq. ID	LIB3196-065-P1-M1-G3
Method	BLASTX
NCBI GI	g1363944
BLAST score	669
E value	1.0e-70
Match length	133
% identity	99
NCBI Description	type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	230568
Seq. ID	LIB3196-065-P1-M1-H1
Method	BLASTX
NCBI GI	g2134996
BLAST score	461
E value	3.0e-46

Match length	131
% identity	74
NCBI Description	desmoplakin I - human

Seq. No.	230569
Seq. ID	LIB3196-065-P1-M1-H11
Method	BLASTX
NCBI GI	g3885884
BLAST score	613
E value	5.0e-64
Match length	121
% identity	94
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	230570
Seq. ID	LIB3196-065-P1-M1-H2
Method	BLASTX
NCBI GI	g72287
BLAST score	601
E value	1.0e-62
Match length	116
% identity	100
NCBI Description	beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No.	230571
Seq. ID	LIB3196-065-P1-M1-H3
Method	BLASTX
NCBI GI	g119350
BLAST score	472
E value	2.0e-47
Match length	103
% identity	89
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana]

Seq. No.	230572
Seq. ID	LIB3196-065-P1-M1-H4
Method	BLASTX
NCBI GI	g732893
BLAST score	548
E value	2.0e-56
Match length	130
% identity	76
NCBI Description	(X85382) tobacco calretulin [Nicotiana tabacum]

Seq. No.	230573
Seq. ID	LIB3196-065-P1-M1-H6
Method	BLASTX
NCBI GI	g3128168
BLAST score	388
E value	1.0e-37
Match length	114

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% identity	55
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]
Seq. No.	230574
Seq. ID	LIB3196-065-P1-M1-H7
Method	BLASTX
NCBI GI	g1345132
BLAST score	533
E value	1.0e-54
Match length	123
% identity	83
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
Seq. No.	230575
Seq. ID	LIB3196-065-P1-M1-H8
Method	BLASTX
NCBI GI	g126719
BLAST score	397
E value	2.0e-50
Match length	106
% identity	94
NCBI Description	T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN >gi_88813_pir__A29472 T-cell surface glycoprotein MAL, splice form a - human >gi_307157 (M15800) MAL protein [Homo sapiens] >gi_435478_emb_CAA54100_ (X76678) MAL-a [Homo sapiens] >gi_2654296_emb_CAA53809_ (X76220) MAL [Homo sapiens] >gi_4505091_ref_NP_002362.1_pMAL_ mal, T-cell differentiation protein
Seq. No.	230576
Seq. ID	LIB3196-065-P1-M1-H9
Method	BLASTX
NCBI GI	g407942
BLAST score	221
E value	4.0e-18
Match length	63
% identity	60
NCBI Description	(U02496) epoxide hydrolase [Solanum tuberosum]
Seq. No.	230577
Seq. ID	LIB3197-001-P1-M1-D12
Method	BLASTX
NCBI GI	g1351202
BLAST score	665
E value	5.0e-70
Match length	142
% identity	89
NCBI Description	TUBULIN BETA CHAIN >gi_312989_emb_CAA42777_ (X60216) beta-tubulin [Glycine max]
Seq. No.	230578
Seq. ID	LIB3197-001-P1-M1-D7
Method	BLASTX

NCBI GI	g1172977
BLAST score	561
E value	8.0e-58
Match length	126
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	230579
Seq. ID	LIB3197-001-P1-M1-D8
Method	BLASTX
NCBI GI	g549597
BLAST score	201
E value	9.0e-16
Match length	91
% identity	44
NCBI Description	ATP-DEPENDENT RNA HELICASE DBP7 >gi_539330_pir__S38093 probable purine nucleotide-binding protein YKR024c - yeast (Saccharomyces cerevisiae) >gi_486449_emb_CAA82096_ (Z28249) ORF YKR024c [Saccharomyces cerevisiae]

Seq. No.	230580
Seq. ID	LIB3197-001-P1-M1-D9
Method	BLASTX
NCBI GI	g1931647
BLAST score	375
E value	5.0e-36
Match length	102
% identity	65
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	230581
Seq. ID	LIB3197-001-P1-M1-E1
Method	BLASTX
NCBI GI	g1403522
BLAST score	417
E value	6.0e-41
Match length	132
% identity	62
NCBI Description	(X57187) chitinase [Phaseolus vulgaris]

Seq. No.	230582
Seq. ID	LIB3197-001-P1-M1-E10
Method	BLASTX
NCBI GI	g2811278
BLAST score	567
E value	1.0e-58
Match length	135
% identity	77
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	230583
Seq. ID	LIB3197-001-P1-M1-E11
Method	BLASTX
NCBI GI	g1890281
BLAST score	356

E value	1.0e-33
Match length	123
% identity	21
NCBI Description	(U89984) transformation-sensitive protein homolog [Acanthamoeba castellanii]

Seq. No.	230584
Seq. ID	LIB3197-001-P1-M1-E12
Method	BLASTX
NCBI GI	g133940
BLAST score	565
E value	4.0e-58
Match length	136
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	230585
Seq. ID	LIB3197-001-P1-M1-E6
Method	BLASTX
NCBI GI	g2979559
BLAST score	335
E value	3.0e-31
Match length	81
% identity	77
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	230586
Seq. ID	LIB3197-001-P1-M1-E7
Method	BLASTX
NCBI GI	g1743354
BLAST score	287
E value	8.0e-26
Match length	62
% identity	82
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	230587
Seq. ID	LIB3197-001-P1-M1-F5
Method	BLASTX
NCBI GI	g3947719
BLAST score	180
E value	3.0e-13
Match length	44
% identity	82
NCBI Description	(AJ012653) ribosomal protein S28 [Prunus persica] >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28 [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655) ribosomal protein S28 [Prunus persica]

Seq. No.	230588
Seq. ID	LIB3197-001-P1-M1-F6
Method	BLASTX
NCBI GI	g1710587

BLAST score	277
E value	2.0e-24
Match length	95
% identity	60
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1196897 (L46848) acidic ribosomal protein P0 [Glycine max]

Seq. No.	230589
Seq. ID	LIB3197-001-P1-M1-F8
Method	BLASTX
NCBI GI	g3721856
BLAST score	492
E value	8.0e-50
Match length	133
% identity	64
NCBI Description	(AB014057) beta-Amyrin Synthase [Panax ginseng]

Seq. No.	230590
Seq. ID	LIB3197-001-P1-M1-G10
Method	BLASTX
NCBI GI	g437327
BLAST score	352
E value	2.0e-33
Match length	136
% identity	53
NCBI Description	(L04497) MYB A; putative [Gossypium hirsutum]

Seq. No.	230591
Seq. ID	LIB3197-001-P1-M1-G11
Method	BLASTX
NCBI GI	g4574320
BLAST score	192
E value	1.0e-14
Match length	62
% identity	66
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]

Seq. No.	230592
Seq. ID	LIB3197-001-P1-M1-G12
Method	BLASTX
NCBI GI	g4322563
BLAST score	149
E value	2.0e-09
Match length	111
% identity	31
NCBI Description	(AF089838) phosphatidylglycerol/phosphatidylinositol transfer protein [Aspergillus oryzae]

Seq. No.	230593
Seq. ID	LIB3197-001-P1-M1-G4
Method	BLASTX
NCBI GI	g4210948
BLAST score	555
E value	5.0e-57
Match length	147
% identity	77

NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.	230594
Seq. ID	LIB3197-001-P1-M1-G6
Method	BLASTX
NCBI GI	g2911060
BLAST score	237
E value	6.0e-20
Match length	96
% identity	36
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana] >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.	230595
Seq. ID	LIB3197-001-P1-M1-G7
Method	BLASTX
NCBI GI	g1172874
BLAST score	217
E value	1.0e-17
Match length	84
% identity	54
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]
Seq. No.	230596
Seq. ID	LIB3197-001-P1-M1-G8
Method	BLASTX
NCBI GI	g1174592
BLAST score	586
E value	8.0e-61
Match length	111
% identity	97
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]
Seq. No.	230597
Seq. ID	LIB3197-001-P1-M1-G9
Method	BLASTX
NCBI GI	g2191150
BLAST score	227
E value	1.0e-18
Match length	67
% identity	81
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]
Seq. No.	230598
Seq. ID	LIB3197-001-P1-M1-H8
Method	BLASTX
NCBI GI	g120673
BLAST score	534
E value	9.0e-55

Match length	126
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]
Seq. No.	230599
Seq. ID	LIB3197-001-P1-M1-H9
Method	BLASTX
NCBI GI	g2231312
BLAST score	196
E value	3.0e-15
Match length	47
% identity	81
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]
Seq. No.	230600
Seq. ID	LIB3197-002-P1-M1-A2
Method	BLASTX
NCBI GI	g3641252
BLAST score	156
E value	2.0e-10
Match length	104
% identity	4
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]
Seq. No.	230601
Seq. ID	LIB3197-002-P1-M1-A5
Method	BLASTX
NCBI GI	g3869088
BLAST score	535
E value	6.0e-55
Match length	102
% identity	99
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]
Seq. No.	230602
Seq. ID	LIB3197-002-P1-M1-A8
Method	BLASTX
NCBI GI	g3925703
BLAST score	454
E value	2.0e-45
Match length	127
% identity	73
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.	230603
Seq. ID	LIB3197-002-P1-M1-A9
Method	BLASTX
NCBI GI	g3377831
BLAST score	138
E value	1.0e-08
Match length	76
% identity	38

NCBI Description	(AF075598) similar to maize transposon MuDR mudrA (GB:M76978) [Arabidopsis thaliana]
Seq. No.	230604
Seq. ID	LIB3197-002-P1-M1-B12
Method	BLASTX
NCBI GI	g495725
BLAST score	406
E value	4.0e-40
Match length	82
% identity	94
NCBI Description	(L25042) acetyl-CoA carboxylase [Medicago sativa]
Seq. No.	230605
Seq. ID	LIB3197-002-P1-M1-B2
Method	BLASTX
NCBI GI	g4455209
BLAST score	347
E value	7.0e-33
Match length	98
% identity	76
NCBI Description	(AL035440) putative Proline synthetase associated protein [Arabidopsis thaliana]
Seq. No.	230606
Seq. ID	LIB3197-002-P1-M1-B3
Method	BLASTX
NCBI GI	g2832625
BLAST score	360
E value	2.0e-34
Match length	86
% identity	79
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	230607
Seq. ID	LIB3197-002-P1-M1-B8
Method	BLASTX
NCBI GI	g3695406
BLAST score	381
E value	5.0e-37
Match length	111
% identity	71
NCBI Description	(AF096373) similar to isoleucyl-tRNA synthetases [Arabidopsis thaliana]
Seq. No.	230608
Seq. ID	LIB3197-002-P1-M1-C10
Method	BLASTX
NCBI GI	g4240116
BLAST score	349
E value	5.0e-33
Match length	105
% identity	67
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	230609
Seq. ID	LIB3197-002-P1-M1-C12
Method	BLASTX
NCBI GI	g3914394
BLAST score	349
E value	4.0e-33
Match length	78
% identity	82
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	230610
Seq. ID	LIB3197-002-P1-M1-C2
Method	BLASTX
NCBI GI	g3318611
BLAST score	205
E value	4.0e-16
Match length	94
% identity	50
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	230611
Seq. ID	LIB3197-002-P1-M1-C3
Method	BLASTX
NCBI GI	g1705678
BLAST score	325
E value	3.0e-30
Match length	137
% identity	39
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No.	230612
Seq. ID	LIB3197-002-P1-M1-C6
Method	BLASTX
NCBI GI	g3335370
BLAST score	152
E value	6.0e-10
Match length	72
% identity	43
NCBI Description	(AC003028) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230613
Seq. ID	LIB3197-002-P1-M1-C8
Method	BLASTX
NCBI GI	g2129499
BLAST score	521
E value	3.0e-53
Match length	109
% identity	91
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	230614
Seq. ID	LIB3197-002-P1-M1-C9
Method	BLASTX
NCBI GI	g4455299
BLAST score	239
E value	4.0e-20
Match length	143
% identity	43
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	230615
Seq. ID	LIB3197-002-P1-M1-D4
Method	BLASTX
NCBI GI	g2286153
BLAST score	513
E value	3.0e-52
Match length	110
% identity	95
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	230616
Seq. ID	LIB3197-002-P1-M1-D6
Method	BLASTX
NCBI GI	g4567311
BLAST score	287
E value	6.0e-26
Match length	69
% identity	70
NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No.	230617
Seq. ID	LIB3197-002-P1-M1-D7
Method	BLASTX
NCBI GI	g3236476
BLAST score	422
E value	1.0e-41
Match length	87
% identity	99
NCBI Description	(AF071195) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	230618
Seq. ID	LIB3197-002-P1-M1-D8
Method	BLASTX
NCBI GI	g2465434
BLAST score	332
E value	3.0e-31
Match length	75
% identity	85
NCBI Description	(AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]

Seq. No.	230619
Seq. ID	LIB3197-002-P1-M1-E11
Method	BLASTX
NCBI GI	g3193301
BLAST score	285

E value	1.0e-25
Match length	124
% identity	53
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	230620
Seq. ID	LIB3197-002-P1-M1-E3
Method	BLASTX
NCBI GI	g2425066
BLAST score	231
E value	9.0e-20
Match length	53
% identity	83
NCBI Description	(AF019147) cysteine proteinase Mir3 [Zea mays]

Seq. No.	230621
Seq. ID	LIB3197-002-P1-M1-E4
Method	BLASTX
NCBI GI	g3309575
BLAST score	227
E value	1.0e-18
Match length	67
% identity	75
NCBI Description	(AF060553) calcium sensor homolog [Arabidopsis thaliana] >gi_4538989_emb_CAB39731.1_ (Y18870) CBL4 protein [Arabidopsis thaliana]

Seq. No.	230622
Seq. ID	LIB3197-002-P1-M1-E5
Method	BLASTX
NCBI GI	g70753
BLAST score	357
E value	2.0e-34
Match length	77
% identity	94
NCBI Description	histone H3 - garden pea >gi_82610_pir__S00373 histone H3 - wheat

Seq. No.	230623
Seq. ID	LIB3197-002-P1-M1-E7
Method	BLASTX
NCBI GI	g2738248
BLAST score	391
E value	3.0e-38
Match length	95
% identity	83
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	230624
Seq. ID	LIB3197-002-P1-M1-F11
Method	BLASTX
NCBI GI	g4006893
BLAST score	336
E value	1.0e-31

Match length	78
% identity	86
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	230625
Seq. ID	LIB3197-002-P1-M1-F2
Method	BLASTX
NCBI GI	g1888485
BLAST score	226
E value	2.0e-23
Match length	72
% identity	73
NCBI Description	(Y11749) dihydroflavonol 4-reductase [Vitis vinifera]

Seq. No.	230626
Seq. ID	LIB3197-002-P1-M1-F6
Method	BLASTX
NCBI GI	g444791
BLAST score	106
E value	8.0e-10
Match length	70
% identity	16
NCBI Description	ubiquitin [Bos taurus]

Seq. No.	230627
Seq. ID	LIB3197-002-P1-M1-F9
Method	BLASTX
NCBI GI	g1703375
BLAST score	649
E value	3.0e-68
Match length	133
% identity	96
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	230628
Seq. ID	LIB3197-002-P1-M1-H11
Method	BLASTX
NCBI GI	g3334144
BLAST score	206
E value	1.0e-16
Match length	62
% identity	66
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	230629
Seq. ID	LIB3197-002-P1-M1-H4
Method	BLASTX
NCBI GI	g1399450
BLAST score	105
E value	2.0e-12
Match length	54
% identity	74
NCBI Description	(U47660) beta-tubulin 2 [Lupinus albus]

Seq. No. 230630

Seq. ID	LIB3197-002-P1-M1-H5
Method	BLASTX
NCBI GI	g3334144
BLAST score	203
E value	1.0e-17
Match length	67
% identity	71
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	230631
Seq. ID	LIB3197-002-P1-M1-H6
Method	BLASTX
NCBI GI	g2493046
BLAST score	273
E value	3.0e-24
Match length	83
% identity	66
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_82297_pir__A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	230632
Seq. ID	LIB3197-002-P1-M1-H7
Method	BLASTX
NCBI GI	g2811278
BLAST score	478
E value	3.0e-48
Match length	104
% identity	85
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	230633
Seq. ID	LIB3197-002-P1-M1-H9
Method	BLASTX
NCBI GI	g136739
BLAST score	287
E value	6.0e-26
Match length	68
% identity	81
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	230634
Seq. ID	LIB3197-003-P1-M1-A1
Method	BLASTX
NCBI GI	g232024
BLAST score	247
E value	1.0e-21
Match length	50
% identity	98
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland

	cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]
Seq. No.	230635
Seq. ID	LIB3197-003-P1-M1-A2
Method	BLASTX
NCBI GI	g2497753
BLAST score	370
E value	2.0e-35
Match length	123
% identity	54
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]
Seq. No.	230636
Seq. ID	LIB3197-003-P1-M1-B1
Method	BLASTX
NCBI GI	g3387808
BLAST score	160
E value	7.0e-11
Match length	134
% identity	27
NCBI Description	(AF035251) tripeptidyl peptidase II; dTPP II; subtilisin-like serine protease [Drosophila melanogaster]
Seq. No.	230637
Seq. ID	LIB3197-003-P1-M1-B9
Method	BLASTX
NCBI GI	g585204
BLAST score	397
E value	9.0e-39
Match length	81
% identity	91
NCBI Description	GLUTAMINE SYNTHETASE ROOT ISOZYME 4 (GLUTAMATE--AMMONIA LIGASE) (GS107) >gi_481809_pir__S39480 glutamate--ammonia ligase (EC 6.3.1.2) 1-4, cytosolic - maize >gi_434330_emb_CAA46722_ (X65929) glutamine synthetase [Zea mays]
Seq. No.	230638
Seq. ID	LIB3197-003-P1-M1-C3
Method	BLASTX
NCBI GI	g3056595
BLAST score	340
E value	5.0e-32
Match length	121
% identity	56
NCBI Description	(AC004255) T1F9.16 [Arabidopsis thaliana]
Seq. No.	230639
Seq. ID	LIB3197-003-P1-M1-D1
Method	BLASTX
NCBI GI	g3687250
BLAST score	168

E value	7.0e-12
Match length	45
% identity	69
NCBI Description	(AC005169) putative arginine n-methyltransferase [Arabidopsis thaliana]

Seq. No.	230640
Seq. ID	LIB3197-003-P1-M1-D2
Method	BLASTX
NCBI GI	g267069
BLAST score	497
E value	2.0e-50
Match length	91
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230641
Seq. ID	LIB3197-003-P1-M1-D8
Method	BLASTX
NCBI GI	g131770
BLAST score	355
E value	8.0e-34
Match length	100
% identity	64
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	230642
Seq. ID	LIB3197-003-P1-M1-E1
Method	BLASTX
NCBI GI	g3901268
BLAST score	221
E value	5.0e-18
Match length	132
% identity	34
NCBI Description	(AF060173) SV2 related protein [Rattus norvegicus]

Seq. No.	230643
Seq. ID	LIB3197-003-P1-M1-E11
Method	BLASTX
NCBI GI	g4580389
BLAST score	405
E value	9.0e-40
Match length	104
% identity	71
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	230644
Seq. ID	LIB3197-003-P1-M1-E2
Method	BLASTX
NCBI GI	g267069

BLAST score	676
E value	2.0e-71
Match length	126
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230645
Seq. ID	LIB3197-003-P1-M1-E3
Method	BLASTX
NCBI GI	g4455202
BLAST score	219
E value	7.0e-18
Match length	75
% identity	57
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No.	230646
Seq. ID	LIB3197-003-P1-M1-E5
Method	BLASTX
NCBI GI	g3334320
BLAST score	518
E value	8.0e-53
Match length	114
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	230647
Seq. ID	LIB3197-003-P1-M1-E9
Method	BLASTX
NCBI GI	g2706450
BLAST score	275
E value	2.0e-24
Match length	71
% identity	77
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	230648
Seq. ID	LIB3197-003-P1-M1-F1
Method	BLASTX
NCBI GI	g1694621
BLAST score	415
E value	1.0e-40
Match length	118
% identity	71
NCBI Description	(D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No.	230649
Seq. ID	LIB3197-003-P1-M1-F2
Method	BLASTX
NCBI GI	g1483218
BLAST score	271
E value	6.0e-24

Match length	63
% identity	79
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	230650
Seq. ID	LIB3197-003-P1-M1-F5
Method	BLASTX
NCBI GI	g729470
BLAST score	182
E value	1.0e-13
Match length	75
% identity	56
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	230651
Seq. ID	LIB3197-003-P1-M1-G10
Method	BLASTX
NCBI GI	g4467153
BLAST score	439
E value	2.0e-43
Match length	104
% identity	81
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	230652
Seq. ID	LIB3197-003-P1-M1-G3
Method	BLASTX
NCBI GI	g3080426
BLAST score	288
E value	6.0e-26
Match length	99
% identity	55
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	230653
Seq. ID	LIB3197-003-P1-M1-G4
Method	BLASTX
NCBI GI	g3298555
BLAST score	247
E value	5.0e-21
Match length	54
% identity	83
NCBI Description	(AC004681) putative homeobox protein, 3' partial [Arabidopsis thaliana]

Seq. No.	230654
Seq. ID	LIB3197-003-P1-M1-G8
Method	BLASTX
NCBI GI	g232031
BLAST score	188

E value	3.0e-14
Match length	65
% identity	52
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	230655
Seq. ID	LIB3197-003-P1-M1-H4
Method	BLASTX
NCBI GI	g2781433
BLAST score	729
E value	1.0e-77
Match length	142
% identity	94
NCBI Description	(AF030052) RSW1-like cellulose synthase catalytic subunit [Oryza sativa subsp. japonica]

Seq. No.	230656
Seq. ID	LIB3197-003-P1-M1-H5
Method	BLASTX
NCBI GI	g2281115
BLAST score	599
E value	3.0e-62
Match length	123
% identity	89
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	230657
Seq. ID	LIB3197-004-P1-M1-A10
Method	BLASTX
NCBI GI	g4309698
BLAST score	166
E value	1.0e-11
Match length	56
% identity	66
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	230658
Seq. ID	LIB3197-004-P1-M1-B1
Method	BLASTX
NCBI GI	g2832625
BLAST score	215
E value	6.0e-35
Match length	95
% identity	79
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	230659
Seq. ID	LIB3197-004-P1-M1-B2
Method	BLASTX
NCBI GI	g2736147
BLAST score	403
E value	2.0e-39

Match length	101
% identity	71
NCBI Description	(AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No.	230660
Seq. ID	LIB3197-004-P1-M1-B4
Method	BLASTX
NCBI GI	g2463666
BLAST score	450
E value	5.0e-45
Match length	85
% identity	100
NCBI Description	(AF006490) adenine nucleotide translocator 2 [Gossypium hirsutum]

Seq. No.	230661
Seq. ID	LIB3197-004-P1-M1-B5
Method	BLASTX
NCBI GI	g3046700
BLAST score	196
E value	2.0e-15
Match length	62
% identity	66
NCBI Description	(AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi_4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No.	230662
Seq. ID	LIB3197-004-P1-M1-B6
Method	BLASTX
NCBI GI	g1587206
BLAST score	521
E value	3.0e-53
Match length	110
% identity	95
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	230663
Seq. ID	LIB3197-004-P1-M1-B9
Method	BLASTX
NCBI GI	g87765
BLAST score	146
E value	1.0e-09
Match length	56
% identity	52
NCBI Description	hypothetical L1 protein (third intron of gene TS) - human >gi_364964_prf__1510254A L1 repetitive element ORF [Homo sapiens]

Seq. No.	230664
Seq. ID	LIB3197-004-P1-M1-C12
Method	BLASTX
NCBI GI	g2462746
BLAST score	629

E value	8.0e-66
Match length	136
% identity	85
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	230665
Seq. ID	LIB3197-004-P1-M1-C4
Method	BLASTX
NCBI GI	g4580523
BLAST score	275
E value	2.0e-24
Match length	113
% identity	51
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	230666
Seq. ID	LIB3197-004-P1-M1-C7
Method	BLASTX
NCBI GI	g4510383
BLAST score	199
E value	7.0e-16
Match length	78
% identity	58
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	230667
Seq. ID	LIB3197-004-P1-M1-C8
Method	BLASTX
NCBI GI	g3236237
BLAST score	425
E value	6.0e-42
Match length	130
% identity	60
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	230668
Seq. ID	LIB3197-004-P1-M1-D1
Method	BLASTX
NCBI GI	g2832680
BLAST score	443
E value	4.0e-44
Match length	131
% identity	39
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	230669
Seq. ID	LIB3197-004-P1-M1-D3
Method	BLASTX
NCBI GI	g3128176
BLAST score	347
E value	9.0e-33
Match length	116
% identity	57
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	230670
Seq. ID	LIB3197-004-P1-M1-D4
Method	BLASTX
NCBI GI	g2506139
BLAST score	336
E value	1.0e-31
Match length	76
% identity	87
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	230671
Seq. ID	LIB3197-004-P1-M1-D5
Method	BLASTX
NCBI GI	g3885329
BLAST score	203
E value	6.0e-25
Match length	74
% identity	84
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	230672
Seq. ID	LIB3197-004-P1-M1-E1
Method	BLASTX
NCBI GI	g3097321
BLAST score	187
E value	5.0e-14
Match length	88
% identity	43
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	230673
Seq. ID	LIB3197-004-P1-M1-E2
Method	BLASTX
NCBI GI	g1408471
BLAST score	455
E value	2.0e-45
Match length	102
% identity	79
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	230674
Seq. ID	LIB3197-004-P1-M1-E3
Method	BLASTX
NCBI GI	g862640
BLAST score	393
E value	2.0e-38
Match length	82
% identity	91
NCBI Description	(U20182) MADS-box protein AGL11 [Arabidopsis thaliana] >gi_4538999_emb_CAB39620.1_ (AL049481) MADS-box protein AGL11 [Arabidopsis thaliana]

Seq. No.	230675

Seq. ID	LIB3197-004-P1-M1-E7
Method	BLASTX
NCBI GI	g2832682
BLAST score	156
E value	8.0e-11
Match length	66
% identity	61
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230676
Seq. ID	LIB3197-004-P1-M1-F1
Method	BLASTX
NCBI GI	g1170898
BLAST score	588
E value	5.0e-61
Match length	139
% identity	85
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial - cider tree >gi_473206_emb_CAA55383_ (X78800) mitochondrial malate dehydrogenase [Eucalyptus gunnii]

Seq. No.	230677
Seq. ID	LIB3197-004-P1-M1-F11
Method	BLASTX
NCBI GI	g2982456
BLAST score	504
E value	3.0e-51
Match length	125
% identity	76
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	230678
Seq. ID	LIB3197-004-P1-M1-F12
Method	BLASTX
NCBI GI	g2982456
BLAST score	165
E value	7.0e-12
Match length	62
% identity	50
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	230679
Seq. ID	LIB3197-004-P1-M1-F2
Method	BLASTX
NCBI GI	g2791834
BLAST score	606
E value	4.0e-63
Match length	120
% identity	97
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	230680
Seq. ID	LIB3197-004-P1-M1-F8
Method	BLASTX
NCBI GI	g401011
BLAST score	454

E value	2.0e-45
Match length	119
% identity	82
NCBI Description	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 2) >gi_279535_pir__JDMU2 DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain (version 2) - Arabidopsis thaliana >gi_16494_emb_CAA36735_ (X52494) DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No.	230681
Seq. ID	LIB3197-004-P1-M1-F9
Method	BLASTX
NCBI GI	g401011
BLAST score	144
E value	6.0e-11
Match length	85
% identity	53
NCBI Description	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 2) >gi_279535_pir__JDMU2 DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain (version 2) - Arabidopsis thaliana >gi_16494_emb_CAA36735_ (X52494) DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No.	230682
Seq. ID	LIB3197-004-P1-M1-G4
Method	BLASTX
NCBI GI	g1220196
BLAST score	400
E value	5.0e-43
Match length	111
% identity	79
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	230683
Seq. ID	LIB3197-004-P1-M1-G6
Method	BLASTX
NCBI GI	g417060
BLAST score	589
E value	4.0e-61
Match length	119
% identity	92
NCBI Description	GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi_1094850_prf__2106409A Gln synthetase [Vigna aconitifolia]

Seq. No.	230684
Seq. ID	LIB3197-004-P1-M1-G7
Method	BLASTX
NCBI GI	g2642429
BLAST score	306
E value	6.0e-28
Match length	134
% identity	53
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	230685
Seq. ID	LIB3197-004-P1-M1-G8
Method	BLASTX
NCBI GI	g462253
BLAST score	289
E value	3.0e-26
Match length	89
% identity	67
NCBI Description	TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP >gi_284975_pir__S26660 HCNGP protein - mouse >gi_57912_emb_CAA48198_ (X68061) HCNGP [Mus musculus]

Seq. No.	230686
Seq. ID	LIB3197-004-P1-M1-G9
Method	BLASTX
NCBI GI	g401322
BLAST score	625
E value	2.0e-65
Match length	127
% identity	96
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	230687
Seq. ID	LIB3197-004-P1-M1-H10
Method	BLASTX
NCBI GI	g4539543
BLAST score	363
E value	6.0e-35
Match length	94
% identity	74
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	230688
Seq. ID	LIB3197-004-P1-M1-H2
Method	BLASTX
NCBI GI	g1518540
BLAST score	416
E value	5.0e-41
Match length	92
% identity	87
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	230689
Seq. ID	LIB3197-004-P1-M1-H3
Method	BLASTX
NCBI GI	g3869088
BLAST score	536
E value	5.0e-55
Match length	103
% identity	99
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	230690
Seq. ID	LIB3197-004-P1-M1-H9

Method	BLASTX
NCBI GI	g4454012
BLAST score	180
E value	2.0e-13
Match length	49
% identity	69
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	230691
Seq. ID	LIB3197-005-P1-M1-A1
Method	BLASTX
NCBI GI	g4455293
BLAST score	387
E value	2.0e-37
Match length	89
% identity	91
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	230692
Seq. ID	LIB3197-005-P1-M1-A10
Method	BLASTX
NCBI GI	g2760334
BLAST score	241
E value	2.0e-20
Match length	86
% identity	55
NCBI Description	(AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No.	230693
Seq. ID	LIB3197-005-P1-M1-A11
Method	BLASTX
NCBI GI	g1076627
BLAST score	219
E value	7.0e-18
Match length	78
% identity	62
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	230694
Seq. ID	LIB3197-005-P1-M1-A2
Method	BLASTX
NCBI GI	g1351856
BLAST score	454
E value	2.0e-45
Match length	108
% identity	84
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	230695
Seq. ID	LIB3197-005-P1-M1-A4
Method	BLASTX
NCBI GI	g1346180

BLAST score	386
E value	2.0e-37
Match length	86
% identity	85
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374) homology with RNA-binding proteins in meristematic tissue [Sinapis alba]

Seq. No.	230696
Seq. ID	LIB3197-005-P1-M1-A5
Method	BLASTX
NCBI GI	g464840
BLAST score	441
E value	7.0e-46
Match length	105
% identity	87
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	230697
Seq. ID	LIB3197-005-P1-M1-A8
Method	BLASTX
NCBI GI	g3377797
BLAST score	471
E value	2.0e-47
Match length	110
% identity	84
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	230698
Seq. ID	LIB3197-005-P1-M1-A9
Method	BLASTX
NCBI GI	g2501565
BLAST score	223
E value	3.0e-18
Match length	83
% identity	49
NCBI Description	HYPOTHETICAL 40.2 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION >gi_1078518_pir__S55087 hypothetical protein YMR101c - yeast (Saccharomyces cerevisiae) >gi_854438_emb_CAA89902_ (Z49807) unknown [Saccharomyces cerevisiae] >gi_4126459_dbj_BAA36578_ (AB013498) cis-prenyltransferase homologue [Saccharomyces cerevisiae]

Seq. No.	230699
Seq. ID	LIB3197-005-P1-M1-B1
Method	BLASTX
NCBI GI	g623586
BLAST score	237
E value	3.0e-20
Match length	47

% identity	100
NCBI Description	(L29273) putative [Nicotiana tabacum]

Seq. No.	230700
Seq. ID	LIB3197-005-P1-M1-B11
Method	BLASTX
NCBI GI	g4371285
BLAST score	234
E value	2.0e-19
Match length	122
% identity	43
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230701
Seq. ID	LIB3197-005-P1-M1-B12
Method	BLASTX
NCBI GI	g1658193
BLAST score	690
E value	6.0e-73
Match length	156
% identity	79
NCBI Description	(U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum bicolor]

Seq. No.	230702
Seq. ID	LIB3197-005-P1-M1-B2
Method	BLASTX
NCBI GI	g3128168
BLAST score	461
E value	3.0e-46
Match length	131
% identity	59
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	230703
Seq. ID	LIB3197-005-P1-M1-B3
Method	BLASTX
NCBI GI	g4580394
BLAST score	231
E value	3.0e-19
Match length	101
% identity	45
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	230704
Seq. ID	LIB3197-005-P1-M1-B4
Method	BLASTX
NCBI GI	g2347199
BLAST score	241
E value	6.0e-21
Match length	56
% identity	80
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	230705

Seq. ID	LIB3197-005-P1-M1-B5
Method	BLASTX
NCBI GI	g125077
BLAST score	675
E value	3.0e-71
Match length	136
% identity	99
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin 13 [Homo sapiens]

Seq. No.	230706
Seq. ID	LIB3197-005-P1-M1-B6
Method	BLASTX
NCBI GI	g4455246
BLAST score	311
E value	2.0e-28
Match length	89
% identity	66
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	230707
Seq. ID	LIB3197-005-P1-M1-B9
Method	BLASTX
NCBI GI	g2500521
BLAST score	226
E value	1.0e-18
Match length	51
% identity	84
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15) >gi_485945_emb_CAA55739_ (X79138) NeIF-4A15 [Nicotiana tabacum]

Seq. No.	230708
Seq. ID	LIB3197-005-P1-M1-C2
Method	BLASTX
NCBI GI	g3869088
BLAST score	552
E value	7.0e-57
Match length	105
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	230709
Seq. ID	LIB3197-005-P1-M1-C4
Method	BLASTX
NCBI GI	g4538923
BLAST score	287
E value	3.0e-46
Match length	148
% identity	68
NCBI Description	(AL049483) predicted protein destination factor [Arabidopsis thaliana]

Seq. No.	230710
Seq. ID	LIB3197-005-P1-M1-D1

Method	BLASTX
NCBI GI	g99992
BLAST score	231
E value	8.0e-20
Match length	67
% identity	63
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) precursor - alfalfa (clone B2) >gi_166418 (M82973) putative endomembrane protein; putative [Medicago sativa]

Seq. No.	230711
Seq. ID	LIB3197-005-P1-M1-D11
Method	BLASTX
NCBI GI	g2292917
BLAST score	682
E value	5.0e-72
Match length	155
% identity	83
NCBI Description	(X99851) galactokinase [Arabidopsis thaliana]

Seq. No.	230712
Seq. ID	LIB3197-005-P1-M1-D12
Method	BLASTX
NCBI GI	g2292917
BLAST score	208
E value	8.0e-21
Match length	93
% identity	65
NCBI Description	(X99851) galactokinase [Arabidopsis thaliana]

Seq. No.	230713
Seq. ID	LIB3197-005-P1-M1-E10
Method	BLASTX
NCBI GI	g4467144
BLAST score	442
E value	7.0e-44
Match length	101
% identity	79
NCBI Description	(AL035540) putative phosphatidylinositol synthase [Arabidopsis thaliana]

Seq. No.	230714
Seq. ID	LIB3197-005-P1-M1-E4
Method	BLASTX
NCBI GI	g4454472
BLAST score	188
E value	4.0e-14
Match length	104
% identity	43
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	230715
Seq. ID	LIB3197-005-P1-M1-E5
Method	BLASTX
NCBI GI	g4454472
BLAST score	177
E value	9.0e-13

Match length	106
% identity	42
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	230716
Seq. ID	LIB3197-005-P1-M1-F1
Method	BLASTX
NCBI GI	g2613143
BLAST score	262
E value	5.0e-23
Match length	72
% identity	72
NCBI Description	(AF030548) tubulin [Oryza sativa]

Seq. No.	230717
Seq. ID	LIB3197-005-P1-M1-F10
Method	BLASTX
NCBI GI	g2465434
BLAST score	272
E value	3.0e-24
Match length	65
% identity	82
NCBI Description	(AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]

Seq. No.	230718
Seq. ID	LIB3197-005-P1-M1-F8
Method	BLASTX
NCBI GI	g3360289
BLAST score	209
E value	1.0e-16
Match length	66
% identity	55
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	230719
Seq. ID	LIB3197-005-P1-M1-G10
Method	BLASTX
NCBI GI	g232024
BLAST score	618
E value	1.0e-64
Match length	116
% identity	100
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	230720
Seq. ID	LIB3197-005-P1-M1-G11
Method	BLASTX
NCBI GI	g3702368
BLAST score	589
E value	4.0e-61
Match length	150
% identity	73

NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]
Seq. No.	230721
Seq. ID	LIB3197-005-P1-M1-G4
Method	BLASTX
NCBI GI	g167324
BLAST score	245
E value	8.0e-21
Match length	46
% identity	96
NCBI Description	(M92051) 5' start site is putative; putative [Gossypium hirsutum]
Seq. No.	230722
Seq. ID	LIB3197-005-P1-M1-G6
Method	BLASTX
NCBI GI	g548774
BLAST score	310
E value	2.0e-28
Match length	83
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]
Seq. No.	230723
Seq. ID	LIB3197-005-P1-M1-G9
Method	BLASTX
NCBI GI	g3805847
BLAST score	141
E value	3.0e-09
Match length	40
% identity	68
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	230724
Seq. ID	LIB3197-005-P1-M1-H1
Method	BLASTX
NCBI GI	g1350680
BLAST score	265
E value	1.0e-23
Match length	72
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L1
Seq. No.	230725
Seq. ID	LIB3197-005-P1-M1-H10
Method	BLASTX
NCBI GI	g3914191
BLAST score	262
E value	8.0e-23
Match length	133
% identity	42
NCBI Description	UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT) >gi_1931579 (U76557) O-GlcNAc

transferase, p110 subunit [Rattus norvegicus]

Seq. No.	230726
Seq. ID	LIB3197-005-P1-M1-H6
Method	BLASTX
NCBI GI	g2811278
BLAST score	381
E value	8.0e-37
Match length	115
% identity	64
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	230727
Seq. ID	LIB3197-005-P1-M1-H7
Method	BLASTX
NCBI GI	g3212869
BLAST score	333
E value	2.0e-32
Match length	94
% identity	77
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	230728
Seq. ID	LIB3197-006-P1-M1-A12
Method	BLASTX
NCBI GI	g1020315
BLAST score	227
E value	1.0e-18
Match length	143
% identity	38
NCBI Description	(U36310) glycerol-3-phosphate dehydrogenase [Homo sapiens] >gi_1389721 (U40367) glycerol-3-phosphate dehydrogenase [Homo sapiens]

Seq. No.	230729
Seq. ID	LIB3197-006-P1-M1-A2
Method	BLASTX
NCBI GI	g1666234
BLAST score	433
E value	6.0e-43
Match length	82
% identity	99
NCBI Description	(U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No.	230730
Seq. ID	LIB3197-006-P1-M1-A3
Method	BLASTX
NCBI GI	g2924520
BLAST score	451
E value	4.0e-45
Match length	109
% identity	81
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	230731

Seq. ID	LIB3197-006-P1-M1-A4
Method	BLASTX
NCBI GI	g2245128
BLAST score	420
E value	3.0e-41
Match length	133
% identity	62
NCBI Description	(Z97344) peroxidase [Arabidopsis thaliana]

Seq. No.	230732
Seq. ID	LIB3197-006-P1-M1-A5
Method	BLASTX
NCBI GI	g4098129
BLAST score	370
E value	2.0e-35
Match length	70
% identity	100
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	230733
Seq. ID	LIB3197-006-P1-M1-A6
Method	BLASTX
NCBI GI	g2245128
BLAST score	409
E value	5.0e-40
Match length	112
% identity	67
NCBI Description	(Z97344) peroxidase [Arabidopsis thaliana]

Seq. No.	230734
Seq. ID	LIB3197-006-P1-M1-B1
Method	BLASTX
NCBI GI	g4097579
BLAST score	413
E value	1.0e-40
Match length	89
% identity	84
NCBI Description	(U64922) NTGP1 [Nicotiana tabacum]

Seq. No.	230735
Seq. ID	LIB3197-006-P1-M1-B10
Method	BLASTX
NCBI GI	g4572679
BLAST score	458
E value	9.0e-46
Match length	121
% identity	71
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No.	230736
Seq. ID	LIB3197-006-P1-M1-B11
Method	BLASTX
NCBI GI	g2662343
BLAST score	639
E value	5.0e-67
Match length	125

% identity	98
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	230737
Seq. ID	LIB3197-006-P1-M1-B12
Method	BLASTX
NCBI GI	g2829206
BLAST score	147
E value	3.0e-09
Match length	31
% identity	90
NCBI Description	(AF044205) proline-rich protein precursor [Gossypium hirsutum]

Seq. No.	230738
Seq. ID	LIB3197-006-P1-M1-B3
Method	BLASTX
NCBI GI	g2895576
BLAST score	158
E value	1.0e-10
Match length	118
% identity	26
NCBI Description	(AF041337) vacuolar proton pump subunit SFD beta isoform [Bos taurus]

Seq. No.	230739
Seq. ID	LIB3197-006-P1-M1-B4
Method	BLASTX
NCBI GI	g2342727
BLAST score	175
E value	1.0e-12
Match length	47
% identity	64
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230740
Seq. ID	LIB3197-006-P1-M1-B6
Method	BLASTX
NCBI GI	g2623310
BLAST score	296
E value	8.0e-27
Match length	77
% identity	74
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3402721 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	230741
Seq. ID	LIB3197-006-P1-M1-B7
Method	BLASTX
NCBI GI	g3860308
BLAST score	158
E value	1.0e-10
Match length	41
% identity	76
NCBI Description	(AJ012681) hypothetical protein [Cicer arietinum]

Seq. No.	230742
Seq. ID	LIB3197-006-P1-M1-C1
Method	BLASTX
NCBI GI	g3024703
BLAST score	289
E value	4.0e-26
Match length	77
% identity	74
NCBI Description	PROBABLE T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_2104461_emb_CAB08778_ (Z95397) Cct7p [Schizosaccharomyces pombe]

Seq. No.	230743
Seq. ID	LIB3197-006-P1-M1-C10
Method	BLASTX
NCBI GI	g1718097
BLAST score	520
E value	5.0e-53
Match length	143
% identity	66
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	230744
Seq. ID	LIB3197-006-P1-M1-C11
Method	BLASTX
NCBI GI	g3881780
BLAST score	152
E value	5.0e-10
Match length	103
% identity	38
NCBI Description	(Z48638) similar to lipid transfer protein [Caenorhabditis elegans]

Seq. No.	230745
Seq. ID	LIB3197-006-P1-M1-C12
Method	BLASTX
NCBI GI	g3269288
BLAST score	490
E value	2.0e-49
Match length	133
% identity	74
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	230746
Seq. ID	LIB3197-006-P1-M1-C2
Method	BLASTX
NCBI GI	g3873872
BLAST score	156
E value	6.0e-11
Match length	36
% identity	69
NCBI Description	(Z81030) cDNA EST CEMSC45R comes from this gene; cDNA EST yk436a5.3 comes from this gene; cDNA EST yk436a5.5 comes

from this gene [Caenorhabditis elegans]

Seq. No.	230747
Seq. ID	LIB3197-006-P1-M1-C4
Method	BLASTX
NCBI GI	g3776009
BLAST score	607
E value	3.0e-63
Match length	150
% identity	74
NCBI Description	(AJ010468) RNA helicase [Arabidopsis thaliana]

Seq. No.	230748
Seq. ID	LIB3197-006-P1-M1-C5
Method	BLASTX
NCBI GI	g4539404
BLAST score	205
E value	4.0e-16
Match length	107
% identity	45
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	230749
Seq. ID	LIB3197-006-P1-M1-D10
Method	BLASTX
NCBI GI	g3885329
BLAST score	480
E value	3.0e-50
Match length	126
% identity	86
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	230750
Seq. ID	LIB3197-006-P1-M1-D11
Method	BLASTX
NCBI GI	g120673
BLAST score	635
E value	2.0e-66
Match length	146
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

Seq. No.	230751
Seq. ID	LIB3197-006-P1-M1-D12
Method	BLASTX
NCBI GI	g2443878
BLAST score	177
E value	8.0e-13
Match length	77
% identity	60
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	230752

Seq. ID	LIB3197-006-P1-M1-D2
Method	BLASTX
NCBI GI	g3915031
BLAST score	765
E value	9.0e-82
Match length	149
% identity	99
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	230753
Seq. ID	LIB3197-006-P1-M1-D3
Method	BLASTX
NCBI GI	g3914394
BLAST score	355
E value	9.0e-34
Match length	79
% identity	82
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	230754
Seq. ID	LIB3197-006-P1-M1-D4
Method	BLASTX
NCBI GI	g1724100
BLAST score	579
E value	6.0e-60
Match length	131
% identity	84
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	230755
Seq. ID	LIB3197-006-P1-M1-D5
Method	BLASTX
NCBI GI	g4468979
BLAST score	453
E value	4.0e-45
Match length	112
% identity	74
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	230756
Seq. ID	LIB3197-006-P1-M1-D8
Method	BLASTX
NCBI GI	g2245378
BLAST score	336
E value	2.0e-31
Match length	83
% identity	72
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 230757

Seq. ID	LIB3197-006-P1-M1-E1
Method	BLASTX
NCBI GI	g992706
BLAST score	552
E value	9.0e-57
Match length	119
% identity	82
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	230758
Seq. ID	LIB3197-006-P1-M1-E10
Method	BLASTX
NCBI GI	g2827709
BLAST score	317
E value	3.0e-29
Match length	99
% identity	59
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	230759
Seq. ID	LIB3197-006-P1-M1-E2
Method	BLASTX
NCBI GI	g2129499
BLAST score	679
E value	1.0e-71
Match length	149
% identity	85
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	230760
Seq. ID	LIB3197-006-P1-M1-E3
Method	BLASTX
NCBI GI	g2827709
BLAST score	307
E value	4.0e-28
Match length	93
% identity	60
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	230761
Seq. ID	LIB3197-006-P1-M1-E7
Method	BLASTX
NCBI GI	g3688600
BLAST score	275
E value	2.0e-24
Match length	101
% identity	54
NCBI Description	(AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No.	230762
Seq. ID	LIB3197-006-P1-M1-E9
Method	BLASTX
NCBI GI	g2827709
BLAST score	321
E value	1.0e-29
Match length	97

% identity	61
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	230763
Seq. ID	LIB3197-006-P1-M1-F1
Method	BLASTX
NCBI GI	g3892056
BLAST score	400
E value	6.0e-39
Match length	94
% identity	83
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	230764
Seq. ID	LIB3197-006-P1-M1-F2
Method	BLASTX
NCBI GI	g2832625
BLAST score	384
E value	3.0e-37
Match length	91
% identity	80
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	230765
Seq. ID	LIB3197-006-P1-M1-F3
Method	BLASTX
NCBI GI	g120669
BLAST score	529
E value	4.0e-54
Match length	123
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	230766
Seq. ID	LIB3197-006-P1-M1-F7
Method	BLASTX
NCBI GI	g3892056
BLAST score	316
E value	4.0e-29
Match length	84
% identity	75
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	230767
Seq. ID	LIB3197-006-P1-M1-F8
Method	BLASTX
NCBI GI	g3097056
BLAST score	295
E value	1.0e-26
Match length	86
% identity	67
NCBI Description	(AJ003139) dihydrofolate reductase-thymidylate synthetase [Daucus carota]

Seq. No.	230768
Seq. ID	LIB3197-006-P1-M1-G1
Method	BLASTX
NCBI GI	g2058282
BLAST score	504
E value	4.0e-51
Match length	140
% identity	67
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	230769
Seq. ID	LIB3197-006-P1-M1-G2
Method	BLASTX
NCBI GI	g2921512
BLAST score	395
E value	2.0e-38
Match length	98
% identity	83
NCBI Description	(AF037460) GF14 protein [Fritillaria agrestis]

Seq. No.	230770
Seq. ID	LIB3197-006-P1-M1-G7
Method	BLASTX
NCBI GI	g2995990
BLAST score	322
E value	8.0e-30
Match length	102
% identity	62
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	230771
Seq. ID	LIB3197-006-P1-M1-G8
Method	BLASTX
NCBI GI	g116923
BLAST score	500
E value	1.0e-50
Match length	137
% identity	69
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	230772
Seq. ID	LIB3197-006-P1-M1-G9
Method	BLASTX
NCBI GI	g2119278
BLAST score	636
E value	1.0e-66
Match length	118
% identity	97
NCBI Description	tubulin beta-1 chain - rice

Seq. No.	230773

Seq. ID	LIB3197-006-P1-M1-H2
Method	BLASTX
NCBI GI	g4379025
BLAST score	175
E value	2.0e-15
Match length	106
% identity	49
NCBI Description	(X03145) pot. ORF VI [Homo sapiens]

Seq. No.	230774
Seq. ID	LIB3197-007-P1-M1-A2
Method	BLASTX
NCBI GI	g1707955
BLAST score	550
E value	1.0e-56
Match length	110
% identity	92
NCBI Description	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 (GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_ (X94320) glutamine synthetase [Vitis vinifera]

Seq. No.	230775
Seq. ID	LIB3197-007-P1-M1-A9
Method	BLASTX
NCBI GI	g1708236
BLAST score	309
E value	8.0e-29
Match length	78
% identity	78
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	230776
Seq. ID	LIB3197-007-P1-M1-B11
Method	BLASTX
NCBI GI	g3047108
BLAST score	218
E value	1.0e-17
Match length	112
% identity	53
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	230777
Seq. ID	LIB3197-007-P1-M1-B12
Method	BLASTX
NCBI GI	g4538929
BLAST score	165
E value	2.0e-11
Match length	58
% identity	59
NCBI Description	(AL049483) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No.	230778
Seq. ID	LIB3197-007-P1-M1-B4
Method	BLASTX
NCBI GI	g267069
BLAST score	339
E value	4.0e-32
Match length	72
% identity	85
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230779
Seq. ID	LIB3197-007-P1-M1-C10
Method	BLASTX
NCBI GI	g1708236
BLAST score	295
E value	2.0e-27
Match length	111
% identity	62
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	230780
Seq. ID	LIB3197-007-P1-M1-C2
Method	BLASTX
NCBI GI	g464621
BLAST score	164
E value	2.0e-11
Match length	47
% identity	68
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	230781
Seq. ID	LIB3197-007-P1-M1-C4
Method	BLASTX
NCBI GI	g416731
BLAST score	143
E value	3.0e-09
Match length	67
% identity	46
NCBI Description	POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir__JQ1107 18.3K protein precursor, pollen - maize >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays]

>gi_1588669_prf__2209273A Zm13 [Zea mays]

Seq. No.	230782
Seq. ID	LIB3197-007-P1-M1-E1
Method	BLASTX
NCBI GI	g1778370
BLAST score	416
E value	7.0e-43
Match length	102
% identity	85
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	230783
Seq. ID	LIB3197-007-P1-M1-E2
Method	BLASTX
NCBI GI	g100203
BLAST score	331
E value	6.0e-31
Match length	108
% identity	63
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	230784
Seq. ID	LIB3197-007-P1-M1-E6
Method	BLASTX
NCBI GI	g1587206
BLAST score	161
E value	4.0e-11
Match length	35
% identity	94
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	230785
Seq. ID	LIB3197-007-P1-M1-F4
Method	BLASTX
NCBI GI	g3873710
BLAST score	272
E value	1.0e-27
Match length	110
% identity	56
NCBI Description	(Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No.	230786
Seq. ID	LIB3197-007-P1-M1-F5
Method	BLASTX
NCBI GI	g267069
BLAST score	583
E value	2.0e-60
Match length	108
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594

	tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	230787
Seq. ID	LIB3197-007-P1-M1-F6
Method	BLASTX
NCBI GI	g2760830
BLAST score	220
E value	7.0e-18
Match length	70
% identity	57
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
Seq. No.	230788
Seq. ID	LIB3197-007-P1-M1-G8
Method	BLASTX
NCBI GI	g2811278
BLAST score	137
E value	1.0e-08
Match length	70
% identity	44
NCBI Description	(AF043284) expansin [Gossypium hirsutum]
Seq. No.	230789
Seq. ID	LIB3197-007-P1-M1-H5
Method	BLASTX
NCBI GI	g3851001
BLAST score	303
E value	1.0e-27
Match length	83
% identity	76
NCBI Description	(AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]
Seq. No.	230790
Seq. ID	LIB3197-007-P1-M1-H7
Method	BLASTX
NCBI GI	g3415117
BLAST score	438
E value	2.0e-43
Match length	109
% identity	42
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]
Seq. No.	230791
Seq. ID	LIB3197-007-P1-M1-H9
Method	BLASTX
NCBI GI	g267069
BLAST score	322
E value	1.0e-54
Match length	110
% identity	92
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230792
Seq. ID	LIB3197-008-P1-M1-A12
Method	BLASTX
NCBI GI	g2146727
BLAST score	374
E value	3.0e-36
Match length	90
% identity	74
NCBI Description	cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 - Arabidopsis thaliana (fragment) >gi_598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	230793
Seq. ID	LIB3197-008-P1-M1-A5
Method	BLASTX
NCBI GI	g1766046
BLAST score	469
E value	4.0e-47
Match length	101
% identity	85
NCBI Description	(U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	230794
Seq. ID	LIB3197-008-P1-M1-A6
Method	BLASTX
NCBI GI	g3641836
BLAST score	168
E value	1.0e-11
Match length	103
% identity	41
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	230795
Seq. ID	LIB3197-008-P1-M1-A8
Method	BLASTX
NCBI GI	g2244765
BLAST score	312
E value	1.0e-28
Match length	93
% identity	55
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230796
Seq. ID	LIB3197-008-P1-M1-B10
Method	BLASTX
NCBI GI	g3252806
BLAST score	158
E value	1.0e-10
Match length	97
% identity	33
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 230797

Seq. ID	LIB3197-008-P1-M1-B12
Method	BLASTX
NCBI GI	g3983665
BLAST score	339
E value	8.0e-32
Match length	88
% identity	77
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No.	230798
Seq. ID	LIB3197-008-P1-M1-B2
Method	BLASTX
NCBI GI	g2760326
BLAST score	232
E value	2.0e-19
Match length	112
% identity	46
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	230799
Seq. ID	LIB3197-008-P1-M1-B5
Method	BLASTX
NCBI GI	g2832625
BLAST score	466
E value	1.0e-46
Match length	114
% identity	78
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	230800
Seq. ID	LIB3197-008-P1-M1-B7
Method	BLASTX
NCBI GI	g3892051
BLAST score	313
E value	6.0e-29
Match length	86
% identity	72
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	230801
Seq. ID	LIB3197-008-P1-M1-B9
Method	BLASTX
NCBI GI	g3269284
BLAST score	245
E value	6.0e-21
Match length	98
% identity	55
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	230802
Seq. ID	LIB3197-008-P1-M1-C1
Method	BLASTX
NCBI GI	g3269284
BLAST score	369
E value	2.0e-35
Match length	112

% identity	69
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	230803
Seq. ID	LIB3197-008-P1-M1-C11
Method	BLASTX
NCBI GI	g3377820
BLAST score	172
E value	2.0e-12
Match length	75
% identity	48
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	230804
Seq. ID	LIB3197-008-P1-M1-C3
Method	BLASTX
NCBI GI	g1076668
BLAST score	732
E value	7.0e-78
Match length	145
% identity	92
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	230805
Seq. ID	LIB3197-008-P1-M1-C4
Method	BLASTX
NCBI GI	g4432846
BLAST score	173
E value	2.0e-12
Match length	99
% identity	54
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	230806
Seq. ID	LIB3197-008-P1-M1-C5
Method	BLASTX
NCBI GI	g2970051
BLAST score	269
E value	9.0e-24
Match length	83
% identity	63
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	230807
Seq. ID	LIB3197-008-P1-M1-C6
Method	BLASTX
NCBI GI	g3377820
BLAST score	136
E value	1.0e-08
Match length	35
% identity	74
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	230808
Seq. ID	LIB3197-008-P1-M1-C7
Method	BLASTX
NCBI GI	g464849
BLAST score	693
E value	2.0e-73
Match length	129
% identity	100
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	230809
Seq. ID	LIB3197-008-P1-M1-D1
Method	BLASTX
NCBI GI	g2344894
BLAST score	358
E value	3.0e-34
Match length	114
% identity	60
NCBI Description	(AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230810
Seq. ID	LIB3197-008-P1-M1-D11
Method	BLASTX
NCBI GI	g1354849
BLAST score	394
E value	3.0e-38
Match length	119
% identity	65
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	230811
Seq. ID	LIB3197-008-P1-M1-D12
Method	BLASTX
NCBI GI	g3337356
BLAST score	504
E value	4.0e-51
Match length	102
% identity	96
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	230812
Seq. ID	LIB3197-008-P1-M1-D4
Method	BLASTX
NCBI GI	g3023195
BLAST score	525
E value	1.0e-53
Match length	127
% identity	80
NCBI Description	14-3-3-LIKE PROTEIN B (SGF14B) >gi_1575727 (U70534) SGF14B [Glycine max]

Seq. No.	230813
Seq. ID	LIB3197-008-P1-M1-D5
Method	BLASTX

NCBI GI	g4376650
BLAST score	145
E value	5.0e-09
Match length	69
% identity	48
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No.	230814
Seq. ID	LIB3197-008-P1-M1-D7
Method	BLASTX
NCBI GI	g3695388
BLAST score	209
E value	1.0e-16
Match length	62
% identity	60
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	230815
Seq. ID	LIB3197-008-P1-M1-E3
Method	BLASTX
NCBI GI	g3402279
BLAST score	574
E value	2.0e-59
Match length	127
% identity	83
NCBI Description	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

Seq. No.	230816
Seq. ID	LIB3197-008-P1-M1-E4
Method	BLASTX
NCBI GI	g4539301
BLAST score	166
E value	1.0e-11
Match length	67
% identity	51
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	230817
Seq. ID	LIB3197-008-P1-M1-E5
Method	BLASTX
NCBI GI	g1332579
BLAST score	236
E value	9.0e-20
Match length	73
% identity	7
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	230818
Seq. ID	LIB3197-008-P1-M1-E8
Method	BLASTX
NCBI GI	g4099611
BLAST score	243
E value	1.0e-20
Match length	137
% identity	37

NCBI Description	(U88873) BUB2-like protein 1 [Mus musculus]
Seq. No.	230819
Seq. ID	LIB3197-008-P1-M1-F1
Method	BLASTX
NCBI GI	g2689631
BLAST score	702
E value	2.0e-74
Match length	140
% identity	99
NCBI Description	(AF022389) ADP-ribosylation factor [Vigna unguiculata]
Seq. No.	230820
Seq. ID	LIB3197-008-P1-M1-F3
Method	BLASTX
NCBI GI	g70644
BLAST score	649
E value	4.0e-68
Match length	131
% identity	19
NCBI Description	ubiquitin precursor - common sunflower (fragment)
Seq. No.	230821
Seq. ID	LIB3197-008-P1-M1-F5
Method	BLASTX
NCBI GI	g1255951
BLAST score	513
E value	3.0e-52
Match length	128
% identity	73
NCBI Description	(X96932) PS60 [Nicotiana tabacum]
Seq. No.	230822
Seq. ID	LIB3197-008-P1-M1-F6
Method	BLASTX
NCBI GI	g1708313
BLAST score	390
E value	8.0e-38
Match length	85
% identity	92
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]
Seq. No.	230823
Seq. ID	LIB3197-008-P1-M1-F8
Method	BLASTX
NCBI GI	g3914424
BLAST score	486
E value	4.0e-49
Match length	112
% identity	81
NCBI Description	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2511592_emb_CAA74027.1_ (Y13693) multicatalytic endopeptidase complex, proteasome component, alpha subunit

[Arabidopsis thaliana]

Seq. No.	230824
Seq. ID	LIB3197-008-P1-M1-G1
Method	BLASTX
NCBI GI	g3881189
BLAST score	448
E value	1.0e-44
Match length	110
% identity	73
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No.	230825
Seq. ID	LIB3197-008-P1-M1-G4
Method	BLASTX
NCBI GI	g2266992
BLAST score	307
E value	4.0e-28
Match length	137
% identity	7
NCBI Description	(U77412) O-linked GlcNAc transferase [Caenorhabditis elegans]

Seq. No.	230826
Seq. ID	LIB3197-008-P1-M1-G7
Method	BLASTX
NCBI GI	g1703375
BLAST score	543
E value	1.0e-55
Match length	112
% identity	96
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	230827
Seq. ID	LIB3197-008-P1-M1-H1
Method	BLASTX
NCBI GI	g1706652
BLAST score	294
E value	2.0e-26
Match length	90
% identity	61
NCBI Description	ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_498862 (U09736) enolase [Entamoeba histolytica]

Seq. No.	230828
Seq. ID	LIB3197-008-P1-M1-H2
Method	BLASTX
NCBI GI	g3176098
BLAST score	430
E value	1.0e-42
Match length	130
% identity	38

NCBI Description	(Y15036) annexin [Medicago truncatula]
Seq. No.	230829
Seq. ID	LIB3197-008-P1-M1-H5
Method	BLASTX
NCBI GI	g3757521
BLAST score	300
E value	3.0e-27
Match length	130
% identity	45
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.	230830
Seq. ID	LIB3197-008-P1-M1-H7
Method	BLASTX
NCBI GI	g400650
BLAST score	187
E value	5.0e-14
Match length	98
% identity	42
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX I-13KD-B) (CI-13KD-B) (B13) >gi_346535_pir__S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 - bovine >gi_238_emb_CAA44903_ (X63218) NADH dehydrogenase [Bos taurus]
Seq. No.	230831
Seq. ID	LIB3197-008-P1-M1-H8
Method	BLASTX
NCBI GI	g4455351
BLAST score	293
E value	2.0e-26
Match length	72
% identity	76
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]
Seq. No.	230832
Seq. ID	LIB3197-010-P1-M1-A1
Method	BLASTX
NCBI GI	g113217
BLAST score	247
E value	3.0e-21
Match length	54
% identity	87
NCBI Description	ACTIN 1 >gi_100149_pir__S07002 actin 1 - carrot
Seq. No.	230833
Seq. ID	LIB3197-010-P1-M1-A12
Method	BLASTX
NCBI GI	g1220196
BLAST score	618
E value	2.0e-64
Match length	134
% identity	87
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.	230834

Seq. ID	LIB3197-010-P1-M1-A3
Method	BLASTX
NCBI GI	g2879811
BLAST score	411
E value	2.0e-40
Match length	92
% identity	85
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	230835
Seq. ID	LIB3197-010-P1-M1-A5
Method	BLASTX
NCBI GI	g4455158
BLAST score	439
E value	3.0e-52
Match length	117
% identity	85
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	230836
Seq. ID	LIB3197-010-P1-M1-A6
Method	BLASTX
NCBI GI	g3169287
BLAST score	261
E value	9.0e-24
Match length	66
% identity	91
NCBI Description	(AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	230837
Seq. ID	LIB3197-010-P1-M1-A9
Method	BLASTX
NCBI GI	g2245100
BLAST score	149
E value	9.0e-10
Match length	91
% identity	44
NCBI Description	(Z97343) DNA-binding protein homolog [Arabidopsis thaliana]

Seq. No.	230838
Seq. ID	LIB3197-010-P1-M1-B1
Method	BLASTX
NCBI GI	g3800951
BLAST score	176
E value	7.0e-13
Match length	68
% identity	49
NCBI Description	(AF100657) No definition line found [Caenorhabditis elegans]

Seq. No.	230839
Seq. ID	LIB3197-010-P1-M1-B6
Method	BLASTX
NCBI GI	g4417271
BLAST score	143
E value	2.0e-09

Match length	43
% identity	70
NCBI Description	(AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	230840
Seq. ID	LIB3197-010-P1-M1-C11
Method	BLASTX
NCBI GI	g832876
BLAST score	169
E value	2.0e-12
Match length	36
% identity	92
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	230841
Seq. ID	LIB3197-010-P1-M1-C2
Method	BLASTX
NCBI GI	g862640
BLAST score	337
E value	3.0e-33
Match length	82
% identity	87
NCBI Description	(U20182) MADS-box protein AGL11 [Arabidopsis thaliana] >gi_4538999_emb_CAB39620.1_ (AL049481) MADS-box protein AGL11 [Arabidopsis thaliana]

Seq. No.	230842
Seq. ID	LIB3197-010-P1-M1-C3
Method	BLASTX
NCBI GI	g4105798
BLAST score	392
E value	4.0e-38
Match length	94
% identity	67
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	230843
Seq. ID	LIB3197-010-P1-M1-C5
Method	BLASTX
NCBI GI	g1362086
BLAST score	334
E value	2.0e-31
Match length	99
% identity	68
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	230844
Seq. ID	LIB3197-010-P1-M1-C7

09604.0004.PCUS00

Method	BLASTX
NCBI GI	g832876
BLAST score	410
E value	4.0e-40
Match length	100
% identity	81
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	230845
Seq. ID	LIB3197-010-P1-M1-D1
Method	BLASTX
NCBI GI	g1076738
BLAST score	431
E value	7.0e-43
Match length	84
% identity	95
NCBI Description	beta-tubulin R2242 - rice

Seq. No.	230846
Seq. ID	LIB3197-010-P1-M1-D12
Method	BLASTX
NCBI GI	g3176874
BLAST score	338
E value	6.0e-32
Match length	102
% identity	65
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	230847
Seq. ID	LIB3197-010-P1-M1-D3
Method	BLASTX
NCBI GI	g4056432
BLAST score	145
E value	5.0e-09
Match length	38
% identity	71
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	230848
Seq. ID	LIB3197-010-P1-M1-D8
Method	BLASTX
NCBI GI	g629806
BLAST score	455
E value	2.0e-47
Match length	108
% identity	85
NCBI Description	tubulin beta chain - rice >gi_493725_emb_CAA55912_ (X79367) beta tubulin [Oryza sativa]

Seq. No.	230849
Seq. ID	LIB3197-010-P1-M1-E3

Method	BLASTX
NCBI GI	g4098128
BLAST score	223
E value	2.0e-18
Match length	52
% identity	85
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	230850
Seq. ID	LIB3197-010-P1-M1-E4
Method	BLASTX
NCBI GI	g3273200
BLAST score	174
E value	1.0e-12
Match length	50
% identity	70
NCBI Description	(AB010917) responce reactor3 [Arabidopsis thaliana] >gi_3894192 (AC005662) response regulator 3 [Arabidopsis thaliana]

Seq. No.	230851
Seq. ID	LIB3197-010-P1-M1-E5
Method	BLASTX
NCBI GI	g2832700
BLAST score	139
E value	1.0e-08
Match length	80
% identity	46
NCBI Description	(AL021713) unknown protein [Arabidopsis thaliana]

Seq. No.	230852
Seq. ID	LIB3197-010-P1-M1-E6
Method	BLASTX
NCBI GI	g100484
BLAST score	190
E value	1.0e-14
Match length	98
% identity	40
NCBI Description	hypothetical protein - garden snapdragon

Seq. No.	230853
Seq. ID	LIB3197-010-P1-M1-F10
Method	BLASTX
NCBI GI	g3395938
BLAST score	340
E value	4.0e-32
Match length	91
% identity	70
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	230854
Seq. ID	LIB3197-010-P1-M1-F11
Method	BLASTX
NCBI GI	g121631
BLAST score	281
E value	3.0e-25

Match length	70
% identity	74
NCBI Description	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco >gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana sylvestris]

Seq. No.	230855
Seq. ID	LIB3197-010-P1-M1-F12
Method	BLASTX
NCBI GI	g1346802
BLAST score	281
E value	3.0e-25
Match length	93
% identity	59
NCBI Description	PROFILIN 1 >gi_1076516_pir__S49351 profilin - kidney bean >gi_556836_emb_CAA57508_ (X81982) profilin [Phaseolus vulgaris]

Seq. No.	230856
Seq. ID	LIB3197-010-P1-M1-F3
Method	BLASTX
NCBI GI	g1706319
BLAST score	158
E value	4.0e-11
Match length	72
% identity	47
NCBI Description	HISTIDINE DECARBOXYLASE (HDC) (TOM92) >gi_481829_pir__S39554 histidine decarboxylase (EC 4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900) histidine decarboxylase [Lycopersicon esculentum]

Seq. No.	230857
Seq. ID	LIB3197-010-P1-M1-G1
Method	BLASTX
NCBI GI	g2661840
BLAST score	166
E value	6.0e-12
Match length	51
% identity	67
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	230858
Seq. ID	LIB3197-010-P1-M1-G12
Method	BLASTX
NCBI GI	g3426039
BLAST score	140
E value	6.0e-18
Match length	76
% identity	57
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	230859
Seq. ID	LIB3197-010-P1-M1-G3
Method	BLASTX
NCBI GI	g2842490
BLAST score	206

E value 1.0e-16
Match length 61
% identity 64
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 230860
Seq. ID LIB3197-010-P1-M1-G7
Method BLASTX
NCBI GI g2347098
BLAST score 334
E value 2.0e-31
Match length 72
% identity 94
NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 230861
Seq. ID LIB3197-010-P1-M1-H1
Method BLASTX
NCBI GI g421876
BLAST score 173
E value 5.0e-13
Match length 59
% identity 63
NCBI Description probable ATP synthase chain - soybean >gi_396230_emb_CAA52349_ (X74296) putative ATP synthase subunit [Glycine max]

Seq. No. 230862
Seq. ID LIB3197-010-P1-M1-H3
Method BLASTX
NCBI GI g2129825
BLAST score 459
E value 5.0e-46
Match length 107
% identity 83
NCBI Description dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 230863
Seq. ID LIB3197-010-P1-M1-H5
Method BLASTX
NCBI GI g2104959
BLAST score 460
E value 4.0e-46
Match length 109
% identity 77
NCBI Description (U96925) immunophilin [Vicia faba]

Seq. No. 230864
Seq. ID LIB3197-010-P1-M1-H6
Method BLASTX
NCBI GI g4454051
BLAST score 221
E value 5.0e-18
Match length 74

% identity	64
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	230865
Seq. ID	LIB3197-010-P1-M1-H8
Method	BLASTX
NCBI GI	g267069
BLAST score	583
E value	2.0e-60
Match length	108
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230866
Seq. ID	LIB3197-010-P1-M1-H9
Method	BLASTX
NCBI GI	g2500717
BLAST score	329
E value	1.0e-30
Match length	100
% identity	58
NCBI Description	STS14 PROTEIN PRECURSOR >gi_2129995_pir__S65052 pistil-specific protein sts14 precursor - potato >gi_1236785_emb_CAA57976_ (X82652) sts14 [Solanum tuberosum] >gi_1589691_prf__2211417A sts14 gene [Solanum tuberosum]

Seq. No.	230867
Seq. ID	LIB3197-011-P1-M1-A11
Method	BLASTX
NCBI GI	g4455208
BLAST score	357
E value	6.0e-34
Match length	114
% identity	68
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	230868
Seq. ID	LIB3197-011-P1-M1-A12
Method	BLASTX
NCBI GI	g3184082
BLAST score	338
E value	1.0e-31
Match length	117
% identity	51
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	230869
Seq. ID	LIB3197-011-P1-M1-A4
Method	BLASTX
NCBI GI	g2252841
BLAST score	176

E value	6.0e-13
Match length	73
% identity	52
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	230870
Seq. ID	LIB3197-011-P1-M1-A6
Method	BLASTX
NCBI GI	g3738257
BLAST score	493
E value	7.0e-50
Match length	105
% identity	92
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	230871
Seq. ID	LIB3197-011-P1-M1-B10
Method	BLASTX
NCBI GI	g2398679
BLAST score	709
E value	3.0e-75
Match length	146
% identity	93
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	230872
Seq. ID	LIB3197-011-P1-M1-B11
Method	BLASTX
NCBI GI	g2702281
BLAST score	379
E value	1.0e-36
Match length	100
% identity	42
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	230873
Seq. ID	LIB3197-011-P1-M1-B4
Method	BLASTX
NCBI GI	g3023847
BLAST score	560
E value	9.0e-58
Match length	115
% identity	36
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	230874
Seq. ID	LIB3197-011-P1-M1-C10
Method	BLASTX
NCBI GI	g2827710
BLAST score	173
E value	2.0e-12
Match length	65

% identity	54
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]

Seq. No.	230875
Seq. ID	LIB3197-011-P1-M1-C11
Method	BLASTX
NCBI GI	g3914431
BLAST score	599
E value	2.0e-62
Match length	135
% identity	85
NCBI Description	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha subunit [Spinacia oleracea]

Seq. No.	230876
Seq. ID	LIB3197-011-P1-M1-C2
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	7.0e-20
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	230877
Seq. ID	LIB3197-011-P1-M1-C3
Method	BLASTX
NCBI GI	g2286153
BLAST score	529
E value	3.0e-54
Match length	126
% identity	80
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	230878
Seq. ID	LIB3197-011-P1-M1-C5
Method	BLASTX
NCBI GI	g1586940
BLAST score	425
E value	6.0e-42
Match length	122
% identity	68
NCBI Description	Ser/Thr kinase [Lycopersicon esculentum]

Seq. No.	230879
Seq. ID	LIB3197-011-P1-M1-C7
Method	BLASTX
NCBI GI	g2245000
BLAST score	335
E value	2.0e-31
Match length	91
% identity	75
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230880
Seq. ID	LIB3197-011-P1-M1-C9
Method	BLASTX
NCBI GI	g1703108
BLAST score	489
E value	2.0e-49
Match length	93
% identity	98
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	230881
Seq. ID	LIB3197-011-P1-M1-D1
Method	BLASTX
NCBI GI	g1710780
BLAST score	193
E value	7.0e-29
Match length	114
% identity	58
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	230882
Seq. ID	LIB3197-011-P1-M1-D7
Method	BLASTX
NCBI GI	g131529
BLAST score	186
E value	6.0e-14
Match length	82
% identity	22
NCBI Description	POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) >gi_53553_emb_CAA36321_ (X52101) 25kDa nuclear protein [Mus musculus]

Seq. No.	230883
Seq. ID	LIB3197-011-P1-M1-E2
Method	BLASTX
NCBI GI	g4455194
BLAST score	290
E value	2.0e-26
Match length	68
% identity	79
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	230884
Seq. ID	LIB3197-011-P1-M1-E9
Method	BLASTX
NCBI GI	g1703375
BLAST score	318
E value	1.0e-29
Match length	66

% identity	97
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]
Seq. No.	230885
Seq. ID	LIB3197-011-P1-M1-F1
Method	BLASTX
NCBI GI	g2462825
BLAST score	271
E value	5.0e-24
Match length	85
% identity	61
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]
Seq. No.	230886
Seq. ID	LIB3197-011-P1-M1-F3
Method	BLASTX
NCBI GI	g267069
BLAST score	440
E value	8.0e-44
Match length	81
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	230887
Seq. ID	LIB3197-011-P1-M1-G1
Method	BLASTX
NCBI GI	g4467146
BLAST score	388
E value	1.0e-37
Match length	142
% identity	52
NCBI Description	(AL035540) galactosidase like protein [Arabidopsis thaliana]
Seq. No.	230888
Seq. ID	LIB3197-011-P1-M1-G7
Method	BLASTX
NCBI GI	g280523
BLAST score	258
E value	2.0e-22
Match length	83
% identity	61
NCBI Description	hypothetical protein B0464.5 - Caenorhabditis elegans
Seq. No.	230889
Seq. ID	LIB3197-011-P1-M1-G8
Method	BLASTX
NCBI GI	g1174592
BLAST score	563
E value	4.0e-58
Match length	110
% identity	95

NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]
Seq. No.	230890
Seq. ID	LIB3197-011-P1-M1-G9
Method	BLASTX
NCBI GI	g3341681
BLAST score	381
E value	9.0e-37
Match length	80
% identity	96
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi_741994_prf__2008312A GTP-binding protein [Arabidopsis thaliana]
Seq. No.	230891
Seq. ID	LIB3197-011-P1-M1-H2
Method	BLASTX
NCBI GI	g4490332
BLAST score	184
E value	9.0e-14
Match length	77
% identity	53
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]
Seq. No.	230892
Seq. ID	LIB3197-011-P1-M1-H3
Method	BLASTX
NCBI GI	g3548803
BLAST score	300
E value	2.0e-27
Match length	85
% identity	66
NCBI Description	(AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
Seq. No.	230893
Seq. ID	LIB3197-012-P1-M1-A10
Method	BLASTX
NCBI GI	g2827143
BLAST score	649
E value	3.0e-68
Match length	127
% identity	93
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	230894
Seq. ID	LIB3197-012-P1-M1-A11
Method	BLASTX
NCBI GI	g4580460
BLAST score	471
E value	2.0e-47
Match length	101
% identity	92

NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]
Seq. No.	230895
Seq. ID	LIB3197-012-P1-M1-A12
Method	BLASTX
NCBI GI	g267069
BLAST score	531
E value	2.0e-54
Match length	98
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	230896
Seq. ID	LIB3197-012-P1-M1-A5
Method	BLASTX
NCBI GI	g4580460
BLAST score	162
E value	1.0e-11
Match length	56
% identity	62
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]
Seq. No.	230897
Seq. ID	LIB3197-012-P1-M1-A6
Method	BLASTX
NCBI GI	g172383
BLAST score	304
E value	9.0e-28
Match length	96
% identity	60
NCBI Description	(M38723) RNA polymerase III [Saccharomyces cerevisiae]
Seq. No.	230898
Seq. ID	LIB3197-012-P1-M1-B10
Method	BLASTX
NCBI GI	g4098521
BLAST score	634
E value	2.0e-66
Match length	131
% identity	91
NCBI Description	(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi_4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana]
Seq. No.	230899
Seq. ID	LIB3197-012-P1-M1-B5
Method	BLASTX
NCBI GI	g1351014
BLAST score	474
E value	1.0e-47
Match length	113
% identity	83

NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]
Seq. No.	230900
Seq. ID	LIB3197-012-P1-M1-B6
Method	BLASTX
NCBI GI	g3643602
BLAST score	322
E value	7.0e-30
Match length	115
% identity	59
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]
Seq. No.	230901
Seq. ID	LIB3197-012-P1-M1-C10
Method	BLASTX
NCBI GI	g3914192
BLAST score	269
E value	1.0e-23
Match length	131
% identity	51
NCBI Description	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX PRECURSOR (E2) (PDC-E2) >gi_3150120_emb_CAA19134_ (AL023595) dihydrolipoamide acetyltransferase component [Schizosaccharomyces pombe]
Seq. No.	230902
Seq. ID	LIB3197-012-P1-M1-C11
Method	BLASTX
NCBI GI	g4574320
BLAST score	157
E value	2.0e-10
Match length	53
% identity	60
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]
Seq. No.	230903
Seq. ID	LIB3197-012-P1-M1-C4
Method	BLASTX
NCBI GI	g120669
BLAST score	578
E value	7.0e-60
Match length	134
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	230904
Seq. ID	LIB3197-012-P1-M1-C5
Method	BLASTX
NCBI GI	g3309170
BLAST score	280

E value	6.0e-25
Match length	115
% identity	48
NCBI Description	(AF071314) COP9 complex subunit 4 [Mus musculus]

Seq. No.	230905
Seq. ID	LIB3197-012-P1-M1-D10
Method	BLASTX
NCBI GI	g4539301
BLAST score	211
E value	7.0e-17
Match length	108
% identity	43
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	230906
Seq. ID	LIB3197-012-P1-M1-D11
Method	BLASTX
NCBI GI	g3063396
BLAST score	533
E value	1.0e-54
Match length	119
% identity	84
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	230907
Seq. ID	LIB3197-012-P1-M1-D4
Method	BLASTX
NCBI GI	g4191778
BLAST score	320
E value	1.0e-29
Match length	105
% identity	63
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	230908
Seq. ID	LIB3197-012-P1-M1-D5
Method	BLASTX
NCBI GI	g2909781
BLAST score	549
E value	2.0e-56
Match length	139
% identity	78
NCBI Description	(AF020288) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]

Seq. No.	230909
Seq. ID	LIB3197-012-P1-M1-E11
Method	BLASTX
NCBI GI	g3915866
BLAST score	608
E value	2.0e-63
Match length	138
% identity	80
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

09604704.950

	>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]
Seq. No.	230910
Seq. ID	LIB3197-012-P1-M1-E4
Method	BLASTX
NCBI GI	g2062167
BLAST score	206
E value	2.0e-16
Match length	78
% identity	51
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
Seq. No.	230911
Seq. ID	LIB3197-012-P1-M1-E5
Method	BLASTX
NCBI GI	g3493172
BLAST score	515
E value	1.0e-52
Match length	111
% identity	91
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]
Seq. No.	230912
Seq. ID	LIB3197-012-P1-M1-F10
Method	BLASTX
NCBI GI	g4469023
BLAST score	551
E value	1.0e-56
Match length	124
% identity	84
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	230913
Seq. ID	LIB3197-012-P1-M1-F11
Method	BLASTX
NCBI GI	g2104219
BLAST score	743
E value	3.0e-79
Match length	144
% identity	100
NCBI Description	(D21853) KIAA0111 [Homo sapiens]
Seq. No.	230914
Seq. ID	LIB3197-012-P1-M1-F12
Method	BLASTX
NCBI GI	g1076627
BLAST score	330
E value	8.0e-31
Match length	110
% identity	63
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase [Nicotiana tabacum]
Seq. No.	230915

Seq. ID	LIB3197-012-P1-M1-F3
Method	BLASTX
NCBI GI	g71532
BLAST score	677
E value	2.0e-71
Match length	138
% identity	99
NCBI Description	keratin, type II cytoskeletal - human (fragment) >gi_34069_emb_CAA24760_ (V01516) keratin [Homo sapiens] >gi_386847 (J00269) keratin [Homo sapiens]

Seq. No.	230916
Seq. ID	LIB3197-012-P1-M1-F5
Method	BLASTX
NCBI GI	g267069
BLAST score	566
E value	2.0e-58
Match length	105
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230917
Seq. ID	LIB3197-012-P1-M1-F7
Method	BLASTX
NCBI GI	g1814424
BLAST score	184
E value	4.0e-14
Match length	47
% identity	83
NCBI Description	(U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No.	230918
Seq. ID	LIB3197-012-P1-M1-F8
Method	BLASTX
NCBI GI	g267069
BLAST score	531
E value	2.0e-54
Match length	98
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230919
Seq. ID	LIB3197-012-P1-M1-G1
Method	BLASTX
NCBI GI	g1001708
BLAST score	273
E value	4.0e-24
Match length	85
% identity	65
NCBI Description	(D64004) NifS [Synechocystis sp.]

Seq. No.	230920
Seq. ID	LIB3197-012-P1-M1-G10
Method	BLASTX
NCBI GI	g4204260
BLAST score	164
E value	2.0e-11
Match length	51
% identity	59
NCBI Description	(AC005223) 25568 [Arabidopsis thaliana]

Seq. No.	230921
Seq. ID	LIB3197-012-P1-M1-G2
Method	BLASTX
NCBI GI	g1495273
BLAST score	546
E value	4.0e-56
Match length	124
% identity	84
NCBI Description	(Z50752) sugar transporter [Arabidopsis thaliana]

Seq. No.	230922
Seq. ID	LIB3197-012-P1-M1-G3
Method	BLASTX
NCBI GI	g3702641
BLAST score	214
E value	3.0e-17
Match length	88
% identity	44
NCBI Description	(AL031825) similar to human 75k autoantigen [Schizosaccharomyces pombe]

Seq. No.	230923
Seq. ID	LIB3197-012-P1-M1-G5
Method	BLASTX
NCBI GI	g3660467
BLAST score	398
E value	9.0e-39
Match length	90
% identity	88
NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]

Seq. No.	230924
Seq. ID	LIB3197-012-P1-M1-G8
Method	BLASTX
NCBI GI	g2642157
BLAST score	267
E value	2.0e-23
Match length	76
% identity	65
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	230925
Seq. ID	LIB3197-012-P1-M1-H1
Method	BLASTX
NCBI GI	g2833386
BLAST score	537

E value	4.0e-55
Match length	128
% identity	85
NCBI Description	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi_2129493_pir__S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi_3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi_1587969_prf__2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No.	230926
Seq. ID	LIB3197-012-P1-M1-H11
Method	BLASTX
NCBI GI	g1255951
BLAST score	598
E value	3.0e-62
Match length	128
% identity	83
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	230927
Seq. ID	LIB3197-012-P1-M1-H3
Method	BLASTX
NCBI GI	g1168410
BLAST score	574
E value	2.0e-59
Match length	135
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2 >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	230928
Seq. ID	LIB3197-012-P1-M1-H4
Method	BLASTX
NCBI GI	g629602
BLAST score	182
E value	2.0e-13
Match length	57
% identity	65
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	230929
Seq. ID	LIB3197-012-P1-M1-H5
Method	BLASTX
NCBI GI	g3738339
BLAST score	627
E value	1.0e-65
Match length	139
% identity	85
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	230930
Seq. ID	LIB3197-012-P1-M1-H6
Method	BLASTX
NCBI GI	g1066859
BLAST score	426
E value	4.0e-42
Match length	121
% identity	67
NCBI Description	(L49020) acetyl-CoA carboxylase [Glycine max]

Seq. No.	230931
Seq. ID	LIB3197-012-P1-M1-H9
Method	BLASTX
NCBI GI	g3451075
BLAST score	613
E value	5.0e-64
Match length	137
% identity	82
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	230932
Seq. ID	LIB3197-013-P1-M1-A1
Method	BLASTX
NCBI GI	g3335226
BLAST score	255
E value	3.0e-22
Match length	53
% identity	18
NCBI Description	(AF077374) small proline-rich protein [Homo sapiens]

Seq. No.	230933
Seq. ID	LIB3197-013-P1-M1-A11
Method	BLASTX
NCBI GI	g1731146
BLAST score	291
E value	3.0e-26
Match length	82
% identity	62
NCBI Description	HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein [Caenorhabditis elegans]

Seq. No.	230934
Seq. ID	LIB3197-013-P1-M1-A2
Method	BLASTX
NCBI GI	g4105472
BLAST score	151
E value	2.0e-12
Match length	122
% identity	49
NCBI Description	(AF046059) cytokine receptor related protein 4 [Homo sapiens]

Seq. No.	230935
Seq. ID	LIB3197-013-P1-M1-A4
Method	BLASTX
NCBI GI	g3582436

BLAST score	201
E value	1.0e-15
Match length	69
% identity	61
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No.	230936
Seq. ID	LIB3197-013-P1-M1-A8
Method	BLASTX
NCBI GI	g3024516
BLAST score	628
E value	9.0e-66
Match length	124
% identity	98
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong similarity to A. thaliana ara-2 (gb_ATHARA2). ESTs gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene. [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related small GTPase [Arabidopsis thaliana]

Seq. No.	230937
Seq. ID	LIB3197-013-P1-M1-B11
Method	BLASTX
NCBI GI	g1762144
BLAST score	349
E value	6.0e-33
Match length	123
% identity	59
NCBI Description	(U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No.	230938
Seq. ID	LIB3197-013-P1-M1-B2
Method	BLASTX
NCBI GI	g3599491
BLAST score	478
E value	3.0e-48
Match length	123
% identity	72
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	230939
Seq. ID	LIB3197-013-P1-M1-B3
Method	BLASTX
NCBI GI	g2384671
BLAST score	361
E value	2.0e-34
Match length	88
% identity	82
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	230940
Seq. ID	LIB3197-013-P1-M1-B5
Method	BLASTX
NCBI GI	g533084
BLAST score	544
E value	2.0e-65

Match length	146
% identity	86
NCBI Description	(U07597) delta-9 stearoyl-acyl carrier protein desaturase precursor [Thunbergia alata]

Seq. No.	230941
Seq. ID	LIB3197-013-P1-M1-C11
Method	BLASTX
NCBI GI	g2827039
BLAST score	344
E value	1.0e-32
Match length	92
% identity	72
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	230942
Seq. ID	LIB3197-013-P1-M1-C2
Method	BLASTX
NCBI GI	g1345785
BLAST score	704
E value	1.0e-74
Match length	142
% identity	96
NCBI Description	CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1) >gi_567935_dbj_BAA05640_ (D26593) chalcone synthase [Camellia sinensis]

Seq. No.	230943
Seq. ID	LIB3197-013-P1-M1-C3
Method	BLASTX
NCBI GI	g267069
BLAST score	579
E value	6.0e-60
Match length	118
% identity	90
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230944
Seq. ID	LIB3197-013-P1-M1-D4
Method	BLASTX
NCBI GI	g1173027
BLAST score	181
E value	3.0e-13
Match length	48
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	230945
Seq. ID	LIB3197-013-P1-M1-E1
Method	BLASTX
NCBI GI	g2980794
BLAST score	240

E value	1.0e-34
Match length	104
% identity	69
NCBI Description	(AL022197) myb - like protein [Arabidopsis thaliana]

Seq. No.	230946
Seq. ID	LIB3197-013-P1-M1-E2
Method	BLASTX
NCBI GI	g2129578
BLAST score	248
E value	4.0e-21
Match length	102
% identity	55
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	230947
Seq. ID	LIB3197-013-P1-M1-F3
Method	BLASTX
NCBI GI	g267069
BLAST score	422
E value	2.0e-61
Match length	118
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230948
Seq. ID	LIB3197-013-P1-M1-G1
Method	BLASTX
NCBI GI	g2244866
BLAST score	251
E value	4.0e-25
Match length	99
% identity	54
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	230949
Seq. ID	LIB3197-013-P1-M1-G3
Method	BLASTX
NCBI GI	g2982259
BLAST score	556
E value	3.0e-57
Match length	128
% identity	80
NCBI Description	(AF051212) probable 60s ribosomal protein L13a [Picea mariana]

Seq. No.	230950
Seq. ID	LIB3197-013-P1-M1-G6
Method	BLASTX
NCBI GI	g4454012

BLAST score	217
E value	1.0e-17
Match length	83
% identity	55
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	230951
Seq. ID	LIB3197-013-P1-M1-G9
Method	BLASTX
NCBI GI	g3851636
BLAST score	315
E value	3.0e-29
Match length	77
% identity	77
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	230952
Seq. ID	LIB3197-013-P1-M1-H10
Method	BLASTX
NCBI GI	g2501432
BLAST score	237
E value	4.0e-20
Match length	71
% identity	69
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir__JC4894 ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating enzyme E2 UbcH-ben [Homo sapiens] >gi_4507793_ref_NP_003339.1_pUBE2N_ ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)

Seq. No.	230953
Seq. ID	LIB3197-013-P1-M1-H2
Method	BLASTX
NCBI GI	g2853081
BLAST score	366
E value	5.0e-35
Match length	83
% identity	83
NCBI Description	(AL021768) ATP binding protein - like [Arabidopsis thaliana]

Seq. No.	230954
Seq. ID	LIB3197-013-P1-M1-H3
Method	BLASTX
NCBI GI	g3914449
BLAST score	614
E value	5.0e-64
Match length	141
% identity	87
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No.	230955
Seq. ID	LIB3197-013-P1-M1-H9
Method	BLASTX
NCBI GI	g3860247
BLAST score	556
E value	3.0e-57
Match length	116
% identity	91
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	230956
Seq. ID	LIB3197-014-P1-M1-A11
Method	BLASTX
NCBI GI	g1362086
BLAST score	429
E value	2.0e-42
Match length	115
% identity	75
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	230957
Seq. ID	LIB3197-014-P1-M1-A12
Method	BLASTX
NCBI GI	g1362086
BLAST score	408
E value	4.0e-40
Match length	105
% identity	77
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	230958
Seq. ID	LIB3197-014-P1-M1-A3
Method	BLASTX
NCBI GI	g3176874
BLAST score	182
E value	1.0e-13
Match length	58
% identity	53
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	230959
Seq. ID	LIB3197-014-P1-M1-C11
Method	BLASTX
NCBI GI	g2738949

BLAST score	481
E value	1.0e-48
Match length	100
% identity	90
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	230960
Seq. ID	LIB3197-014-P1-M1-C12
Method	BLASTX
NCBI GI	g2501578
BLAST score	165
E value	2.0e-11
Match length	55
% identity	64
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	230961
Seq. ID	LIB3197-014-P1-M1-C2
Method	BLASTX
NCBI GI	g3023857
BLAST score	311
E value	1.0e-39
Match length	105
% identity	41
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_629591_pir__S48839 guanine nucleotide regulatory protein - rape >gi_563335_emb_CAA83924_ (Z33643) guanine nucleotide regulatory protein [Brassica napus]

Seq. No.	230962
Seq. ID	LIB3197-014-P1-M1-C6
Method	BLASTX
NCBI GI	g4049341
BLAST score	209
E value	6.0e-30
Match length	100
% identity	75
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	230963
Seq. ID	LIB3197-014-P1-M1-D1
Method	BLASTX
NCBI GI	g1345971
BLAST score	304
E value	7.0e-28
Match length	118
% identity	52
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_541947_pir__JQ2339 omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean >gi_408792 (L22965) omega-3 fatty acid desaturase [Glycine soja]

Seq. No.	230964

Seq. ID	LIB3197-014-P1-M1-D12
Method	BLASTX
NCBI GI	g1724102
BLAST score	418
E value	3.0e-41
Match length	99
% identity	84
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	230965
Seq. ID	LIB3197-014-P1-M1-D2
Method	BLASTX
NCBI GI	g2982262
BLAST score	197
E value	3.0e-15
Match length	108
% identity	44
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	230966
Seq. ID	LIB3197-014-P1-M1-D6
Method	BLASTX
NCBI GI	g2982466
BLAST score	145
E value	3.0e-09
Match length	49
% identity	61
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	230967
Seq. ID	LIB3197-014-P1-M1-E1
Method	BLASTX
NCBI GI	g2160156
BLAST score	496
E value	2.0e-50
Match length	113
% identity	81
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No.	230968
Seq. ID	LIB3197-014-P1-M1-E2
Method	BLASTX
NCBI GI	g2811278
BLAST score	382
E value	2.0e-37
Match length	77
% identity	88
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	230969
Seq. ID	LIB3197-014-P1-M1-F1
Method	BLASTX
NCBI GI	g1169009
BLAST score	323

E value	4.0e-30
Match length	118
% identity	51
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir__S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi_437777_emb_CAA52814_ (X74814) 0-Methyltransferase [Eucalyptus gunnii]

Seq. No.	230970
Seq. ID	LIB3197-014-P1-M1-F2
Method	BLASTX
NCBI GI	g1888485
BLAST score	252
E value	3.0e-23
Match length	77
% identity	73
NCBI Description	(Y11749) dihydroflavonol 4-reductase [Vitis vinifera]

Seq. No.	230971
Seq. ID	LIB3197-014-P1-M1-G11
Method	BLASTX
NCBI GI	g2739168
BLAST score	217
E value	1.0e-17
Match length	76
% identity	57
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	230972
Seq. ID	LIB3197-014-P1-M1-G9
Method	BLASTX
NCBI GI	g136107
BLAST score	153
E value	3.0e-10
Match length	87
% identity	31
NCBI Description	TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL AMINOPEPTIDASE) >gi_1082875_pir__S54376 tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880 (M73047) tripeptidyl peptidase II [Homo sapiens] >gi_4507657_ref_NP_003282.1_pTPP2_ tripeptidyl peptidase II

Seq. No.	230973
Seq. ID	LIB3197-014-P1-M1-H1
Method	BLASTX
NCBI GI	g729470
BLAST score	183
E value	1.0e-13
Match length	83
% identity	49
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_

(Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	230974
Seq. ID	LIB3197-014-P1-M1-H10
Method	BLASTX
NCBI GI	g2832625
BLAST score	273
E value	2.0e-24
Match length	101
% identity	57
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	230975
Seq. ID	LIB3197-014-P1-M1-H2
Method	BLASTX
NCBI GI	g3913002
BLAST score	110
E value	1.0e-08
Match length	62
% identity	56
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL9 HOMOLOG (TM5) >gi_629674_pir__S23728 TDR5 protein - tomato >gi_19358_emb_CAA43010_ (X60480) TDR5 [Lycopersicon esculentum] >gi_19384_emb_CAA43170_ (X60758) TDR5 [Lycopersicon esculentum]

Seq. No.	230976
Seq. ID	LIB3197-015-P1-M1-A10
Method	BLASTX
NCBI GI	g3152594
BLAST score	370
E value	8.0e-36
Match length	87
% identity	11
NCBI Description	(AC002986) Contains repeats similar to RECA protein gb_L26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]

Seq. No.	230977
Seq. ID	LIB3197-015-P1-M1-A3
Method	BLASTX
NCBI GI	g1747296
BLAST score	343
E value	2.0e-32
Match length	95
% identity	68
NCBI Description	(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

Seq. No.	230978
Seq. ID	LIB3197-015-P1-M1-A6
Method	BLASTX
NCBI GI	g1362107
BLAST score	218
E value	8.0e-18
Match length	44

% identity	95
NCBI Description	GUT8-2a protein - common tobacco

Seq. No.	230979
Seq. ID	LIB3197-015-P1-M1-B1
Method	BLASTX
NCBI GI	g2262164
BLAST score	329
E value	1.0e-30
Match length	105
% identity	65
NCBI Description	(AC002329) putative obtusifoliol 14-alpha demethylase [Arabidopsis thaliana]

Seq. No.	230980
Seq. ID	LIB3197-015-P1-M1-B2
Method	BLASTX
NCBI GI	g1703108
BLAST score	732
E value	7.0e-78
Match length	145
% identity	98
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	230981
Seq. ID	LIB3197-015-P1-M1-B3
Method	BLASTX
NCBI GI	g116054
BLAST score	469
E value	3.0e-47
Match length	102
% identity	90
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK). >gi_280393_pir__A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean >gi_169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]

Seq. No.	230982
Seq. ID	LIB3197-015-P1-M1-B6
Method	BLASTX
NCBI GI	g4262151
BLAST score	403
E value	2.0e-39
Match length	116
% identity	66
NCBI Description	(AC005275) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	230983
Seq. ID	LIB3197-015-P1-M1-B7
Method	BLASTX
NCBI GI	g2129698
BLAST score	225
E value	2.0e-18

Match length	54
% identity	74
NCBI Description	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi_1054633_emb_CAA63387_ (X92728) protein kinase [Arabidopsis thaliana]

Seq. No.	230984
Seq. ID	LIB3197-015-P1-M1-B8
Method	BLASTX
NCBI GI	g1061040
BLAST score	617
E value	2.0e-64
Match length	130
% identity	85
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	230985
Seq. ID	LIB3197-015-P1-M1-B9
Method	BLASTX
NCBI GI	g3694872
BLAST score	527
E value	7.0e-54
Match length	124
% identity	81
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	230986
Seq. ID	LIB3197-015-P1-M1-C1
Method	BLASTX
NCBI GI	g1666228
BLAST score	391
E value	3.0e-38
Match length	75
% identity	99
NCBI Description	(U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin [Pisum sativum] >gi_1724137 (U81046) actin [Pisum sativum] >gi_1724139 (U81047) actin [Pisum sativum]

Seq. No.	230987
Seq. ID	LIB3197-015-P1-M1-C2
Method	BLASTX
NCBI GI	g3914501
BLAST score	531
E value	2.0e-54
Match length	120
% identity	86
NCBI Description	ASPARTATE CARBAMOYLTRANSFERASE 3 PRECURSOR (ASPARTATE TRANSCARBAMYLASE 3) (ATCASE 3) >gi_609344 (U05293) aspartate carbamoyltransferase [Pisum sativum]

Seq. No.	230988
Seq. ID	LIB3197-015-P1-M1-C4
Method	BLASTX
NCBI GI	g267069
BLAST score	362

E value	8.0e-35
Match length	69
% identity	96
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	230989
Seq. ID	LIB3197-015-P1-M1-D11
Method	BLASTX
NCBI GI	g4098128
BLAST score	393
E value	2.0e-38
Match length	91
% identity	85
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	230990
Seq. ID	LIB3197-015-P1-M1-D12
Method	BLASTX
NCBI GI	g1944216
BLAST score	379
E value	8.0e-37
Match length	82
% identity	87
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	230991
Seq. ID	LIB3197-015-P1-M1-D4
Method	BLASTX
NCBI GI	g1724102
BLAST score	209
E value	3.0e-17
Match length	45
% identity	91
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	230992
Seq. ID	LIB3197-015-P1-M1-E11
Method	BLASTX
NCBI GI	g3097321
BLAST score	243
E value	1.0e-20
Match length	114
% identity	46
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	230993
Seq. ID	LIB3197-015-P1-M1-F11
Method	BLASTX
NCBI GI	g4263711
BLAST score	341
E value	4.0e-32
Match length	122
% identity	58

NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	230994
Seq. ID	LIB3197-015-P1-M1-F3
Method	BLASTX
NCBI GI	g3212871
BLAST score	169
E value	6.0e-12
Match length	90
% identity	48
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	230995
Seq. ID	LIB3197-015-P1-M1-F6
Method	BLASTX
NCBI GI	g3757514
BLAST score	589
E value	4.0e-61
Match length	128
% identity	88
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	230996
Seq. ID	LIB3197-015-P1-M1-F8
Method	BLASTX
NCBI GI	g2662343
BLAST score	261
E value	6.0e-23
Match length	71
% identity	77
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	230997
Seq. ID	LIB3197-015-P1-M1-G1
Method	BLASTX
NCBI GI	g346685
BLAST score	353
E value	8.0e-34
Match length	88
% identity	77
NCBI Description	developmentally-regulated GTP-binding protein - mouse

Seq. No.	230998
Seq. ID	LIB3197-015-P1-M1-G10
Method	BLASTX
NCBI GI	g2392025
BLAST score	211
E value	8.0e-17
Match length	45
% identity	84
NCBI Description	(D88420) stromal ascorbate peroxidase [Cucurbita sp.]

Seq. No.	230999
Seq. ID	LIB3197-015-P1-M1-G11

Method	BLASTX
NCBI GI	g4263519
BLAST score	463
E value	2.0e-46
Match length	96
% identity	93
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

Seq. No.	231000
Seq. ID	LIB3197-015-P1-M1-G7
Method	BLASTX
NCBI GI	g4508073
BLAST score	463
E value	2.0e-46
Match length	141
% identity	62
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	231001
Seq. ID	LIB3197-015-P1-M1-H1
Method	BLASTX
NCBI GI	g2829911
BLAST score	375
E value	3.0e-36
Match length	103
% identity	30
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	231002
Seq. ID	LIB3197-015-P1-M1-H10
Method	BLASTX
NCBI GI	g4056502
BLAST score	338
E value	1.0e-33
Match length	95
% identity	80
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	231003
Seq. ID	LIB3197-015-P1-M1-H11
Method	BLASTX
NCBI GI	g3097321
BLAST score	190
E value	2.0e-14
Match length	83
% identity	45
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	231004
Seq. ID	LIB3197-015-P1-M1-H3
Method	BLASTX
NCBI GI	g3757514
BLAST score	252
E value	8.0e-22
Match length	64
% identity	73

NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	231005
Seq. ID	LIB3197-015-P1-M1-H4
Method	BLASTX
NCBI GI	g2828291
BLAST score	393
E value	4.0e-38
Match length	115
% identity	72
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	231006
Seq. ID	LIB3197-015-P1-M1-H8
Method	BLASTX
NCBI GI	g3757514
BLAST score	220
E value	5.0e-18
Match length	89
% identity	57
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	231007
Seq. ID	LIB3197-015-P1-M1-H9
Method	BLASTX
NCBI GI	g2887459
BLAST score	511
E value	3.0e-52
Match length	102
% identity	99
NCBI Description	(AB010922) actin [Cucumis sativus]

Seq. No.	231008
Seq. ID	LIB3197-016-P1-M1-A10
Method	BLASTX
NCBI GI	g3193306
BLAST score	334
E value	3.0e-31
Match length	132
% identity	56
NCBI Description	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]

Seq. No.	231009
Seq. ID	LIB3197-016-P1-M1-A11
Method	BLASTX
NCBI GI	g267069
BLAST score	466
E value	7.0e-47
Match length	86
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916

09594050 - 10010000

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231010
Seq. ID	LIB3197-016-P1-M1-A12
Method	BLASTX
NCBI GI	g3560264
BLAST score	168
E value	1.0e-11
Match length	102
% identity	38
NCBI Description	(AL031535) sol1 family protein [Schizosaccharomyces pombe]

Seq. No.	231011
Seq. ID	LIB3197-016-P1-M1-A5
Method	BLASTX
NCBI GI	g120669
BLAST score	592
E value	2.0e-61
Match length	116
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231012
Seq. ID	LIB3197-016-P1-M1-A6
Method	BLASTX
NCBI GI	g2739387
BLAST score	147
E value	2.0e-09
Match length	114
% identity	32
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231013
Seq. ID	LIB3197-016-P1-M1-A7
Method	BLASTX
NCBI GI	g2811278
BLAST score	420
E value	2.0e-41
Match length	84
% identity	94
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231014
Seq. ID	LIB3197-016-P1-M1-B11
Method	BLASTX
NCBI GI	g3953471
BLAST score	371
E value	6.0e-36
Match length	92
% identity	74
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No. 231015

Seq. ID	LIB3197-016-P1-M1-B12
Method	BLASTX
NCBI GI	g3540182
BLAST score	162
E value	1.0e-18
Match length	101
% identity	58
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	231016
Seq. ID	LIB3197-016-P1-M1-B2
Method	BLASTX
NCBI GI	g3287696
BLAST score	159
E value	8.0e-14
Match length	50
% identity	76
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	231017
Seq. ID	LIB3197-016-P1-M1-B6
Method	BLASTX
NCBI GI	g1657382
BLAST score	675
E value	3.0e-71
Match length	136
% identity	90
NCBI Description	(Y09101) cholinephosphate cytidylyltransferase [Pisum sativum]

Seq. No.	231018
Seq. ID	LIB3197-016-P1-M1-C10
Method	BLASTX
NCBI GI	g4138209
BLAST score	155
E value	3.0e-10
Match length	67
% identity	42
NCBI Description	(AJ223071) serine/threonine kinase protein MSTK2L,long-form [Mus musculus]

Seq. No.	231019
Seq. ID	LIB3197-016-P1-M1-C4
Method	BLASTX
NCBI GI	g3211975
BLAST score	336
E value	2.0e-31
Match length	72
% identity	94
NCBI Description	(AF068195) putative glialblastoma cell differentiation-related protein [Homo sapiens]

Seq. No.	231020
Seq. ID	LIB3197-016-P1-M1-C6

Method	BLASTX
NCBI GI	g1408471
BLAST score	492
E value	9.0e-50
Match length	113
% identity	78
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	231021
Seq. ID	LIB3197-016-P1-M1-D10
Method	BLASTX
NCBI GI	g4263695
BLAST score	231
E value	3.0e-19
Match length	126
% identity	11
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No.	231022
Seq. ID	LIB3197-016-P1-M1-D12
Method	BLASTX
NCBI GI	g132939
BLAST score	432
E value	5.0e-43
Match length	99
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	231023
Seq. ID	LIB3197-016-P1-M1-D4
Method	BLASTX
NCBI GI	g116602
BLAST score	186
E value	2.0e-14
Match length	63
% identity	68
NCBI Description	COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN]

Seq. No.	231024
Seq. ID	LIB3197-016-P1-M1-E5
Method	BLASTX
NCBI GI	g122097
BLAST score	296
E value	1.0e-29
Match length	82
% identity	86
NCBI Description	HISTONE H4 >gi_103010_pir__S18003 histone H4 - midge (Chironomus thummi thummi) >gi_103052_pir__S09656 histone H4 - fruit fly (Drosophila hydei) >gi_103199_pir__S10098 histone H4 - fruit fly (Drosophila melanogaster) >gi_542539_pir__S40437 histone H4 - midge (Chironomus thummi thummi) >gi_1085859_pir__B56654 histone H4 -

Tigriopus californicus >gi_2119026_pir__B56580 histone H4 - midge (Chironomus thummi thummi) >gi_7084_emb_CAA39772_ (X56335) histone H4 [Chironomus thummi] >gi_7434_emb_CAA36806_ (X52576) histone H4 [Drosophila hydei] >gi_7440_emb_CAA34920_ (X17072) histone H4 [Drosophila hydei] >gi_8071_emb_CAA32435_ (X14215) H4 histone [Drosophila melanogaster] >gi_10616_emb_CAA36639_ (X52393) histone H4 [Tigriopus californicus] >gi_161896 (M84797) histone H4 [Tigriopus californicus] >gi_297562_emb_CAA51323_ (X72803) histone H4 [Chironomus thummi] >gi_1419478_emb_CAA66066_ (X97436) histone H4 [Drosophila hydei] >gi_1419480_emb_CAA66067_ (X97437) histone H4 [Drosophila melanogaster] >gi_1419482_emb_CAA66068_ (X97438) histone H4 [Drosophila melanogaster] >gi_1882999_emb_CAA62808_ (X91508) histone H4 [Acrolepiopsis assectella] >gi_1885324_emb_CAA62814_ (X91514) histone H4 [Myrmica ruginodis]

Seq. No.	231025
Seq. ID	LIB3197-016-P1-M1-F11
Method	BLASTX
NCBI GI	g1370190
BLAST score	177
E value	1.0e-19
Match length	86
% identity	64
NCBI Description	(Z73944) RAB8A [Lotus japonicus]

Seq. No.	231026
Seq. ID	LIB3197-016-P1-M1-F4
Method	BLASTX
NCBI GI	g232024
BLAST score	251
E value	8.0e-22
Match length	81
% identity	64
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	231027
Seq. ID	LIB3197-016-P1-M1-F6
Method	BLASTX
NCBI GI	g2289961
BLAST score	346
E value	1.0e-32
Match length	90
% identity	79
NCBI Description	(U82434) AtRAB8 [Arabidopsis thaliana]

Seq. No.	231028
Seq. ID	LIB3197-016-P1-M1-G12
Method	BLASTX
NCBI GI	g2062167
BLAST score	348

E value	4.0e-33
Match length	71
% identity	89
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	231029
Seq. ID	LIB3197-016-P1-M1-G4
Method	BLASTX
NCBI GI	g4263790
BLAST score	202
E value	4.0e-16
Match length	70
% identity	59
NCBI Description	(AC006068) putative ch-TOG protein [Arabidopsis thaliana]

Seq. No.	231030
Seq. ID	LIB3197-016-P1-M1-H12
Method	BLASTX
NCBI GI	g1168256
BLAST score	210
E value	4.0e-17
Match length	53
% identity	70
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	231031
Seq. ID	LIB3197-016-P1-M1-H5
Method	BLASTX
NCBI GI	g81811
BLAST score	145
E value	4.0e-09
Match length	31
% identity	90
NCBI Description	ribosomal protein S11 - soybean (fragment) >gi_170054 (M31024) ribosomal protein S11 [Glycine max]

Seq. No.	231032
Seq. ID	LIB3197-016-P1-M1-H6
Method	BLASTX
NCBI GI	g1168256
BLAST score	594
E value	9.0e-62
Match length	127
% identity	82
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	231033
Seq. ID	LIB3197-016-P1-M1-H9

Method	BLASTX
NCBI GI	g2160169
BLAST score	184
E value	1.0e-13
Match length	73
% identity	55
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	231034
Seq. ID	LIB3197-017-P1-M1-A10
Method	BLASTX
NCBI GI	g1174162
BLAST score	593
E value	1.0e-61
Match length	111
% identity	93
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	231035
Seq. ID	LIB3197-017-P1-M1-A12
Method	BLASTX
NCBI GI	g125080
BLAST score	744
E value	3.0e-79
Match length	151
% identity	99
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	231036
Seq. ID	LIB3197-017-P1-M1-B11
Method	BLASTX
NCBI GI	g2244850
BLAST score	190
E value	9.0e-22
Match length	109
% identity	64
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231037
Seq. ID	LIB3197-017-P1-M1-B4
Method	BLASTX
NCBI GI	g4056479
BLAST score	266
E value	2.0e-23
Match length	80
% identity	66
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	231038
Seq. ID	LIB3197-017-P1-M1-B6
Method	BLASTX

NCBI GI	g2244750
BLAST score	611
E value	2.0e-64
Match length	129
% identity	94
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	231039
Seq. ID	LIB3197-017-P1-M1-E11
Method	BLASTX
NCBI GI	g2760334
BLAST score	413
E value	2.0e-40
Match length	87
% identity	83
NCBI Description	(AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No.	231040
Seq. ID	LIB3197-017-P1-M1-E12
Method	BLASTX
NCBI GI	g2154715
BLAST score	208
E value	7.0e-17
Match length	67
% identity	69
NCBI Description	(Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No.	231041
Seq. ID	LIB3197-017-P1-M1-E5
Method	BLASTX
NCBI GI	g464621
BLAST score	261
E value	8.0e-23
Match length	96
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	231042
Seq. ID	LIB3197-017-P1-M1-F10
Method	BLASTX
NCBI GI	g4337175
BLAST score	454
E value	2.0e-45
Match length	127
% identity	69
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	231043
Seq. ID	LIB3197-017-P1-M1-F12

Method	BLASTX
NCBI GI	g2213595
BLAST score	350
E value	3.0e-33
Match length	109
% identity	60
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	231044
Seq. ID	LIB3197-017-P1-M1-F4
Method	BLASTX
NCBI GI	g82264
BLAST score	210
E value	1.0e-16
Match length	43
% identity	91
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)8I) - potato (fragment) >gi_498789_emb_CAA56109_ (X79597) cytochrome c1 [Solanum tuberosum]

Seq. No.	231045
Seq. ID	LIB3197-017-P1-M1-G10
Method	BLASTX
NCBI GI	g1495251
BLAST score	348
E value	3.0e-33
Match length	91
% identity	70
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	231046
Seq. ID	LIB3197-017-P1-M1-G12
Method	BLASTX
NCBI GI	g1771162
BLAST score	260
E value	1.0e-22
Match length	118
% identity	48
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	231047
Seq. ID	LIB3197-017-P1-M1-G4
Method	BLASTX
NCBI GI	g2654208
BLAST score	97
E value	1.0e-08
Match length	40
% identity	88
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia oleracea]

Seq. No.	231048
Seq. ID	LIB3197-017-P1-M1-G6

Method	BLASTX
NCBI GI	g4204300
BLAST score	202
E value	9.0e-16
Match length	79
% identity	52
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	231049
Seq. ID	LIB3197-019-Q1-M1-A10
Method	BLASTX
NCBI GI	g3097321
BLAST score	185
E value	9.0e-14
Match length	89
% identity	44
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	231050
Seq. ID	LIB3197-019-Q1-M1-A11
Method	BLASTX
NCBI GI	g3097321
BLAST score	191
E value	2.0e-14
Match length	104
% identity	38
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	231051
Seq. ID	LIB3197-019-Q1-M1-A2
Method	BLASTX
NCBI GI	g120669
BLAST score	425
E value	5.0e-42
Match length	87
% identity	90
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231052
Seq. ID	LIB3197-019-Q1-M1-A3
Method	BLASTX
NCBI GI	g2829902
BLAST score	399
E value	5.0e-39
Match length	109
% identity	73
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	231053
Seq. ID	LIB3197-019-Q1-M1-A6
Method	BLASTX
NCBI GI	g4510344

BLAST score	149
E value	1.0e-09
Match length	84
% identity	42
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231054
Seq. ID	LIB3197-019-Q1-M1-A7
Method	BLASTX
NCBI GI	g1703115
BLAST score	510
E value	6.0e-52
Match length	93
% identity	100
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	231055
Seq. ID	LIB3197-019-Q1-M1-A8
Method	BLASTX
NCBI GI	g1486472
BLAST score	421
E value	2.0e-41
Match length	96
% identity	84
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	231056
Seq. ID	LIB3197-019-Q1-M1-B11
Method	BLASTX
NCBI GI	g2811278
BLAST score	333
E value	4.0e-31
Match length	123
% identity	78
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231057
Seq. ID	LIB3197-019-Q1-M1-B2
Method	BLASTX
NCBI GI	g2832625
BLAST score	307
E value	2.0e-28
Match length	69
% identity	81
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	231058
Seq. ID	LIB3197-019-Q1-M1-B7
Method	BLASTX
NCBI GI	g1209756
BLAST score	147
E value	1.0e-09
Match length	54

% identity	63
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	231059
Seq. ID	LIB3197-019-Q1-M1-B8
Method	BLASTX
NCBI GI	g2244734
BLAST score	545
E value	4.0e-56
Match length	121
% identity	89
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	231060
Seq. ID	LIB3197-019-Q1-M1-C1
Method	BLASTX
NCBI GI	g3914740
BLAST score	190
E value	6.0e-15
Match length	50
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	231061
Seq. ID	LIB3197-019-Q1-M1-C12
Method	BLASTX
NCBI GI	g2623296
BLAST score	141
E value	1.0e-08
Match length	50
% identity	58
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231062
Seq. ID	LIB3197-019-Q1-M1-C3
Method	BLASTX
NCBI GI	g3924611
BLAST score	187
E value	4.0e-14
Match length	123
% identity	36
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231063
Seq. ID	LIB3197-019-Q1-M1-C7
Method	BLASTX
NCBI GI	g400384
BLAST score	149
E value	1.0e-09
Match length	104
% identity	35
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE B14 SUBUNIT (COMPLEX I-B14) (CI-B14) >gi_346536_pir__S28245 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B14 - bovine >gi_240_emb_CAA44896_ (X63211) NADH dehydrogenase [Bos taurus]

Seq. No.	231064
Seq. ID	LIB3197-019-Q1-M1-C9
Method	BLASTX
NCBI GI	g2129559
BLAST score	496
E value	3.0e-50
Match length	110
% identity	87
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	231065
Seq. ID	LIB3197-019-Q1-M1-D1
Method	BLASTX
NCBI GI	g4490756
BLAST score	339
E value	6.0e-32
Match length	86
% identity	78
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231066
Seq. ID	LIB3197-019-Q1-M1-D10
Method	BLASTX
NCBI GI	g3024017
BLAST score	468
E value	6.0e-47
Match length	99
% identity	92
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	231067
Seq. ID	LIB3197-019-Q1-M1-D11
Method	BLASTX
NCBI GI	g3913295
BLAST score	704
E value	1.0e-74
Match length	138
% identity	91
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_ (X83217) caffeic O-methyltransferase [Prunus dulcis]

Seq. No.	231068
Seq. ID	LIB3197-019-Q1-M1-D12
Method	BLASTX
NCBI GI	g4204300
BLAST score	194
E value	7.0e-15

Match length	75
% identity	52
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	231069
Seq. ID	LIB3197-019-Q1-M1-D3
Method	BLASTX
NCBI GI	g120668
BLAST score	531
E value	2.0e-54
Match length	116
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82399_pir__A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var. distichum]

Seq. No.	231070
Seq. ID	LIB3197-019-Q1-M1-D7
Method	BLASTX
NCBI GI	g3334113
BLAST score	192
E value	1.0e-14
Match length	37
% identity	97
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	231071
Seq. ID	LIB3197-019-Q1-M1-D9
Method	BLASTX
NCBI GI	g4335864
BLAST score	562
E value	4.0e-58
Match length	116
% identity	85
NCBI Description	(AF052040) calreticulin [Berberis stolonifera]

Seq. No.	231072
Seq. ID	LIB3197-019-Q1-M1-E1
Method	BLASTX
NCBI GI	g88052
BLAST score	290
E value	5.0e-35
Match length	83
% identity	95
NCBI Description	keratin K5, 58K type II, epidermal (version 2) - human (fragment)

Seq. No.	231073
Seq. ID	LIB3197-019-Q1-M1-E2
Method	BLASTX
NCBI GI	g3236237
BLAST score	274

E value	2.0e-24
Match length	90
% identity	60
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	231074
Seq. ID	LIB3197-019-Q1-M1-E3
Method	BLASTX
NCBI GI	g1174600
BLAST score	379
E value	1.0e-36
Match length	72
% identity	96
NCBI Description	TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717) beta-tubulin [Oryza sativa]

Seq. No.	231075
Seq. ID	LIB3197-019-Q1-M1-E4
Method	BLASTX
NCBI GI	g4314378
BLAST score	251
E value	1.0e-21
Match length	101
% identity	52
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	231076
Seq. ID	LIB3197-019-Q1-M1-E5
Method	BLASTX
NCBI GI	g1587206
BLAST score	443
E value	3.0e-44
Match length	93
% identity	95
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	231077
Seq. ID	LIB3197-019-Q1-M1-E9
Method	BLASTX
NCBI GI	g3242728
BLAST score	215
E value	3.0e-17
Match length	134
% identity	36
NCBI Description	(AC003040) unknown protein [Arabidopsis thaliana]

Seq. No.	231078
Seq. ID	LIB3197-019-Q1-M1-F1
Method	BLASTX
NCBI GI	g1362086
BLAST score	458
E value	7.0e-46
Match length	96
% identity	91
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

	>gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]
Seq. No.	231079
Seq. ID	LIB3197-019-Q1-M1-F10
Method	BLASTX
NCBI GI	g1843527
BLAST score	472
E value	2.0e-47
Match length	124
% identity	43
NCBI Description	(U73747) annexin [Gossypium hirsutum]
Seq. No.	231080
Seq. ID	LIB3197-019-Q1-M1-F12
Method	BLASTX
NCBI GI	g4490737
BLAST score	336
E value	2.0e-31
Match length	122
% identity	59
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	231081
Seq. ID	LIB3197-019-Q1-M1-F5
Method	BLASTX
NCBI GI	g4521249
BLAST score	289
E value	4.0e-26
Match length	75
% identity	73
NCBI Description	(AB013912) DNA helicase [Mus musculus]
Seq. No.	231082
Seq. ID	LIB3197-019-Q1-M1-G10
Method	BLASTX
NCBI GI	g1168728
BLAST score	485
E value	6.0e-49
Match length	114
% identity	82
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	231083
Seq. ID	LIB3197-019-Q1-M1-G11
Method	BLASTX
NCBI GI	g585451
BLAST score	264
E value	4.0e-23
Match length	91
% identity	58
NCBI Description	MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 62 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)

	(NAD-ME) >gi_1076667_pir__B53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 62K chain precursor, mitochondrial - potato >gi_438249_emb_CAA80559_ (Z23023) malate dehydrogenase [Solanum tuberosum]
Seq. No.	231084
Seq. ID	LIB3197-019-Q1-M1-G12
Method	BLASTX
NCBI GI	g1843527
BLAST score	484
E value	8.0e-49
Match length	127
% identity	44
NCBI Description	(U73747) annexin [Gossypium hirsutum]
Seq. No.	231085
Seq. ID	LIB3197-019-Q1-M1-G2
Method	BLASTX
NCBI GI	g232024
BLAST score	454
E value	2.0e-45
Match length	109
% identity	82
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]
Seq. No.	231086
Seq. ID	LIB3197-019-Q1-M1-G3
Method	BLASTX
NCBI GI	g2653446
BLAST score	278
E value	8.0e-25
Match length	95
% identity	63
NCBI Description	(AB009077) proton pyrophosphatase [Vigna radiata]
Seq. No.	231087
Seq. ID	LIB3197-019-Q1-M1-G4
Method	BLASTX
NCBI GI	g464775
BLAST score	430
E value	1.0e-42
Match length	86
% identity	92
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]
Seq. No.	231088
Seq. ID	LIB3197-019-Q1-M1-G5
Method	BLASTX
NCBI GI	g2501448
BLAST score	248
E value	8.0e-26

Match length	72
% identity	86
NCBI Description	UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923_ (X99609) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No.	231089
Seq. ID	LIB3197-019-Q1-M1-G6
Method	BLASTX
NCBI GI	g3023858
BLAST score	566
E value	2.0e-58
Match length	114
% identity	33
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	231090
Seq. ID	LIB3197-019-Q1-M1-G7
Method	BLASTX
NCBI GI	g629806
BLAST score	291
E value	8.0e-40
Match length	96
% identity	86
NCBI Description	tubulin beta chain - rice >gi_493725_emb_CAA55912_ (X79367) beta tubulin [Oryza sativa]

Seq. No.	231091
Seq. ID	LIB3197-019-Q1-M1-G8
Method	BLASTX
NCBI GI	g3892051
BLAST score	234
E value	3.0e-29
Match length	82
% identity	80
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	231092
Seq. ID	LIB3197-019-Q1-M1-G9
Method	BLASTX
NCBI GI	g119354
BLAST score	530
E value	3.0e-54
Match length	115
% identity	88
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	231093
Seq. ID	LIB3197-019-Q1-M1-H11
Method	BLASTX
NCBI GI	g4220537

BLAST score	548
E value	2.0e-56
Match length	126
% identity	81
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	231094
Seq. ID	LIB3197-019-Q1-M1-H12
Method	BLASTX
NCBI GI	g3023841
BLAST score	170
E value	5.0e-12
Match length	56
% identity	62
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi_1695179_emb_CAA70704_ (Y09513) G protein beta subunit [Nicotiana plumbaginifolia]

Seq. No.	231095
Seq. ID	LIB3197-019-Q1-M1-H2
Method	BLASTX
NCBI GI	g1710581
BLAST score	400
E value	4.0e-39
Match length	97
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	231096
Seq. ID	LIB3197-019-Q1-M1-H4
Method	BLASTX
NCBI GI	g2661840
BLAST score	380
E value	1.0e-36
Match length	105
% identity	67
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	231097
Seq. ID	LIB3197-019-Q1-M1-H6
Method	BLASTX
NCBI GI	g2244847
BLAST score	304
E value	9.0e-28
Match length	103
% identity	57
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	231098
Seq. ID	LIB3197-020-Q1-M1-A11
Method	BLASTX
NCBI GI	g2062167
BLAST score	468
E value	6.0e-47

Match length	99
% identity	87
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	231099
Seq. ID	LIB3197-020-Q1-M1-A12
Method	BLASTX
NCBI GI	g2853087
BLAST score	172
E value	3.0e-12
Match length	74
% identity	50
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	231100
Seq. ID	LIB3197-020-Q1-M1-B10
Method	BLASTX
NCBI GI	g1524370
BLAST score	242
E value	4.0e-38
Match length	115
% identity	73
NCBI Description	(X92491) TOM20 [Solanum tuberosum]

Seq. No.	231101
Seq. ID	LIB3197-020-Q1-M1-B12
Method	BLASTX
NCBI GI	g267069
BLAST score	591
E value	2.0e-61
Match length	109
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231102
Seq. ID	LIB3197-020-Q1-M1-B5
Method	BLASTX
NCBI GI	g3063710
BLAST score	306
E value	5.0e-28
Match length	71
% identity	75
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	231103
Seq. ID	LIB3197-020-Q1-M1-C11
Method	BLASTX
NCBI GI	g1703129
BLAST score	620
E value	9.0e-65
Match length	117
% identity	100
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis

thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	231104
Seq. ID	LIB3197-020-Q1-M1-C12
Method	BLASTX
NCBI GI	g2677828
BLAST score	398
E value	1.0e-38
Match length	116
% identity	66
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	231105
Seq. ID	LIB3197-020-Q1-M1-D12
Method	BLASTX
NCBI GI	g3914449
BLAST score	735
E value	3.0e-78
Match length	145
% identity	99
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No.	231106
Seq. ID	LIB3197-020-Q1-M1-E10
Method	BLASTX
NCBI GI	g3386614
BLAST score	445
E value	3.0e-44
Match length	118
% identity	40
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	231107
Seq. ID	LIB3197-020-Q1-M1-E11
Method	BLASTX
NCBI GI	g464849
BLAST score	763
E value	1.0e-81
Match length	143
% identity	100
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	231108
Seq. ID	LIB3197-020-Q1-M1-E12
Method	BLASTX
NCBI GI	g2832625
BLAST score	429
E value	2.0e-42
Match length	101
% identity	81
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	231109
Seq. ID	LIB3197-020-Q1-M1-E4
Method	BLASTX
NCBI GI	g1053047
BLAST score	232
E value	7.0e-20
Match length	52
% identity	88
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	231110
Seq. ID	LIB3197-020-Q1-M1-E6
Method	BLASTX
NCBI GI	g267069
BLAST score	265
E value	1.0e-23
Match length	52
% identity	88
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231111
Seq. ID	LIB3197-020-Q1-M1-F10
Method	BLASTX
NCBI GI	g2213595
BLAST score	363
E value	1.0e-34
Match length	134
% identity	53
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	231112
Seq. ID	LIB3197-020-Q1-M1-F11
Method	BLASTX
NCBI GI	g231496
BLAST score	355
E value	1.0e-33
Match length	70
% identity	97
NCBI Description	ACTIN 58 >gi_100421_pir__S20094 actin - potato >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]

Seq. No.	231113
Seq. ID	LIB3197-020-Q1-M1-F12
Method	BLASTX
NCBI GI	g231683
BLAST score	381
E value	1.0e-36
Match length	114
% identity	61
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana

	>gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]
Seq. No.	231114
Seq. ID	LIB3197-020-Q1-M1-F4
Method	BLASTX
NCBI GI	g3821730
BLAST score	223
E value	3.0e-18
Match length	69
% identity	67
NCBI Description	(Z99991) formate dehydrogenase [Solanum tuberosum]
Seq. No.	231115
Seq. ID	LIB3197-020-Q1-M1-F5
Method	BLASTX
NCBI GI	g3695059
BLAST score	452
E value	4.0e-45
Match length	134
% identity	69
NCBI Description	(AF064787) rac GTPase activating protein 1 [Lotus japonicus]
Seq. No.	231116
Seq. ID	LIB3197-020-Q1-M1-G12
Method	BLASTX
NCBI GI	g3885328
BLAST score	201
E value	9.0e-16
Match length	63
% identity	57
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	231117
Seq. ID	LIB3197-020-Q1-M1-G4
Method	BLASTX
NCBI GI	g3024764
BLAST score	234
E value	1.0e-19
Match length	116
% identity	49
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (UBIQUITIN THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) >gi_3287373 (AC002397) ISOT [Mus musculus]
Seq. No.	231118
Seq. ID	LIB3197-020-Q1-M1-G5
Method	BLASTX
NCBI GI	g3881780
BLAST score	173
E value	2.0e-12
Match length	116
% identity	38
NCBI Description	(Z48638) similar to lipid transfer protein [Caenorhabditis

elegans]

Seq. No.	231119
Seq. ID	LIB3197-020-Q1-M1-G9
Method	BLASTX
NCBI GI	g2213595
BLAST score	357
E value	5.0e-34
Match length	106
% identity	63
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	231120
Seq. ID	LIB3197-020-Q1-M1-H11
Method	BLASTX
NCBI GI	g3643598
BLAST score	419
E value	9.0e-44
Match length	106
% identity	86
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	231121
Seq. ID	LIB3197-020-Q1-M1-H2
Method	BLASTX
NCBI GI	g232024
BLAST score	184
E value	3.0e-14
Match length	55
% identity	67
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	231122
Seq. ID	LIB3197-020-Q1-M1-H5
Method	BLASTX
NCBI GI	g3212877
BLAST score	437
E value	2.0e-43
Match length	101
% identity	79
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	231123
Seq. ID	LIB3197-020-Q1-M1-H8
Method	BLASTX
NCBI GI	g3869088
BLAST score	605
E value	5.0e-63
Match length	116
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	231124
Seq. ID	LIB3197-020-Q1-M1-H9
Method	BLASTX
NCBI GI	g131770
BLAST score	378
E value	2.0e-36
Match length	105
% identity	66
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	231125
Seq. ID	LIB3197-021-Q1-M1-A1
Method	BLASTX
NCBI GI	g3913008
BLAST score	299
E value	2.0e-30
Match length	86
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	231126
Seq. ID	LIB3197-021-Q1-M1-A11
Method	BLASTX
NCBI GI	g1666228
BLAST score	374
E value	3.0e-47
Match length	95
% identity	99
NCBI Description	(U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin [Pisum sativum] >gi_1724137 (U81046) actin [Pisum sativum] >gi_1724139 (U81047) actin [Pisum sativum]

Seq. No.	231127
Seq. ID	LIB3197-021-Q1-M1-A12
Method	BLASTX
NCBI GI	g3212869
BLAST score	512
E value	4.0e-52
Match length	111
% identity	86
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	231128
Seq. ID	LIB3197-021-Q1-M1-A2
Method	BLASTX
NCBI GI	g4033468
BLAST score	401
E value	4.0e-39
Match length	112
% identity	46
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP40

>gi_2582641_emb_CAA67800_ (X99437) splicing factor [Arabidopsis thaliana] >gi_2980800_emb_CAA18176_ (AL022197) splicing factor At-SRp40 [Arabidopsis thaliana]

Seq. No.	231129
Seq. ID	LIB3197-021-Q1-M1-A5
Method	BLASTX
NCBI GI	g4204300
BLAST score	149
E value	1.0e-09
Match length	56
% identity	57
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	231130
Seq. ID	LIB3197-021-Q1-M1-A6
Method	BLASTX
NCBI GI	g4098331
BLAST score	620
E value	8.0e-65
Match length	114
% identity	97
NCBI Description	(U76896) beta-tubulin 5 [Triticum aestivum]

Seq. No.	231131
Seq. ID	LIB3197-021-Q1-M1-A8
Method	BLASTX
NCBI GI	g4455199
BLAST score	210
E value	3.0e-17
Match length	49
% identity	80
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	231132
Seq. ID	LIB3197-021-Q1-M1-B1
Method	BLASTX
NCBI GI	g3176098
BLAST score	383
E value	5.0e-37
Match length	127
% identity	35
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	231133
Seq. ID	LIB3197-021-Q1-M1-B10
Method	BLASTX
NCBI GI	g2827755
BLAST score	278
E value	1.0e-24
Match length	96
% identity	62
NCBI Description	INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE PHOSPHOHYDROLASE) (PPASE) >gi_951323 (U31467) pyrophosphatase [Vigna radiata]

Seq. No.	231134

Seq. ID	LIB3197-021-Q1-M1-B11
Method	BLASTX
NCBI GI	g3377797
BLAST score	556
E value	3.0e-57
Match length	123
% identity	86
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	231135
Seq. ID	LIB3197-021-Q1-M1-B12
Method	BLASTX
NCBI GI	g2664210
BLAST score	300
E value	7.0e-32
Match length	109
% identity	66
NCBI Description	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	231136
Seq. ID	LIB3197-021-Q1-M1-B4
Method	BLASTX
NCBI GI	g2626840
BLAST score	282
E value	3.0e-25
Match length	130
% identity	44
NCBI Description	(D89729) CRM1 protein [Homo sapiens] >gi_4507943_ref_NP_003391.1_pXPO1_ exportin 1 (CRM1, yeast, homolog)

Seq. No.	231137
Seq. ID	LIB3197-021-Q1-M1-B5
Method	BLASTX
NCBI GI	g3776560
BLAST score	289
E value	5.0e-26
Match length	132
% identity	48
NCBI Description	(AC005388) Similar to gb_U51990 hPrp18 (splicing factor) gene from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	231138
Seq. ID	LIB3197-021-Q1-M1-B6
Method	BLASTX
NCBI GI	g131770
BLAST score	409
E value	5.0e-40
Match length	115
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24

ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	231139
Seq. ID	LIB3197-021-Q1-M1-B7
Method	BLASTX
NCBI GI	g2119934
BLAST score	446
E value	2.0e-44
Match length	92
% identity	93
NCBI Description	translation initiation factor eIF-4A.7 - common tobacco

Seq. No.	231140
Seq. ID	LIB3197-021-Q1-M1-B9
Method	BLASTX
NCBI GI	g2738949
BLAST score	540
E value	2.0e-55
Match length	113
% identity	88
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	231141
Seq. ID	LIB3197-021-Q1-M1-C1
Method	BLASTX
NCBI GI	g1724102
BLAST score	502
E value	6.0e-51
Match length	114
% identity	84
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	231142
Seq. ID	LIB3197-021-Q1-M1-C2
Method	BLASTX
NCBI GI	g4371285
BLAST score	485
E value	5.0e-49
Match length	133
% identity	69
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231143
Seq. ID	LIB3197-021-Q1-M1-C3
Method	BLASTX
NCBI GI	g3337349
BLAST score	148
E value	9.0e-10
Match length	41
% identity	61
NCBI Description	(AC004481) putative protein kinase [Arabidopsis thaliana]

Seq. No. 231144

Seq. ID	LIB3197-021-Q1-M1-C4
Method	BLASTX
NCBI GI	g1174536
BLAST score	139
E value	5.0e-09
Match length	40
% identity	62
NCBI Description	ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE--TRNA LIGASE) (ASNRS) >gi_1073865_pir__B64115 asparagine--tRNA ligase (EC 6.1.1.22) - Haemophilus influenzae (strain Rd KW20) >gi_1574761 (U32810) asparaginyl-tRNA synthetase (asnS) [Haemophilus influenzae Rd]

Seq. No.	231145
Seq. ID	LIB3197-021-Q1-M1-C7
Method	BLASTX
NCBI GI	g3249066
BLAST score	340
E value	5.0e-32
Match length	121
% identity	61
NCBI Description	(AC004473) Similar to S. cerevisiae SIK1P protein gb_984964. ESTs gb_F15433 and gb_AA395158 come from this gene. [Arabidopsis thaliana]

Seq. No.	231146
Seq. ID	LIB3197-021-Q1-M1-C9
Method	BLASTX
NCBI GI	g3885328
BLAST score	178
E value	5.0e-13
Match length	43
% identity	72
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	231147
Seq. ID	LIB3197-021-Q1-M1-D1
Method	BLASTX
NCBI GI	g4206124
BLAST score	660
E value	2.0e-69
Match length	135
% identity	95
NCBI Description	(AF097668) T-complex protein 1 epsilon subunit [Mesembryanthemum crystallinum]

Seq. No.	231148
Seq. ID	LIB3197-021-Q1-M1-D10
Method	BLASTX
NCBI GI	g2443348
BLAST score	282
E value	3.0e-25
Match length	117
% identity	44
NCBI Description	(AB001379) cytochrome P450 [Glycyrrhiza echinata]

Seq. No.	231149
Seq. ID	LIB3197-021-Q1-M1-D3
Method	BLASTX
NCBI GI	g3319457
BLAST score	172
E value	3.0e-12
Match length	98
% identity	39
NCBI Description	(AF077542) contains similarity to O-linked GlcNAc transferases [Caenorhabditis elegans]

Seq. No.	231150
Seq. ID	LIB3197-021-Q1-M1-D6
Method	BLASTX
NCBI GI	g4469005
BLAST score	150
E value	3.0e-15
Match length	84
% identity	57
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231151
Seq. ID	LIB3197-021-Q1-M1-D7
Method	BLASTX
NCBI GI	g4454012
BLAST score	457
E value	1.0e-45
Match length	123
% identity	67
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	231152
Seq. ID	LIB3197-021-Q1-M1-D9
Method	BLASTX
NCBI GI	g586076
BLAST score	557
E value	2.0e-57
Match length	109
% identity	89
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	231153
Seq. ID	LIB3197-021-Q1-M1-E1
Method	BLASTX
NCBI GI	g113621
BLAST score	298
E value	3.0e-27
Match length	90
% identity	72
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No.	231154
Seq. ID	LIB3197-021-Q1-M1-E10
Method	BLASTX
NCBI GI	g464444
BLAST score	546
E value	4.0e-56
Match length	118
% identity	90
NCBI Description	PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome - Arabidopsis thaliana >gi_166830 (M98495) proteasome [Arabidopsis thaliana]

Seq. No.	231155
Seq. ID	LIB3197-021-Q1-M1-E11
Method	BLASTX
NCBI GI	g2811278
BLAST score	257
E value	7.0e-40
Match length	118
% identity	73
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231156
Seq. ID	LIB3197-021-Q1-M1-E2
Method	BLASTX
NCBI GI	g1703129
BLAST score	561
E value	7.0e-58
Match length	105
% identity	98
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	231157
Seq. ID	LIB3197-021-Q1-M1-E3
Method	BLASTX
NCBI GI	g3367534
BLAST score	282
E value	8.0e-52
Match length	132
% identity	77
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	231158
Seq. ID	LIB3197-021-Q1-M1-E6
Method	BLASTX
NCBI GI	g267069
BLAST score	560
E value	9.0e-58
Match length	104
% identity	98

NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231159
Seq. ID	LIB3197-021-Q1-M1-E7
Method	BLASTX
NCBI GI	g1346349
BLAST score	500
E value	1.0e-50
Match length	102
% identity	97
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II - human >gi_908805 (L42612) keratin type II [Homo sapiens]

Seq. No.	231160
Seq. ID	LIB3197-021-Q1-M1-E8
Method	BLASTX
NCBI GI	g2811278
BLAST score	558
E value	1.0e-57
Match length	119
% identity	87
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231161
Seq. ID	LIB3197-021-Q1-M1-E9
Method	BLASTX
NCBI GI	g1843525
BLAST score	250
E value	1.0e-21
Match length	50
% identity	98
NCBI Description	(U73746) annexin [Gossypium hirsutum]

Seq. No.	231162
Seq. ID	LIB3197-021-Q1-M1-F1
Method	BLASTX
NCBI GI	g1170567
BLAST score	350
E value	2.0e-33
Match length	72
% identity	88
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	231163
Seq. ID	LIB3197-021-Q1-M1-F10
Method	BLASTX
NCBI GI	g3881976
BLAST score	223
E value	7.0e-19
Match length	64
% identity	64

NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]
Seq. No.	231164
Seq. ID	LIB3197-021-Q1-M1-F12
Method	BLASTX
NCBI GI	g3269289
BLAST score	177
E value	7.0e-13
Match length	50
% identity	68
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]
Seq. No.	231165
Seq. ID	LIB3197-021-Q1-M1-F3
Method	BLASTX
NCBI GI	g112863
BLAST score	596
E value	5.0e-62
Match length	135
% identity	81
NCBI Description	STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR >gi_100227_pir__S12209 hypothetical protein - tomato >gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon esculentum]
Seq. No.	231166
Seq. ID	LIB3197-021-Q1-M1-F4
Method	BLASTX
NCBI GI	g4512705
BLAST score	537
E value	3.0e-55
Match length	117
% identity	87
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	231167
Seq. ID	LIB3197-021-Q1-M1-F5
Method	BLASTX
NCBI GI	g339878
BLAST score	198
E value	6.0e-16
Match length	64
% identity	59
NCBI Description	(M55169) tripeptidyl peptidase II [Homo sapiens]
Seq. No.	231168
Seq. ID	LIB3197-021-Q1-M1-F6
Method	BLASTX
NCBI GI	g2062172
BLAST score	351
E value	3.0e-33
Match length	73
% identity	89
NCBI Description	(AC001645) unknown protein [Arabidopsis thaliana]
Seq. No.	231169

Seq. ID	LIB3197-021-Q1-M1-F7
Method	BLASTX
NCBI GI	g2435519
BLAST score	385
E value	3.0e-37
Match length	133
% identity	58
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	231170
Seq. ID	LIB3197-021-Q1-M1-F9
Method	BLASTX
NCBI GI	g3128228
BLAST score	640
E value	4.0e-67
Match length	133
% identity	90
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	231171
Seq. ID	LIB3197-021-Q1-M1-G1
Method	BLASTX
NCBI GI	g2326345
BLAST score	223
E value	3.0e-18
Match length	109
% identity	43
NCBI Description	(Y11187) PRL1 protein [Arabidopsis thaliana]

Seq. No.	231172
Seq. ID	LIB3197-021-Q1-M1-G12
Method	BLASTX
NCBI GI	g586076
BLAST score	643
E value	2.0e-67
Match length	122
% identity	97
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	231173
Seq. ID	LIB3197-021-Q1-M1-G2
Method	BLASTX
NCBI GI	g1708401
BLAST score	493
E value	6.0e-50
Match length	105
% identity	91
NCBI Description	ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)

Seq. No. 231174

Seq. ID	LIB3197-021-Q1-M1-G3
Method	BLASTX
NCBI GI	g231496
BLAST score	572
E value	3.0e-59
Match length	108
% identity	98
NCBI Description	ACTIN 58 >gi_100421_pir__S20094 actin - potato >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]

Seq. No.	231175
Seq. ID	LIB3197-021-Q1-M1-G6
Method	BLASTX
NCBI GI	g2580440
BLAST score	158
E value	1.0e-10
Match length	60
% identity	53
NCBI Description	(D87261) PCF2 [Oryza sativa]

Seq. No.	231176
Seq. ID	LIB3197-021-Q1-M1-G7
Method	BLASTX
NCBI GI	g2119934
BLAST score	446
E value	2.0e-44
Match length	92
% identity	93
NCBI Description	translation initiation factor eIF-4A.7 - common tobacco

Seq. No.	231177
Seq. ID	LIB3197-021-Q1-M1-G9
Method	BLASTX
NCBI GI	g2598575
BLAST score	249
E value	3.0e-21
Match length	124
% identity	40
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	231178
Seq. ID	LIB3197-021-Q1-M1-H11
Method	BLASTX
NCBI GI	g309557
BLAST score	555
E value	3.0e-57
Match length	119
% identity	91
NCBI Description	(L21007) chaperonin 60 [Zea mays]

Seq. No.	231179
Seq. ID	LIB3197-021-Q1-M1-H12
Method	BLASTX
NCBI GI	g3860272
BLAST score	660
E value	2.0e-69
Match length	132

% identity	98
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	231180
Seq. ID	LIB3197-021-Q1-M1-H4
Method	BLASTX
NCBI GI	g1931639
BLAST score	172
E value	2.0e-12
Match length	91
% identity	37
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	231181
Seq. ID	LIB3197-021-Q1-M1-H5
Method	BLASTX
NCBI GI	g1710663
BLAST score	188
E value	4.0e-15
Match length	99
% identity	48
NCBI Description	PUTATIVE DNA-DIRECTED RNA POLYMERASE III 130 KD POLYPEPTIDE (RNA POLYMERASE III SUBUNIT 2) >gi_1204209_emb_CAA93558_ (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe]

Seq. No.	231182
Seq. ID	LIB3197-022-Q1-M1-A3
Method	BLASTX
NCBI GI	g3493172
BLAST score	411
E value	2.0e-40
Match length	91
% identity	89
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	231183
Seq. ID	LIB3197-022-Q1-M1-A6
Method	BLASTX
NCBI GI	g1724102
BLAST score	493
E value	7.0e-50
Match length	112
% identity	84
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	231184
Seq. ID	LIB3197-022-Q1-M1-A7
Method	BLASTX
NCBI GI	g4539327
BLAST score	312
E value	5.0e-29
Match length	63
% identity	92

NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]
Seq. No.	231185
Seq. ID	LIB3197-022-Q1-M1-A8
Method	BLASTX
NCBI GI	g3212869
BLAST score	439
E value	1.0e-43
Match length	93
% identity	87
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	231186
Seq. ID	LIB3197-022-Q1-M1-A9
Method	BLASTX
NCBI GI	g4389512
BLAST score	255
E value	3.0e-22
Match length	101
% identity	54
NCBI Description	(AC007059) Human homolog of Mus musculus wizS protein [AA 64-934] [Homo sapiens]
Seq. No.	231187
Seq. ID	LIB3197-022-Q1-M1-B11
Method	BLASTX
NCBI GI	g2462746
BLAST score	563
E value	4.0e-58
Match length	124
% identity	84
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]
Seq. No.	231188
Seq. ID	LIB3197-022-Q1-M1-B3
Method	BLASTX
NCBI GI	g3319921
BLAST score	271
E value	7.0e-24
Match length	97
% identity	61
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]
Seq. No.	231189
Seq. ID	LIB3197-022-Q1-M1-B6
Method	BLASTX
NCBI GI	g2209358
BLAST score	567
E value	1.0e-58
Match length	138
% identity	75
NCBI Description	(AF004812) beta-D-galactosidase [Mangifera indica]

Seq. No.	231190
Seq. ID	LIB3197-022-Q1-M1-B8
Method	BLASTX
NCBI GI	g3420006
BLAST score	259
E value	2.0e-22
Match length	89
% identity	55
NCBI Description	(AF000306) steroid sulfotransferase 2 [Brassica napus]

Seq. No.	231191
Seq. ID	LIB3197-022-Q1-M1-C1
Method	BLASTX
NCBI GI	g3095111
BLAST score	143
E value	6.0e-09
Match length	91
% identity	37
NCBI Description	(AF051894) 15 kDa selenoprotein [Homo sapiens]

Seq. No.	231192
Seq. ID	LIB3197-022-Q1-M1-C10
Method	BLASTX
NCBI GI	g4455158
BLAST score	216
E value	1.0e-17
Match length	60
% identity	68
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	231193
Seq. ID	LIB3197-022-Q1-M1-C12
Method	BLASTX
NCBI GI	g2341034
BLAST score	556
E value	3.0e-57
Match length	113
% identity	97
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	231194
Seq. ID	LIB3197-022-Q1-M1-C2
Method	BLASTX
NCBI GI	g2493131
BLAST score	537
E value	3.0e-55
Match length	112
% identity	96
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No.	231195
Seq. ID	LIB3197-022-Q1-M1-C3
Method	BLASTX
NCBI GI	g2853219

BLAST score	577
E value	8.0e-60
Match length	127
% identity	82
NCBI Description	(AJ000923) glutathione transferase [Carica papaya]

Seq. No.	231196
Seq. ID	LIB3197-022-Q1-M1-C7
Method	BLASTX
NCBI GI	g1170567
BLAST score	541
E value	2.0e-55
Match length	111
% identity	89
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	231197
Seq. ID	LIB3197-022-Q1-M1-D1
Method	BLASTX
NCBI GI	g4335763
BLAST score	225
E value	2.0e-18
Match length	81
% identity	49
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	231198
Seq. ID	LIB3197-022-Q1-M1-D10
Method	BLASTX
NCBI GI	g4508073
BLAST score	435
E value	4.0e-43
Match length	113
% identity	69
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	231199
Seq. ID	LIB3197-022-Q1-M1-D11
Method	BLASTX
NCBI GI	g3550982
BLAST score	501
E value	1.0e-52
Match length	123
% identity	86
NCBI Description	(AB010690) mutM homologue-1 [Arabidopsis thaliana]

Seq. No.	231200
Seq. ID	LIB3197-022-Q1-M1-D12
Method	BLASTX
NCBI GI	g2738949
BLAST score	579
E value	5.0e-60
Match length	119
% identity	89
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 231201
Seq. ID LIB3197-022-Q1-M1-D4
Method BLASTX
NCBI GI g2062167
BLAST score 267
E value 1.0e-23
Match length 57
% identity 84
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 231202
Seq. ID LIB3197-022-Q1-M1-D5
Method BLASTX
NCBI GI g2104681
BLAST score 146
E value 3.0e-09
Match length 129
% identity 37
NCBI Description (X97907) transcription factor [Vicia faba]

Seq. No. 231203
Seq. ID LIB3197-022-Q1-M1-D6
Method BLASTX
NCBI GI g1703375
BLAST score 384
E value 3.0e-37
Match length 88
% identity 86
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No. 231204
Seq. ID LIB3197-022-Q1-M1-D8
Method BLASTX
NCBI GI g2454184
BLAST score 577
E value 9.0e-60
Match length 117
% identity 94
NCBI Description (U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No. 231205
Seq. ID LIB3197-022-Q1-M1-E1
Method BLASTX
NCBI GI g4454463
BLAST score 192
E value 3.0e-15
Match length 48
% identity 28
NCBI Description (AC006234) putative leucine rich protein kinase [Arabidopsis thaliana]

Seq. No. 231206

Seq. ID	LIB3197-022-Q1-M1-E12
Method	BLASTX
NCBI GI	g1351856
BLAST score	617
E value	2.0e-64
Match length	127
% identity	91
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	231207
Seq. ID	LIB3197-022-Q1-M1-E3
Method	BLASTX
NCBI GI	g2924509
BLAST score	233
E value	2.0e-19
Match length	91
% identity	51
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No.	231208
Seq. ID	LIB3197-022-Q1-M1-E5
Method	BLASTX
NCBI GI	g3668089
BLAST score	234
E value	2.0e-19
Match length	83
% identity	51
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	231209
Seq. ID	LIB3197-022-Q1-M1-E9
Method	BLASTX
NCBI GI	g3128186
BLAST score	236
E value	9.0e-20
Match length	67
% identity	67
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231210
Seq. ID	LIB3197-022-Q1-M1-F1
Method	BLASTX
NCBI GI	g2811278
BLAST score	424
E value	8.0e-42
Match length	122
% identity	65
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231211
Seq. ID	LIB3197-022-Q1-M1-F4
Method	BLASTX
NCBI GI	g3668097
BLAST score	425

E value	4.0e-42
Match length	101
% identity	82
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	231212
Seq. ID	LIB3197-022-Q1-M1-F7
Method	BLASTX
NCBI GI	g2832625
BLAST score	378
E value	2.0e-36
Match length	90
% identity	80
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	231213
Seq. ID	LIB3197-022-Q1-M1-F9
Method	BLASTX
NCBI GI	g2827552
BLAST score	332
E value	4.0e-31
Match length	91
% identity	58
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	231214
Seq. ID	LIB3197-022-Q1-M1-G10
Method	BLASTX
NCBI GI	g1711532
BLAST score	282
E value	3.0e-26
Match length	123
% identity	54
NCBI Description	SSU72 PROTEIN >gi_2131928_pir__S63180 hypothetical protein YNL222w - yeast (Saccharomyces cerevisiae) >gi_1173490 (U20390) Ssu72p [Saccharomyces cerevisiae] >gi_1302241_emb_CAA96125_ (Z71498) ORF YNL222w [Saccharomyces cerevisiae] >gi_1589662_prf__2211396A SSU72 protein [Saccharomyces cerevisiae]

Seq. No.	231215
Seq. ID	LIB3197-022-Q1-M1-G11
Method	BLASTX
NCBI GI	g2583108
BLAST score	225
E value	1.0e-18
Match length	90
% identity	54
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	231216
Seq. ID	LIB3197-022-Q1-M1-G2
Method	BLASTX
NCBI GI	g1076738
BLAST score	461
E value	4.0e-46

Match length	89
% identity	96
NCBI Description	beta-tubulin R2242 - rice

Seq. No.	231217
Seq. ID	LIB3197-022-Q1-M1-G3
Method	BLASTX
NCBI GI	g3641837
BLAST score	440
E value	9.0e-44
Match length	124
% identity	73
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	231218
Seq. ID	LIB3197-022-Q1-M1-G5
Method	BLASTX
NCBI GI	g3249098
BLAST score	162
E value	4.0e-11
Match length	105
% identity	44
NCBI Description	(AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481 and gb_N64971 come from this gene. [Arabidopsis thaliana]

Seq. No.	231219
Seq. ID	LIB3197-022-Q1-M1-G7
Method	BLASTX
NCBI GI	g4038043
BLAST score	174
E value	2.0e-12
Match length	115
% identity	34
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	231220
Seq. ID	LIB3197-022-Q1-M1-G8
Method	BLASTX
NCBI GI	g100488
BLAST score	331
E value	7.0e-31
Match length	124
% identity	53
NCBI Description	TNP2 protein - garden snapdragon

Seq. No.	231221
Seq. ID	LIB3197-022-Q1-M1-H1
Method	BLASTX
NCBI GI	g71634
BLAST score	332
E value	3.0e-31
Match length	65
% identity	98
NCBI Description	actin 1 - rice

Seq. No.	231222
Seq. ID	LIB3197-022-Q1-M1-H10
Method	BLASTX
NCBI GI	g3334322
BLAST score	431
E value	9.0e-43
Match length	82
% identity	99
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_2108347 (U55036) small GTP-binding protein Bsar1b [Brassica rapa]

Seq. No.	231223
Seq. ID	LIB3197-022-Q1-M1-H7
Method	BLASTX
NCBI GI	g2895576
BLAST score	162
E value	4.0e-11
Match length	130
% identity	25
NCBI Description	(AF041337) vacuolar proton pump subunit SFD beta isoform [Bos taurus]

Seq. No.	231224
Seq. ID	LIB3197-022-Q1-M1-H8
Method	BLASTX
NCBI GI	g1174592
BLAST score	614
E value	4.0e-64
Match length	138
% identity	90
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	231225
Seq. ID	LIB3197-023-Q1-M1-A4
Method	BLASTX
NCBI GI	g475048
BLAST score	614
E value	5.0e-64
Match length	131
% identity	63
NCBI Description	(X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]

Seq. No.	231226
Seq. ID	LIB3197-023-Q1-M1-A5
Method	BLASTX
NCBI GI	g1408471
BLAST score	523
E value	2.0e-53
Match length	116
% identity	81
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	231227
Seq. ID	LIB3197-023-Q1-M1-A8
Method	BLASTX
NCBI GI	g4580394
BLAST score	410
E value	4.0e-40
Match length	137
% identity	53
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	231228
Seq. ID	LIB3197-023-Q1-M1-B4
Method	BLASTX
NCBI GI	g1330401
BLAST score	200
E value	2.0e-15
Match length	81
% identity	46
NCBI Description	(U58762) T27F7.1 gene product [Caenorhabditis elegans]

Seq. No.	231229
Seq. ID	LIB3197-023-Q1-M1-B8
Method	BLASTX
NCBI GI	g464849
BLAST score	593
E value	1.0e-61
Match length	120
% identity	97
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	231230
Seq. ID	LIB3197-023-Q1-M1-C1
Method	BLASTX
NCBI GI	g4220537
BLAST score	363
E value	1.0e-34
Match length	140
% identity	51
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	231231
Seq. ID	LIB3197-023-Q1-M1-C7
Method	BLASTX
NCBI GI	g4240116
BLAST score	373
E value	8.0e-36
Match length	107
% identity	73
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	231232
Seq. ID	LIB3197-023-Q1-M1-C9

Method	BLASTX
NCBI GI	g3603401
BLAST score	347
E value	5.0e-33
Match length	96
% identity	68
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	231233
Seq. ID	LIB3197-023-Q1-M1-D1
Method	BLASTX
NCBI GI	g3122703
BLAST score	173
E value	5.0e-13
Match length	66
% identity	53
NCBI Description	60S RIBOSOMAL PROTEIN L23A >gi_2641201 (AF031542) ribosomal protein L23a [Fritillaria agrestis]

Seq. No.	231234
Seq. ID	LIB3197-023-Q1-M1-D3
Method	BLASTX
NCBI GI	g2662343
BLAST score	644
E value	1.0e-67
Match length	123
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	231235
Seq. ID	LIB3197-023-Q1-M1-D7
Method	BLASTX
NCBI GI	g3122703
BLAST score	327
E value	2.0e-30
Match length	86
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L23A >gi_2641201 (AF031542) ribosomal protein L23a [Fritillaria agrestis]

Seq. No.	231236
Seq. ID	LIB3197-023-Q1-M1-D9
Method	BLASTX
NCBI GI	g3420801
BLAST score	473
E value	1.0e-47
Match length	140
% identity	66
NCBI Description	(AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana]

Seq. No.	231237
Seq. ID	LIB3197-023-Q1-M1-E1
Method	BLASTX
NCBI GI	g4455223
BLAST score	236
E value	9.0e-20

Match length	64
% identity	37
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]
Seq. No.	231238
Seq. ID	LIB3197-023-Q1-M1-E2
Method	BLASTX
NCBI GI	g541954
BLAST score	583
E value	2.0e-60
Match length	140
% identity	84
NCBI Description	ubiquitin extension protein - white lupine >gi_438111_emb_CAA80334_ (Z22613) ubiquitin extension protein [Lupinus albus]
Seq. No.	231239
Seq. ID	LIB3197-023-Q1-M1-E7
Method	BLASTX
NCBI GI	g2811278
BLAST score	572
E value	3.0e-59
Match length	119
% identity	88
NCBI Description	(AF043284) expansin [Gossypium hirsutum]
Seq. No.	231240
Seq. ID	LIB3197-023-Q1-M1-E9
Method	BLASTX
NCBI GI	g2811278
BLAST score	665
E value	5.0e-70
Match length	135
% identity	89
NCBI Description	(AF043284) expansin [Gossypium hirsutum]
Seq. No.	231241
Seq. ID	LIB3197-023-Q1-M1-F1
Method	BLASTX
NCBI GI	g2829910
BLAST score	147
E value	3.0e-09
Match length	99
% identity	11
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.	231242
Seq. ID	LIB3197-023-Q1-M1-F7
Method	BLASTX
NCBI GI	g3986750
BLAST score	470
E value	4.0e-47
Match length	94
% identity	89
NCBI Description	(AF107464) serine/threonine protein phosphatase type 2A

[Hevea brasiliensis]

Seq. No.	231243
Seq. ID	LIB3197-023-Q1-M1-G2
Method	BLASTX
NCBI GI	g2996012
BLAST score	451
E value	6.0e-45
Match length	113
% identity	75
NCBI Description	(AF054455) cytosolic phosphoglucose isomerase; PgiC [Leavenworthia crassa]

Seq. No.	231244
Seq. ID	LIB3197-023-Q1-M1-G7
Method	BLASTX
NCBI GI	g3355471
BLAST score	181
E value	2.0e-13
Match length	96
% identity	38
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	231245
Seq. ID	LIB3197-023-Q1-M1-G8
Method	BLASTX
NCBI GI	g4454012
BLAST score	566
E value	2.0e-58
Match length	147
% identity	71
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	231246
Seq. ID	LIB3197-023-Q1-M1-H10
Method	BLASTX
NCBI GI	g3122572
BLAST score	297
E value	2.0e-27
Match length	74
% identity	77
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	231247
Seq. ID	LIB3197-023-Q1-M1-H11
Method	BLASTX
NCBI GI	g1370162
BLAST score	469
E value	3.0e-47
Match length	99

% identity	92
NCBI Description	(X97853) RAB1A [Lotus japonicus]

Seq. No.	231248
Seq. ID	LIB3197-023-Q1-M1-H2
Method	BLASTX
NCBI GI	g2493416
BLAST score	148
E value	1.0e-09
Match length	76
% identity	38
NCBI Description	S100 CALCIUM-BINDING PROTEIN A13 >gi_2134853_pir__JC5064 calcium-binding protein S100 A13 - human >gi_1694828_emb_CAA68188_ (X99920) S100 calcium-binding protein A13 (S100A13) [Homo sapiens]

Seq. No.	231249
Seq. ID	LIB3197-023-Q1-M1-H3
Method	BLASTX
NCBI GI	g3551249
BLAST score	155
E value	3.0e-10
Match length	65
% identity	48
NCBI Description	(AB012704) 184 [Daucus carota]

Seq. No.	231250
Seq. ID	LIB3197-023-Q1-M1-H5
Method	BLASTX
NCBI GI	g3059131
BLAST score	291
E value	3.0e-26
Match length	94
% identity	57
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	231251
Seq. ID	LIB3197-023-Q1-M1-H6
Method	BLASTX
NCBI GI	g1781103
BLAST score	250
E value	2.0e-21
Match length	110
% identity	43
NCBI Description	(Z83864) menG [Mycobacterium tuberculosis]

Seq. No.	231252
Seq. ID	LIB3197-023-Q1-M1-H7
Method	BLASTX
NCBI GI	g1644427
BLAST score	334
E value	3.0e-31
Match length	74
% identity	85
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	231253

Seq. ID	LIB3197-024-Q1-M1-A2
Method	BLASTX
NCBI GI	g1171866
BLAST score	215
E value	2.0e-17
Match length	83
% identity	54
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No.	231254
Seq. ID	LIB3197-024-Q1-M1-A7
Method	BLASTX
NCBI GI	g4006875
BLAST score	180
E value	3.0e-13
Match length	74
% identity	49
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	231255
Seq. ID	LIB3197-024-Q1-M1-A9
Method	BLASTX
NCBI GI	g4510348
BLAST score	205
E value	2.0e-16
Match length	60
% identity	67
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	231256
Seq. ID	LIB3197-024-Q1-M1-B1
Method	BLASTX
NCBI GI	g4455202
BLAST score	217
E value	1.0e-17
Match length	74
% identity	58
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No.	231257
Seq. ID	LIB3197-024-Q1-M1-B8
Method	BLASTX
NCBI GI	g1856971
BLAST score	346
E value	8.0e-33
Match length	88
% identity	81
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	231258
Seq. ID	LIB3197-024-Q1-M1-C1

Method	BLASTX
NCBI GI	g3059131
BLAST score	305
E value	6.0e-28
Match length	97
% identity	57
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	231259
Seq. ID	LIB3197-024-Q1-M1-C8
Method	BLASTX
NCBI GI	g232024
BLAST score	670
E value	1.0e-70
Match length	129
% identity	98
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	231260
Seq. ID	LIB3197-024-Q1-M1-C9
Method	BLASTX
NCBI GI	g3122673
BLAST score	409
E value	3.0e-40
Match length	105
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	231261
Seq. ID	LIB3197-024-Q1-M1-D1
Method	BLASTX
NCBI GI	g232024
BLAST score	609
E value	1.0e-63
Match length	114
% identity	100
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	231262
Seq. ID	LIB3197-024-Q1-M1-D2
Method	BLASTX
NCBI GI	g2507281
BLAST score	621
E value	6.0e-65
Match length	112
% identity	98
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	231263
Seq. ID	LIB3197-024-Q1-M1-D7
Method	BLASTX
NCBI GI	g1173198
BLAST score	412
E value	1.0e-40
Match length	88
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	231264
Seq. ID	LIB3197-024-Q1-M1-D8
Method	BLASTX
NCBI GI	g114121
BLAST score	257
E value	3.0e-22
Match length	81
% identity	62
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_101185_pir__B36167 ADP-ribosylation factor 1 - yeast (Saccharomyces cerevisiae) >gi_171073 (J03276) ADP-ribosylation factor [Saccharomyces cerevisiae] >gi_1004303_emb_CAA58255_ (X83276) ADP-ribosylationfactor 2 [Saccharomyces cerevisiae] >gi_1431314_emb_CAA98769_ (Z74240) ORF YDL192w [Saccharomyces cerevisiae]

Seq. No.	231265
Seq. ID	LIB3197-024-Q1-M1-D9
Method	BLASTX
NCBI GI	g4538897
BLAST score	327
E value	1.0e-30
Match length	90
% identity	69
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	231266
Seq. ID	LIB3197-024-Q1-M1-E2
Method	BLASTX
NCBI GI	g2062167
BLAST score	465
E value	1.0e-46
Match length	97
% identity	88
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	231267
Seq. ID	LIB3197-024-Q1-M1-E6
Method	BLASTX
NCBI GI	g82040
BLAST score	361
E value	1.0e-34
Match length	98

% identity	20
NCBI Description	ubiquitin precursor - flax (fragment) >gi_168304 (M57895) ubiquitin [Linum usitatissimum]

Seq. No.	231268
Seq. ID	LIB3197-024-Q1-M1-E8
Method	BLASTX
NCBI GI	g1710585
BLAST score	360
E value	2.0e-34
Match length	84
% identity	85
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1143507_emb_CAA63786_ (X93587) P0 ribosomal protein [Lupinus luteus]

Seq. No.	231269
Seq. ID	LIB3197-024-Q1-M1-F10
Method	BLASTX
NCBI GI	g267069
BLAST score	430
E value	1.0e-42
Match length	79
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231270
Seq. ID	LIB3197-024-Q1-M1-F11
Method	BLASTX
NCBI GI	g4455309
BLAST score	495
E value	4.0e-50
Match length	137
% identity	70
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231271
Seq. ID	LIB3197-024-Q1-M1-F12
Method	BLASTX
NCBI GI	g2459445
BLAST score	314
E value	7.0e-29
Match length	111
% identity	31
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	231272
Seq. ID	LIB3197-024-Q1-M1-F2
Method	BLASTX
NCBI GI	g120669
BLAST score	446
E value	2.0e-44
Match length	89
% identity	92

NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	231273
Seq. ID	LIB3197-024-Q1-M1-F3
Method	BLASTX
NCBI GI	g120672
BLAST score	223
E value	1.0e-18
Match length	58
% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66016_pir__DEPZG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - parsley >gi_20549_emb_CAA42902_ (X60344) glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]
Seq. No.	231274
Seq. ID	LIB3197-024-Q1-M1-F4
Method	BLASTX
NCBI GI	g2493318
BLAST score	211
E value	5.0e-17
Match length	67
% identity	57
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]
Seq. No.	231275
Seq. ID	LIB3197-024-Q1-M1-F6
Method	BLASTX
NCBI GI	g586076
BLAST score	584
E value	1.0e-60
Match length	107
% identity	98
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]
Seq. No.	231276
Seq. ID	LIB3197-024-Q1-M1-F9
Method	BLASTX
NCBI GI	g1694976
BLAST score	354
E value	1.0e-33
Match length	100
% identity	67
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]
Seq. No.	231277

Seq. ID	LIB3197-024-Q1-M1-G1
Method	BLASTX
NCBI GI	g2811278
BLAST score	551
E value	1.0e-56
Match length	133
% identity	76
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231278
Seq. ID	LIB3197-024-Q1-M1-G11
Method	BLASTX
NCBI GI	g4544399
BLAST score	303
E value	1.0e-27
Match length	124
% identity	44
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	231279
Seq. ID	LIB3197-024-Q1-M1-G12
Method	BLASTX
NCBI GI	g3395422
BLAST score	375
E value	5.0e-36
Match length	138
% identity	54
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana] >gi_3786022 (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231280
Seq. ID	LIB3197-024-Q1-M1-G2
Method	BLASTX
NCBI GI	g2764732
BLAST score	392
E value	4.0e-38
Match length	87
% identity	93
NCBI Description	(AJ002490) ndhB [Arabidopsis thaliana]

Seq. No.	231281
Seq. ID	LIB3197-024-Q1-M1-G5
Method	BLASTX
NCBI GI	g3953471
BLAST score	328
E value	1.0e-30
Match length	75
% identity	81
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	231282
Seq. ID	LIB3197-024-Q1-M1-G6
Method	BLASTX
NCBI GI	g2760839
BLAST score	253

E value	8.0e-22
Match length	72
% identity	61
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	231283
Seq. ID	LIB3197-024-Q1-M1-G7
Method	BLASTX
NCBI GI	g231757
BLAST score	575
E value	2.0e-59
Match length	131
% identity	87
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_99653_pir__S18568 lignin-bispecific O-methyltransferase (EC 2.1.1.-) - quaking aspen >gi_20951_emb_CAA44006_ (X62096) lignin bispecific acid/5-hydroxyferulic acid methyltransferase [Populus tremuloides] >gi_2226267 (U13171) caffeic acid/5-hydroxyferulic acid O-methyltransferase [Populus tremuloides]

Seq. No.	231284
Seq. ID	LIB3197-024-Q1-M1-G8
Method	BLASTX
NCBI GI	g1928981
BLAST score	529
E value	4.0e-54
Match length	113
% identity	93
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	231285
Seq. ID	LIB3197-024-Q1-M1-G9
Method	BLASTX
NCBI GI	g416758
BLAST score	184
E value	9.0e-14
Match length	92
% identity	42
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	231286
Seq. ID	LIB3197-024-Q1-M1-H11
Method	BLASTX
NCBI GI	g1708191
BLAST score	351
E value	3.0e-33
Match length	126
% identity	55
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No.	231287
Seq. ID	LIB3197-024-Q1-M1-H2
Method	BLASTX
NCBI GI	g3097321
BLAST score	199
E value	2.0e-15
Match length	104
% identity	39
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	231288
Seq. ID	LIB3197-024-Q1-M1-H4
Method	BLASTX
NCBI GI	g2811031
BLAST score	127
E value	7.0e-13
Match length	72
% identity	58
NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi_2109299_gb_AAB58165.1_ (AF000132) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	231289
Seq. ID	LIB3197-024-Q1-M1-H6
Method	BLASTX
NCBI GI	g4567262
BLAST score	301
E value	9.0e-49
Match length	107
% identity	86
NCBI Description	(AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No.	231290
Seq. ID	LIB3197-024-Q1-M1-H7
Method	BLASTX
NCBI GI	g547684
BLAST score	558
E value	2.0e-57
Match length	112
% identity	96
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100336_pir__S18865 heat shock protein 82 - common tobacco (fragment) >gi_19880_emb_CAA44877_ (X63195) heat shock protein 82 [Nicotiana tabacum]

Seq. No.	231291
Seq. ID	LIB3197-025-Q1-M1-A12
Method	BLASTX
NCBI GI	g2507281
BLAST score	675
E value	3.0e-71
Match length	122
% identity	99
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	231292
Seq. ID	LIB3197-025-Q1-M1-A7
Method	BLASTX
NCBI GI	g2739046
BLAST score	162
E value	3.0e-11
Match length	89
% identity	37
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	231293
Seq. ID	LIB3197-025-Q1-M1-A9
Method	BLASTX
NCBI GI	g3283893
BLAST score	192
E value	1.0e-14
Match length	110
% identity	36
NCBI Description	(AF070626) unknown [Homo sapiens]

Seq. No.	231294
Seq. ID	LIB3197-025-Q1-M1-B12
Method	BLASTX
NCBI GI	g2738949
BLAST score	568
E value	1.0e-58
Match length	118
% identity	88
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	231295
Seq. ID	LIB3197-025-Q1-M1-B2
Method	BLASTX
NCBI GI	g1408471
BLAST score	505
E value	3.0e-51
Match length	113
% identity	81
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	231296
Seq. ID	LIB3197-025-Q1-M1-B3
Method	BLASTX
NCBI GI	g123613
BLAST score	407
E value	8.0e-40
Match length	92
% identity	86
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_100222_pir__S14949 heat shock cognate protein 70 - tomato >gi_19256_emb_CAA37970_ (X54029) heat shock protein cognate 70 [Lycopersicon esculentum]

Seq. No.	231297
Seq. ID	LIB3197-025-Q1-M1-B5
Method	BLASTX
NCBI GI	g2129499
BLAST score	605
E value	5.0e-63
Match length	126
% identity	90
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	231298
Seq. ID	LIB3197-025-Q1-M1-B6
Method	BLASTX
NCBI GI	g4235430
BLAST score	426
E value	4.0e-42
Match length	134
% identity	67
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	231299
Seq. ID	LIB3197-025-Q1-M1-B7
Method	BLASTX
NCBI GI	g3176874
BLAST score	417
E value	6.0e-41
Match length	134
% identity	61
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	231300
Seq. ID	LIB3197-025-Q1-M1-B9
Method	BLASTX
NCBI GI	g2961357
BLAST score	583
E value	2.0e-60
Match length	140
% identity	80
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	231301
Seq. ID	LIB3197-025-Q1-M1-C1
Method	BLASTX
NCBI GI	g1168328
BLAST score	141
E value	1.0e-08
Match length	51
% identity	61
NCBI Description	ACTIN-LIKE PROTEIN 3 >gi_629878_pir__S48844 actin-like protein - slime mold (Dictyostelium discoideum) >gi_2130164_pir__S69002 actin-like protein - slime mold (Dictyostelium discoideum) >gi_563346_emb_CAA86553_ (Z46418) actin-like protein [Dictyostelium discoideum]

Seq. No.	231302

Seq. ID	LIB3197-025-Q1-M1-C12
Method	BLASTX
NCBI GI	g586076
BLAST score	636
E value	1.0e-66
Match length	118
% identity	98
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	231303
Seq. ID	LIB3197-025-Q1-M1-C4
Method	BLASTX
NCBI GI	g3695023
BLAST score	322
E value	7.0e-30
Match length	141
% identity	50
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	231304
Seq. ID	LIB3197-025-Q1-M1-C5
Method	BLASTX
NCBI GI	g2706450
BLAST score	342
E value	3.0e-32
Match length	85
% identity	81
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	231305
Seq. ID	LIB3197-025-Q1-M1-C7
Method	BLASTX
NCBI GI	g3328240
BLAST score	336
E value	2.0e-31
Match length	108
% identity	58
NCBI Description	(AF064775) early nodule-specific protein [Medicago truncatula]

Seq. No.	231306
Seq. ID	LIB3197-025-Q1-M1-D11
Method	BLASTX
NCBI GI	g2462781
BLAST score	511
E value	5.0e-52
Match length	133
% identity	74
NCBI Description	(U73175) carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana]

Seq. No.	231307
Seq. ID	LIB3197-025-Q1-M1-D6
Method	BLASTX

NCBI GI	g3869088
BLAST score	637
E value	9.0e-67
Match length	122
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	231308
Seq. ID	LIB3197-025-Q1-M1-E10
Method	BLASTX
NCBI GI	g2160322
BLAST score	465
E value	1.0e-46
Match length	92
% identity	92
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]

Seq. No.	231309
Seq. ID	LIB3197-025-Q1-M1-E4
Method	BLASTX
NCBI GI	g3928099
BLAST score	269
E value	1.0e-23
Match length	128
% identity	23
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	231310
Seq. ID	LIB3197-025-Q1-M1-E6
Method	BLASTX
NCBI GI	g3695388
BLAST score	185
E value	8.0e-14
Match length	60
% identity	57
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	231311
Seq. ID	LIB3197-026-Q1-M1-A1
Method	BLASTX
NCBI GI	g71634
BLAST score	517
E value	1.0e-52
Match length	95
% identity	100
NCBI Description	actin 1 - rice

Seq. No.	231312
Seq. ID	LIB3197-026-Q1-M1-A10
Method	BLASTX
NCBI GI	g267069
BLAST score	551
E value	1.0e-56
Match length	102
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594

	tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	231313
Seq. ID	LIB3197-026-Q1-M1-A11
Method	BLASTX
NCBI GI	g4106515
BLAST score	513
E value	3.0e-52
Match length	123
% identity	77
NCBI Description	(AF092743) CAK associated cyclinH homolog [Populus tremula x Populus tremuloides]
Seq. No.	231314
Seq. ID	LIB3197-026-Q1-M1-A12
Method	BLASTX
NCBI GI	g3915031
BLAST score	573
E value	2.0e-59
Match length	109
% identity	98
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]
Seq. No.	231315
Seq. ID	LIB3197-026-Q1-M1-A2
Method	BLASTX
NCBI GI	g267073
BLAST score	561
E value	7.0e-58
Match length	107
% identity	94
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]
Seq. No.	231316
Seq. ID	LIB3197-026-Q1-M1-A3
Method	BLASTX
NCBI GI	g2129499
BLAST score	379
E value	5.0e-37
Match length	78
% identity	87
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	231317
Seq. ID	LIB3197-026-Q1-M1-A5
Method	BLASTX
NCBI GI	g267069
BLAST score	616

E value	3.0e-64
Match length	114
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231318
Seq. ID	LIB3197-026-Q1-M1-A8
Method	BLASTX
NCBI GI	g267069
BLAST score	640
E value	4.0e-67
Match length	121
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231319
Seq. ID	LIB3197-026-Q1-M1-A9
Method	BLASTX
NCBI GI	g1168728
BLAST score	373
E value	3.0e-36
Match length	86
% identity	76
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	231320
Seq. ID	LIB3197-026-Q1-M1-B1
Method	BLASTX
NCBI GI	g2130073
BLAST score	525
E value	1.0e-53
Match length	121
% identity	86
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	231321
Seq. ID	LIB3197-026-Q1-M1-B10
Method	BLASTX
NCBI GI	g2290528
BLAST score	185
E value	8.0e-14
Match length	70
% identity	47
NCBI Description	(U94746) ATAN11 [Arabidopsis thaliana]

Seq. No.	231322
Seq. ID	LIB3197-026-Q1-M1-B11

Method	BLASTX
NCBI GI	g2914706
BLAST score	410
E value	3.0e-40
Match length	85
% identity	85
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	231323
Seq. ID	LIB3197-026-Q1-M1-B12
Method	BLASTX
NCBI GI	g728938
BLAST score	589
E value	3.0e-61
Match length	130
% identity	87
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472) inorganic pyrophosphatse ase' [Hordeum vulgare]

Seq. No.	231324
Seq. ID	LIB3197-026-Q1-M1-B2
Method	BLASTX
NCBI GI	g2661840
BLAST score	392
E value	4.0e-38
Match length	109
% identity	67
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	231325
Seq. ID	LIB3197-026-Q1-M1-B3
Method	BLASTX
NCBI GI	g2529683
BLAST score	556
E value	2.0e-57
Match length	129
% identity	78
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	231326
Seq. ID	LIB3197-026-Q1-M1-B4
Method	BLASTX
NCBI GI	g82307
BLAST score	633
E value	3.0e-66
Match length	117
% identity	93
NCBI Description	myb protein 306 - garden snapdragon >gi_256828_bbs_115017 Myb oncoprotein homolog {clone 306} [Antirrhinum majus=snapdragons, J1:522, flowers, Peptide, 316 aa]

Seq. No.	231327
Seq. ID	LIB3197-026-Q1-M1-B6
Method	BLASTX

NCBI GI	g1841870
BLAST score	155
E value	7.0e-11
Match length	37
% identity	84
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	231328
Seq. ID	LIB3197-026-Q1-M1-C1
Method	BLASTX
NCBI GI	g2462929
BLAST score	455
E value	2.0e-45
Match length	119
% identity	69
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	231329
Seq. ID	LIB3197-026-Q1-M1-C10
Method	BLASTX
NCBI GI	g4325345
BLAST score	489
E value	2.0e-49
Match length	137
% identity	25
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	231330
Seq. ID	LIB3197-026-Q1-M1-C2
Method	BLASTX
NCBI GI	g3646373
BLAST score	534
E value	8.0e-55
Match length	105
% identity	92
NCBI Description	(AJ011078) RGP1 protein [Oryza sativa]

Seq. No.	231331
Seq. ID	LIB3197-026-Q1-M1-C3
Method	BLASTX
NCBI GI	g461812
BLAST score	178
E value	5.0e-13
Match length	73
% identity	48
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	231332
Seq. ID	LIB3197-026-Q1-M1-C5
Method	BLASTX

NCBI GI	g3763933
BLAST score	139
E value	7.0e-09
Match length	68
% identity	56
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	231333
Seq. ID	LIB3197-026-Q1-M1-C6
Method	BLASTX
NCBI GI	g267069
BLAST score	524
E value	1.0e-53
Match length	98
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231334
Seq. ID	LIB3197-026-Q1-M1-D10
Method	BLASTX
NCBI GI	g3334115
BLAST score	286
E value	1.0e-25
Match length	81
% identity	75
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	231335
Seq. ID	LIB3197-026-Q1-M1-D11
Method	BLASTX
NCBI GI	g3212869
BLAST score	621
E value	6.0e-65
Match length	132
% identity	84
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	231336
Seq. ID	LIB3197-026-Q1-M1-D12
Method	BLASTX
NCBI GI	g549060
BLAST score	504
E value	3.0e-51
Match length	137
% identity	67
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	231337

Seq. ID	LIB3197-026-Q1-M1-D6
Method	BLASTX
NCBI GI	g1351974
BLAST score	613
E value	5.0e-64
Match length	119
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325 ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_ (X80042) ADP-ribosylation factor [Zea mays]

Seq. No.	231338
Seq. ID	LIB3197-026-Q1-M1-E1
Method	BLASTX
NCBI GI	g132944
BLAST score	564
E value	3.0e-58
Match length	115
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	231339
Seq. ID	LIB3197-026-Q1-M1-E11
Method	BLASTX
NCBI GI	g3062806
BLAST score	434
E value	5.0e-43
Match length	135
% identity	57
NCBI Description	(D86198) dolichol-phosphate-mannose synthase [Homo sapiens] >gi_4503363_ref_NP_003850.1_pDPM1_ UNKNOWN

Seq. No.	231340
Seq. ID	LIB3197-026-Q1-M1-E2
Method	BLASTX
NCBI GI	g2369766
BLAST score	473
E value	2.0e-47
Match length	128
% identity	69
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	231341
Seq. ID	LIB3197-026-Q1-M1-E3
Method	BLASTX
NCBI GI	g1694711
BLAST score	237
E value	7.0e-20
Match length	90
% identity	46
NCBI Description	(Y09581) FRO1 [Arabidopsis thaliana]

Seq. No.	231342
Seq. ID	LIB3197-026-Q1-M1-E4

Method	BLASTX
NCBI GI	g3128228
BLAST score	682
E value	4.0e-72
Match length	137
% identity	92
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	231343
Seq. ID	LIB3197-026-Q1-M1-E8
Method	BLASTX
NCBI GI	g3023847
BLAST score	340
E value	3.0e-32
Match length	72
% identity	64
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	231344
Seq. ID	LIB3197-026-Q1-M1-E9
Method	BLASTX
NCBI GI	g3334320
BLAST score	473
E value	1.0e-47
Match length	104
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	231345
Seq. ID	LIB3197-026-Q1-M1-F1
Method	BLASTX
NCBI GI	g3170525
BLAST score	160
E value	6.0e-11
Match length	56
% identity	57
NCBI Description	(AF054615) cellulase [Fragaria x ananassa]

Seq. No.	231346
Seq. ID	LIB3197-026-Q1-M1-F11
Method	BLASTX
NCBI GI	g4580461
BLAST score	197
E value	3.0e-15
Match length	77
% identity	58
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	231347
Seq. ID	LIB3197-026-Q1-M1-F2
Method	BLASTX
NCBI GI	g2914700

BLAST score	680
E value	8.0e-72
Match length	142
% identity	54
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	231348
Seq. ID	LIB3197-026-Q1-M1-F3
Method	BLASTX
NCBI GI	g2982303
BLAST score	297
E value	4.0e-27
Match length	66
% identity	83
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	231349
Seq. ID	LIB3197-026-Q1-M1-F7
Method	BLASTX
NCBI GI	g547683
BLAST score	510
E value	4.0e-52
Match length	104
% identity	93
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	231350
Seq. ID	LIB3197-026-Q1-M1-F8
Method	BLASTX
NCBI GI	g3183088
BLAST score	209
E value	1.0e-16
Match length	71
% identity	56
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	231351
Seq. ID	LIB3197-026-Q1-M1-G1
Method	BLASTX
NCBI GI	g120669
BLAST score	351
E value	3.0e-33
Match length	96
% identity	69
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231352
Seq. ID	LIB3197-026-Q1-M1-G2
Method	BLASTX
NCBI GI	g2213594
BLAST score	352
E value	2.0e-33
Match length	116
% identity	57
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	231353
Seq. ID	LIB3197-026-Q1-M1-G3
Method	BLASTX
NCBI GI	g1172874
BLAST score	139
E value	1.0e-08
Match length	52
% identity	50
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	231354
Seq. ID	LIB3197-026-Q1-M1-G7
Method	BLASTX
NCBI GI	g120669
BLAST score	385
E value	2.0e-37
Match length	75
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231355
Seq. ID	LIB3197-026-Q1-M1-G8
Method	BLASTX
NCBI GI	g3759177
BLAST score	364
E value	7.0e-35
Match length	121
% identity	70
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	231356
Seq. ID	LIB3197-026-Q1-M1-H10
Method	BLASTX
NCBI GI	g2894378
BLAST score	361
E value	2.0e-34
Match length	139

% identity	55
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.	231357
Seq. ID	LIB3197-026-Q1-M1-H12
Method	BLASTX
NCBI GI	g2529685
BLAST score	527
E value	7.0e-54
Match length	122
% identity	86
NCBI Description	(AC002535) putative dimethyladenosine transferase [Arabidopsis thaliana]
Seq. No.	231358
Seq. ID	LIB3197-026-Q1-M1-H3
Method	BLASTX
NCBI GI	g135449
BLAST score	655
E value	7.0e-69
Match length	142
% identity	89
NCBI Description	TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1 tubulin [Zea mays]
Seq. No.	231359
Seq. ID	LIB3197-026-Q1-M1-H5
Method	BLASTX
NCBI GI	g99737
BLAST score	461
E value	4.0e-46
Match length	142
% identity	65
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.	231360
Seq. ID	LIB3197-026-Q1-M1-H8
Method	BLASTX
NCBI GI	g267069
BLAST score	245
E value	2.0e-21
Match length	56
% identity	82
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	231361
Seq. ID	LIB3197-027-Q1-M1-A1
Method	BLASTX
NCBI GI	g3421094
BLAST score	247
E value	1.0e-21

Match length	52
% identity	90
NCBI Description	(AF043527) 20S proteasome subunit PAF2 [Arabidopsis thaliana]

Seq. No.	231362
Seq. ID	LIB3197-027-Q1-M1-A10
Method	BLASTX
NCBI GI	g3269284
BLAST score	381
E value	8.0e-37
Match length	114
% identity	69
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	231363
Seq. ID	LIB3197-027-Q1-M1-A11
Method	BLASTX
NCBI GI	g441457
BLAST score	623
E value	4.0e-65
Match length	117
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	231364
Seq. ID	LIB3197-027-Q1-M1-A12
Method	BLASTX
NCBI GI	g4580394
BLAST score	180
E value	2.0e-13
Match length	83
% identity	42
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	231365
Seq. ID	LIB3197-027-Q1-M1-A6
Method	BLASTX
NCBI GI	g1174470
BLAST score	313
E value	1.0e-28
Match length	92
% identity	59
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	231366
Seq. ID	LIB3197-027-Q1-M1-A7
Method	BLASTX
NCBI GI	g464846
BLAST score	426
E value	5.0e-42
Match length	84

% identity	93
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	231367
Seq. ID	LIB3197-027-Q1-M1-A8
Method	BLASTX
NCBI GI	g1370198
BLAST score	286
E value	1.0e-25
Match length	77
% identity	77
NCBI Description	(Z73948) RAB8E [Lotus japonicus]

Seq. No.	231368
Seq. ID	LIB3197-027-Q1-M1-A9
Method	BLASTX
NCBI GI	g2995384
BLAST score	159
E value	8.0e-11
Match length	60
% identity	58
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	231369
Seq. ID	LIB3197-027-Q1-M1-B1
Method	BLASTX
NCBI GI	g1170508
BLAST score	492
E value	7.0e-50
Match length	105
% identity	88
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi_2119931_pir__S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi_475219_emb_CAA55639_ (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi_475221_emb_CAA55640_ (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]

Seq. No.	231370
Seq. ID	LIB3197-027-Q1-M1-B12
Method	BLASTX
NCBI GI	g2558655
BLAST score	237
E value	7.0e-20
Match length	134
% identity	43
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	231371
Seq. ID	LIB3197-027-Q1-M1-B2
Method	BLASTX
NCBI GI	g1170508
BLAST score	182
E value	6.0e-14

Match length	62
% identity	60
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi_2119931_pir__S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi_475219_emb_CAA55639_ (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi_475221_emb_CAA55640_ (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]

Seq. No.	231372
Seq. ID	LIB3197-027-Q1-M1-B5
Method	BLASTX
NCBI GI	g418854
BLAST score	757
E value	8.0e-81
Match length	152
% identity	18
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ (X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum]

Seq. No.	231373
Seq. ID	LIB3197-027-Q1-M1-B6
Method	BLASTX
NCBI GI	g3879145
BLAST score	164
E value	3.0e-11
Match length	80
% identity	44
NCBI Description	(Z93386) predicted using Genefinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	231374
Seq. ID	LIB3197-027-Q1-M1-B8
Method	BLASTX
NCBI GI	g3193222
BLAST score	164
E value	3.0e-11
Match length	36
% identity	89
NCBI Description	(AF068687) malate dehydrogenase [Glycine max]

Seq. No.	231375
Seq. ID	LIB3197-027-Q1-M1-C1
Method	BLASTX
NCBI GI	g4309972
BLAST score	164
E value	2.0e-11
Match length	119
% identity	38
NCBI Description	(AC002983) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231376
Seq. ID	LIB3197-027-Q1-M1-C11

Method	BLASTX
NCBI GI	g2253384
BLAST score	747
E value	1.0e-79
Match length	150
% identity	95
NCBI Description	(AF007100) biotin carboxylase precursor [Glycine max]

Seq. No.	231377
Seq. ID	LIB3197-027-Q1-M1-C5
Method	BLASTX
NCBI GI	g4105696
BLAST score	676
E value	3.0e-71
Match length	132
% identity	95
NCBI Description	(AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No.	231378
Seq. ID	LIB3197-027-Q1-M1-C6
Method	BLASTX
NCBI GI	g3163946
BLAST score	565
E value	4.0e-67
Match length	151
% identity	89
NCBI Description	(AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No.	231379
Seq. ID	LIB3197-027-Q1-M1-C7
Method	BLASTX
NCBI GI	g529516
BLAST score	287
E value	1.0e-25
Match length	85
% identity	60
NCBI Description	(L29099) beta-fructosidase [Solanum tuberosum]

Seq. No.	231380
Seq. ID	LIB3197-027-Q1-M1-C9
Method	BLASTX
NCBI GI	g2811278
BLAST score	587
E value	6.0e-61
Match length	123
% identity	88
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231381
Seq. ID	LIB3197-027-Q1-M1-D10
Method	BLASTX
NCBI GI	g3608137
BLAST score	264
E value	5.0e-23
Match length	125
% identity	45
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	231382
Seq. ID	LIB3197-027-Q1-M1-D11
Method	BLASTX
NCBI GI	g2924520
BLAST score	649
E value	4.0e-68
Match length	144
% identity	85
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	231383
Seq. ID	LIB3197-027-Q1-M1-D12
Method	BLASTX
NCBI GI	g4056496
BLAST score	283
E value	8.0e-45
Match length	142
% identity	64
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	231384
Seq. ID	LIB3197-027-Q1-M1-D2
Method	BLASTX
NCBI GI	g4103959
BLAST score	594
E value	1.0e-61
Match length	116
% identity	60
NCBI Description	(AF030033) calmodulin [Phaseolus vulgaris]

Seq. No.	231385
Seq. ID	LIB3197-027-Q1-M1-D3
Method	BLASTX
NCBI GI	g2369714
BLAST score	468
E value	6.0e-47
Match length	101
% identity	91
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	231386
Seq. ID	LIB3197-027-Q1-M1-D4
Method	BLASTX
NCBI GI	g3660467
BLAST score	396
E value	2.0e-38
Match length	134
% identity	64
NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]

Seq. No.	231387
Seq. ID	LIB3197-027-Q1-M1-D5
Method	BLASTX
NCBI GI	g832876

BLAST score	579
E value	6.0e-60
Match length	128
% identity	88
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	231388
Seq. ID	LIB3197-027-Q1-M1-D7
Method	BLASTX
NCBI GI	g267069
BLAST score	509
E value	7.0e-52
Match length	94
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231389
Seq. ID	LIB3197-027-Q1-M1-D8
Method	BLASTX
NCBI GI	g1399273
BLAST score	329
E value	1.0e-30
Match length	138
% identity	52
NCBI Description	(U31834) calmodulin-domain protein kinase CDPK isoform 5 [Arabidopsis thaliana] >gi_3080419_emb_CAA18738_ (AL022604) calmodulin-domain protein kinase CDPK isoform 5 (CPK5) [Arabidopsis thaliana]

Seq. No.	231390
Seq. ID	LIB3197-027-Q1-M1-D9
Method	BLASTX
NCBI GI	g1174592
BLAST score	670
E value	1.0e-70
Match length	133
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	231391
Seq. ID	LIB3197-027-Q1-M1-E1
Method	BLASTX
NCBI GI	g2996012
BLAST score	267
E value	6.0e-33
Match length	103
% identity	71
NCBI Description	(AF054455) cytosolic phosphoglucose isomerase; PgiC [Leavenworthia crassa]

Seq. No.	231392
Seq. ID	LIB3197-027-Q1-M1-E10
Method	BLASTX
NCBI GI	g3738324
BLAST score	256
E value	4.0e-22
Match length	99
% identity	48
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	231393
Seq. ID	LIB3197-027-Q1-M1-E4
Method	BLASTX
NCBI GI	g3158376
BLAST score	488
E value	3.0e-49
Match length	131
% identity	75
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	231394
Seq. ID	LIB3197-027-Q1-M1-E6
Method	BLASTX
NCBI GI	g3337356
BLAST score	593
E value	1.0e-61
Match length	119
% identity	97
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	231395
Seq. ID	LIB3197-027-Q1-M1-E8
Method	BLASTX
NCBI GI	g3834321
BLAST score	652
E value	2.0e-68
Match length	136
% identity	91
NCBI Description	(AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	231396
Seq. ID	LIB3197-027-Q1-M1-F10
Method	BLASTX
NCBI GI	g4559358
BLAST score	171
E value	4.0e-12
Match length	52
% identity	56
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	231397
Seq. ID	LIB3197-027-Q1-M1-F11

Method	BLASTX
NCBI GI	g1931639
BLAST score	234
E value	9.0e-20
Match length	126
% identity	39
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	231398
Seq. ID	LIB3197-027-Q1-M1-F3
Method	BLASTX
NCBI GI	g4008441
BLAST score	334
E value	2.0e-36
Match length	131
% identity	63
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	231399
Seq. ID	LIB3197-027-Q1-M1-F4
Method	BLASTX
NCBI GI	g3402679
BLAST score	710
E value	3.0e-75
Match length	150
% identity	87
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	231400
Seq. ID	LIB3197-027-Q1-M1-F8
Method	BLASTX
NCBI GI	g3097321
BLAST score	226
E value	1.0e-18
Match length	116
% identity	41
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	231401
Seq. ID	LIB3197-027-Q1-M1-F9
Method	BLASTX
NCBI GI	g1706403
BLAST score	338
E value	9.0e-32
Match length	69
% identity	94
NCBI Description	GLUTAMATE DEHYDROGENASE (GDH) >gi_1085815_pir__S54797 glutamate dehydrogenase (EC 1.4.1.2) - Vitis vinifera >gi_806595_emb_CAA60507_ (X86924) glutamate dehydrogenase [Vitis vinifera]

Seq. No.	231402
Seq. ID	LIB3197-027-Q1-M1-G1
Method	BLASTX

NCBI GI	g2500399
BLAST score	283
E value	3.0e-29
Match length	87
% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098) ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls, embryos, Peptide, 253 aa] [Ambystoma mexicanum]

Seq. No.	231403
Seq. ID	LIB3197-027-Q1-M1-G10
Method	BLASTX
NCBI GI	g2119353
BLAST score	197
E value	5.0e-27
Match length	125
% identity	28
NCBI Description	calmodulin - moss (Physcomitrella patens)

Seq. No.	231404
Seq. ID	LIB3197-027-Q1-M1-G12
Method	BLASTX
NCBI GI	g3169287
BLAST score	711
E value	2.0e-75
Match length	135
% identity	100
NCBI Description	(AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	231405
Seq. ID	LIB3197-027-Q1-M1-G4
Method	BLASTX
NCBI GI	g267082
BLAST score	513
E value	3.0e-52
Match length	100
% identity	93
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	231406
Seq. ID	LIB3197-027-Q1-M1-G5
Method	BLASTX
NCBI GI	g2344894
BLAST score	415
E value	8.0e-41
Match length	125
% identity	64
NCBI Description	(AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231407
Seq. ID	LIB3197-027-Q1-M1-G7
Method	BLASTX
NCBI GI	g3202000
BLAST score	638

E value	6.0e-67
Match length	128
% identity	97
NCBI Description	(AF068846) scaffold attachment factor A [Homo sapiens]

Seq. No.	231408
Seq. ID	LIB3197-027-Q1-M1-G8
Method	BLASTX
NCBI GI	g1170949
BLAST score	484
E value	7.0e-49
Match length	130
% identity	68
NCBI Description	SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir__S38327 protein kinase - Arabidopsis thaliana >gi_166811 (L07249) protein kinase [Arabidopsis thaliana]

Seq. No.	231409
Seq. ID	LIB3197-027-Q1-M1-G9
Method	BLASTX
NCBI GI	g3334661
BLAST score	290
E value	4.0e-26
Match length	91
% identity	58
NCBI Description	(Y10490) putative cytochrome P450 [Glycine max]

Seq. No.	231410
Seq. ID	LIB3197-027-Q1-M1-H1
Method	BLASTX
NCBI GI	g2130017
BLAST score	214
E value	3.0e-17
Match length	63
% identity	63
NCBI Description	hypothetical protein - common sunflower >gi_1040729_emb_CAA60621_ (X87143) cytochrome b5 containing fusion protein [Helianthus annuus]

Seq. No.	231411
Seq. ID	LIB3197-027-Q1-M1-H2
Method	BLASTX
NCBI GI	g267069
BLAST score	383
E value	3.0e-67
Match length	128
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231412
Seq. ID	LIB3197-027-Q1-M1-H3
Method	BLASTX
NCBI GI	g267069
BLAST score	670

E value	1.0e-70
Match length	127
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231413
Seq. ID	LIB3197-027-Q1-M1-H5
Method	BLASTX
NCBI GI	g2501555
BLAST score	482
E value	1.0e-48
Match length	120
% identity	71
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	231414
Seq. ID	LIB3197-027-Q1-M1-H6
Method	BLASTX
NCBI GI	g3342798
BLAST score	175
E value	1.0e-12
Match length	71
% identity	52
NCBI Description	(AF061240) glutamine cyclotransferase precursor [Carica papaya]

Seq. No.	231415
Seq. ID	LIB3197-027-Q1-M1-H7
Method	BLASTX
NCBI GI	g2130017
BLAST score	384
E value	4.0e-37
Match length	112
% identity	62
NCBI Description	hypothetical protein - common sunflower >gi_1040729_emb_CAA60621_ (X87143) cytochrome b5 containing fusion protein [Helianthus annuus]

Seq. No.	231416
Seq. ID	LIB3197-027-Q1-M1-H8
Method	BLASTX
NCBI GI	g3860277
BLAST score	400
E value	2.0e-45
Match length	123
% identity	78
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	231417
Seq. ID	LIB3197-027-Q1-M1-H9
Method	BLASTX

NCBI GI	g3157943
BLAST score	381
E value	8.0e-37
Match length	117
% identity	60
NCBI Description	(AC002131) Contains similarity to BAP31 protein gb_X81816 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	231418
Seq. ID	LIB3197-028-Q1-M1-A10
Method	BLASTX
NCBI GI	g4544399
BLAST score	537
E value	5.0e-55
Match length	147
% identity	69
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	231419
Seq. ID	LIB3197-028-Q1-M1-A12
Method	BLASTX
NCBI GI	g464846
BLAST score	405
E value	1.0e-39
Match length	83
% identity	89
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	231420
Seq. ID	LIB3197-028-Q1-M1-A6
Method	BLASTX
NCBI GI	g2996012
BLAST score	525
E value	1.0e-53
Match length	128
% identity	77
NCBI Description	(AF054455) cytosolic phosphoglucose isomerase; PgiC [Leavenworthia crassa]

Seq. No.	231421
Seq. ID	LIB3197-028-Q1-M1-A8
Method	BLASTX
NCBI GI	g135406
BLAST score	396
E value	8.0e-39
Match length	76
% identity	93
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	231422
Seq. ID	LIB3197-028-Q1-M1-B10

Method	BLASTX
NCBI GI	g2062167
BLAST score	462
E value	3.0e-46
Match length	99
% identity	87
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	231423
Seq. ID	LIB3197-028-Q1-M1-B11
Method	BLASTX
NCBI GI	g4417289
BLAST score	149
E value	1.0e-09
Match length	84
% identity	54
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	231424
Seq. ID	LIB3197-028-Q1-M1-B2
Method	BLASTX
NCBI GI	g135406
BLAST score	174
E value	2.0e-12
Match length	72
% identity	49
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	231425
Seq. ID	LIB3197-028-Q1-M1-B6
Method	BLASTX
NCBI GI	g3892051
BLAST score	161
E value	3.0e-11
Match length	87
% identity	44
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	231426
Seq. ID	LIB3197-028-Q1-M1-C12
Method	BLASTX
NCBI GI	g312179
BLAST score	524
E value	2.0e-53
Match length	105
% identity	93
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	231427
Seq. ID	LIB3197-028-Q1-M1-C2
Method	BLASTX
NCBI GI	g2511529
BLAST score	305
E value	5.0e-28
Match length	78
% identity	77
NCBI Description	(AF002697) E1B 19K/Bcl-2-binding protein Nip3 [Homo sapiens]

Seq. No.	231428
Seq. ID	LIB3197-028-Q1-M1-C3
Method	BLASTX
NCBI GI	g3915826
BLAST score	399
E value	5.0e-39
Match length	99
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	231429
Seq. ID	LIB3197-028-Q1-M1-C5
Method	BLASTX
NCBI GI	g2119278
BLAST score	630
E value	6.0e-66
Match length	120
% identity	95
NCBI Description	tubulin beta-1 chain - rice

Seq. No.	231430
Seq. ID	LIB3197-028-Q1-M1-C7
Method	BLASTX
NCBI GI	g730917
BLAST score	239
E value	2.0e-20
Match length	93
% identity	56
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_626947_pir__S48232 TCP1 complex beta chain - yeast (Saccharomyces cerevisiae) >gi_454887_emb_CAA54745_ (X77675) TCP1-related chaperonin [Saccharomyces cerevisiae] >gi_557781_emb_CAA86136_ (Z38059) tcp1beta, len: 527, CAI: 0.19, chaperone protein [Saccharomyces cerevisiae] >gi_571510 (U16761) Bin3p [Saccharomyces cerevisiae]

Seq. No.	231431
Seq. ID	LIB3197-028-Q1-M1-D10
Method	BLASTX
NCBI GI	g2911075
BLAST score	244
E value	9.0e-21
Match length	71
% identity	63
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	231432
Seq. ID	LIB3197-028-Q1-M1-D11
Method	BLASTX
NCBI GI	g135406
BLAST score	590
E value	3.0e-61
Match length	116
% identity	95
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	231433
Seq. ID	LIB3197-028-Q1-M1-D12
Method	BLASTX
NCBI GI	g303750
BLAST score	472
E value	2.0e-47
Match length	91
% identity	100
NCBI Description	(D12548) GTP-binding protein [Pisum sativum] >gi_738940_prf__2001457H GTP-binding protein [Pisum sativum]

Seq. No.	231434
Seq. ID	LIB3197-028-Q1-M1-D2
Method	BLASTX
NCBI GI	g113621
BLAST score	265
E value	1.0e-23
Match length	63
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays]

Seq. No.	231435
Seq. ID	LIB3197-028-Q1-M1-D4
Method	BLASTX
NCBI GI	g2982311
BLAST score	631
E value	5.0e-66
Match length	128
% identity	88
NCBI Description	(AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No.	231436
Seq. ID	LIB3197-028-Q1-M1-D5
Method	BLASTX
NCBI GI	g1332411
BLAST score	497
E value	2.0e-50

Match length	114
% identity	81
NCBI Description	(D85102) dihydroflavonol 4-reductase [Rosa hybrida]

Seq. No.	231437
Seq. ID	LIB3197-028-Q1-M1-D7
Method	BLASTX
NCBI GI	g3152582
BLAST score	270
E value	8.0e-24
Match length	73
% identity	66
NCBI Description	(AC002986) YUP8H12R.20 [Arabidopsis thaliana]

Seq. No.	231438
Seq. ID	LIB3197-028-Q1-M1-D9
Method	BLASTX
NCBI GI	g3128176
BLAST score	262
E value	7.0e-23
Match length	87
% identity	54
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	231439
Seq. ID	LIB3197-028-Q1-M1-E1
Method	BLASTX
NCBI GI	g2253010
BLAST score	577
E value	8.0e-60
Match length	122
% identity	89
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	231440
Seq. ID	LIB3197-028-Q1-M1-E10
Method	BLASTX
NCBI GI	g3776084
BLAST score	272
E value	6.0e-24
Match length	85
% identity	59
NCBI Description	(Y18251) NtN2 [Medicago truncatula]

Seq. No.	231441
Seq. ID	LIB3197-028-Q1-M1-E11
Method	BLASTX
NCBI GI	g2651308
BLAST score	340
E value	6.0e-32
Match length	117
% identity	67
NCBI Description	(AC002336) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	231442

Seq. ID	LIB3197-028-Q1-M1-E4
Method	BLASTX
NCBI GI	g2129473
BLAST score	247
E value	5.0e-21
Match length	91
% identity	51
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	231443
Seq. ID	LIB3197-028-Q1-M1-E5
Method	BLASTX
NCBI GI	g4033424
BLAST score	433
E value	8.0e-43
Match length	99
% identity	82
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No.	231444
Seq. ID	LIB3197-028-Q1-M1-E9
Method	BLASTX
NCBI GI	g2342735
BLAST score	233
E value	2.0e-19
Match length	52
% identity	87
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	231445
Seq. ID	LIB3197-028-Q1-M1-F10
Method	BLASTX
NCBI GI	g82040
BLAST score	744
E value	3.0e-79
Match length	149
% identity	28
NCBI Description	ubiquitin precursor - flax (fragment) >gi_168304 (M57895) ubiquitin [Linum usitatissimum]

Seq. No.	231446
Seq. ID	LIB3197-028-Q1-M1-F12
Method	BLASTX
NCBI GI	g2970051
BLAST score	441
E value	9.0e-44
Match length	109
% identity	77
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	231447
Seq. ID	LIB3197-028-Q1-M1-F2
Method	BLASTX
NCBI GI	g3420239

BLAST score	207
E value	1.0e-20
Match length	68
% identity	84
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	231448
Seq. ID	LIB3197-028-Q1-M1-F3
Method	BLASTX
NCBI GI	g232024
BLAST score	744
E value	2.0e-79
Match length	139
% identity	100
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	231449
Seq. ID	LIB3197-028-Q1-M1-F4
Method	BLASTX
NCBI GI	g3098571
BLAST score	232
E value	3.0e-19
Match length	134
% identity	37
NCBI Description	(AF049028) BURP domain containing protein [Brassica napus]

Seq. No.	231450
Seq. ID	LIB3197-028-Q1-M1-F5
Method	BLASTX
NCBI GI	g2827550
BLAST score	193
E value	1.0e-14
Match length	57
% identity	65
NCBI Description	(AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	231451
Seq. ID	LIB3197-028-Q1-M1-F8
Method	BLASTX
NCBI GI	g2464905
BLAST score	275
E value	2.0e-24
Match length	110
% identity	54
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	231452
Seq. ID	LIB3197-028-Q1-M1-F9
Method	BLASTX
NCBI GI	g1009232
BLAST score	162
E value	4.0e-11

Match length	66
% identity	58
NCBI Description	(L38828) EF-1-alpha-related GTP-binding protein [Nicotiana tabacum]

Seq. No.	231453
Seq. ID	LIB3197-028-Q1-M1-G10
Method	BLASTX
NCBI GI	g1256509
BLAST score	511
E value	5.0e-52
Match length	106
% identity	84
NCBI Description	(X92943) pectate lyase [Musa acuminata]

Seq. No.	231454
Seq. ID	LIB3197-028-Q1-M1-G11
Method	BLASTX
NCBI GI	g2811278
BLAST score	576
E value	6.0e-64
Match length	135
% identity	88
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231455
Seq. ID	LIB3197-028-Q1-M1-G12
Method	BLASTX
NCBI GI	g728938
BLAST score	692
E value	3.0e-73
Match length	148
% identity	91
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472) inorganic pyrophosphatse ase' [Hordeum vulgare]

Seq. No.	231456
Seq. ID	LIB3197-028-Q1-M1-G2
Method	BLASTX
NCBI GI	g1449179
BLAST score	161
E value	5.0e-11
Match length	54
% identity	54
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	231457
Seq. ID	LIB3197-028-Q1-M1-G3
Method	BLASTX
NCBI GI	g1041706
BLAST score	524
E value	2.0e-53
Match length	111

% identity	84
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	231458
Seq. ID	LIB3197-028-Q1-M1-G5
Method	BLASTX
NCBI GI	g2935298
BLAST score	400
E value	6.0e-39
Match length	123
% identity	66
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	231459
Seq. ID	LIB3197-028-Q1-M1-G6
Method	BLASTX
NCBI GI	g4545231
BLAST score	514
E value	2.0e-52
Match length	101
% identity	99
NCBI Description	(AF116243) RAS-related GTP-binding protein [Gossypium hirsutum]

Seq. No.	231460
Seq. ID	LIB3197-028-Q1-M1-G7
Method	BLASTX
NCBI GI	g2811278
BLAST score	548
E value	3.0e-56
Match length	135
% identity	76
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231461
Seq. ID	LIB3197-028-Q1-M1-G8
Method	BLASTX
NCBI GI	g1361974
BLAST score	453
E value	3.0e-45
Match length	145
% identity	59
NCBI Description	cysteine proteinase - clove pink (fragment) >gi_595986 (U17135) cysteine proteinase [Dianthus caryophyllus]

Seq. No.	231462
Seq. ID	LIB3197-028-Q1-M1-H1
Method	BLASTX
NCBI GI	g3885328
BLAST score	391
E value	5.0e-41
Match length	104
% identity	83
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	231463
Seq. ID	LIB3197-028-Q1-M1-H4
Method	BLASTX
NCBI GI	g120673
BLAST score	626
E value	2.0e-65
Match length	146
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

Seq. No.	231464
Seq. ID	LIB3197-029-Q1-M1-A1
Method	BLASTX
NCBI GI	g4580455
BLAST score	415
E value	7.0e-41
Match length	113
% identity	75
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	231465
Seq. ID	LIB3197-029-Q1-M1-A10
Method	BLASTX
NCBI GI	g4056488
BLAST score	189
E value	6.0e-21
Match length	67
% identity	76
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	231466
Seq. ID	LIB3197-029-Q1-M1-A11
Method	BLASTX
NCBI GI	g872116
BLAST score	422
E value	1.0e-41
Match length	103
% identity	80
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	231467
Seq. ID	LIB3197-029-Q1-M1-A2
Method	BLASTX
NCBI GI	g464849
BLAST score	600
E value	2.0e-62
Match length	129
% identity	92
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	231468

Seq. ID	LIB3197-029-Q1-M1-A3
Method	BLASTX
NCBI GI	g3915031
BLAST score	177
E value	2.0e-16
Match length	69
% identity	74
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	231469
Seq. ID	LIB3197-029-Q1-M1-A5
Method	BLASTX
NCBI GI	g1771162
BLAST score	180
E value	2.0e-13
Match length	86
% identity	49
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	231470
Seq. ID	LIB3197-029-Q1-M1-A6
Method	BLASTX
NCBI GI	g3858935
BLAST score	567
E value	1.0e-58
Match length	128
% identity	83
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	231471
Seq. ID	LIB3197-029-Q1-M1-A7
Method	BLASTX
NCBI GI	g2129499
BLAST score	663
E value	5.0e-70
Match length	133
% identity	92
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	231472
Seq. ID	LIB3197-029-Q1-M1-B1
Method	BLASTX
NCBI GI	g3426037
BLAST score	598
E value	3.0e-62
Match length	137
% identity	52
NCBI Description	(AC005168) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No.	231473
Seq. ID	LIB3197-029-Q1-M1-B12
Method	BLASTX
NCBI GI	g2252842
BLAST score	164
E value	2.0e-11
Match length	93
% identity	44
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	231474
Seq. ID	LIB3197-029-Q1-M1-B2
Method	BLASTX
NCBI GI	g3914403
BLAST score	307
E value	3.0e-28
Match length	113
% identity	58
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II) >gi_2370335_emb_CAA73866_ (Y13466) protoporphyrinogen oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_ (AB020500) mitochondrial protoporphyrinogen oxidase [Nicotiana tabacum] >gi_4105188 (AF044129) protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]

Seq. No.	231475
Seq. ID	LIB3197-029-Q1-M1-B4
Method	BLASTX
NCBI GI	g3377797
BLAST score	501
E value	7.0e-51
Match length	125
% identity	78
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	231476
Seq. ID	LIB3197-029-Q1-M1-B5
Method	BLASTX
NCBI GI	g2062167
BLAST score	313
E value	5.0e-29
Match length	64
% identity	88
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	231477
Seq. ID	LIB3197-029-Q1-M1-B6
Method	BLASTX
NCBI GI	g3142301

BLAST score	217
E value	1.0e-17
Match length	113
% identity	49
NCBI Description	(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630

Seq. No.	231478
Seq. ID	LIB3197-029-Q1-M1-C1
Method	BLASTX
NCBI GI	g4128197
BLAST score	155
E value	2.0e-10
Match length	52
% identity	60
NCBI Description	(U75273) acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No.	231479
Seq. ID	LIB3197-029-Q1-M1-C10
Method	BLASTX
NCBI GI	g1169534
BLAST score	593
E value	9.0e-62
Match length	122
% identity	94
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus communis]

Seq. No.	231480
Seq. ID	LIB3197-029-Q1-M1-C11
Method	BLASTX
NCBI GI	g1173256
BLAST score	637
E value	9.0e-67
Match length	123
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	231481
Seq. ID	LIB3197-029-Q1-M1-C12
Method	BLASTX
NCBI GI	g2499611
BLAST score	450
E value	8.0e-45
Match length	90
% identity	93
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein

kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
>gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis thaliana]

Seq. No.	231482
Seq. ID	LIB3197-029-Q1-M1-C4
Method	BLASTX
NCBI GI	g3421087
BLAST score	544
E value	6.0e-56
Match length	110
% identity	97
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	231483
Seq. ID	LIB3197-029-Q1-M1-C5
Method	BLASTX
NCBI GI	g2414624
BLAST score	265
E value	4.0e-23
Match length	96
% identity	51
NCBI Description	(Z99259) ATP synthase subunit [Schizosaccharomyces pombe]

Seq. No.	231484
Seq. ID	LIB3197-029-Q1-M1-C7
Method	BLASTX
NCBI GI	g3337350
BLAST score	480
E value	1.0e-48
Match length	104
% identity	92
NCBI Description	(AC004481) putative permease [Arabidopsis thaliana]

Seq. No.	231485
Seq. ID	LIB3197-029-Q1-M1-D1
Method	BLASTX
NCBI GI	g1707020
BLAST score	207
E value	1.0e-16
Match length	89
% identity	28
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231486
Seq. ID	LIB3197-029-Q1-M1-D11
Method	BLASTX
NCBI GI	g3860263
BLAST score	237
E value	6.0e-20
Match length	62
% identity	65
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No. 231487

Seq. ID	LIB3197-029-Q1-M1-D2
Method	BLASTX
NCBI GI	g2497543
BLAST score	163
E value	2.0e-11
Match length	39
% identity	77
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	231488
Seq. ID	LIB3197-029-Q1-M1-D3
Method	BLASTX
NCBI GI	g3097321
BLAST score	194
E value	7.0e-15
Match length	84
% identity	45
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	231489
Seq. ID	LIB3197-029-Q1-M1-D4
Method	BLASTX
NCBI GI	g4314378
BLAST score	227
E value	7.0e-19
Match length	96
% identity	46
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	231490
Seq. ID	LIB3197-029-Q1-M1-D6
Method	BLASTX
NCBI GI	g3249081
BLAST score	311
E value	1.0e-28
Match length	121
% identity	18
NCBI Description	(AC004473) Strong similarity to AR0GP2 gene gb_1762634 from Lycopersicon esculentum. [Arabidopsis thaliana]

Seq. No.	231491
Seq. ID	LIB3197-029-Q1-M1-D7
Method	BLASTX
NCBI GI	g2500192
BLAST score	491
E value	9.0e-50
Match length	95
% identity	97
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC3 >gi_1304413 (U43501) Rac-like protein [Arabidopsis thaliana] >gi_2645643 (AF031427) Rho-like GTP binding protein [Arabidopsis thaliana] >gi_2924513_emb_CAA17767.1_ (AL022023) Rho1Ps homolog/ Rac-like protein [Arabidopsis thaliana]

Seq. No. 231492

Seq. ID	LIB3197-029-Q1-M1-E10
Method	BLASTX
NCBI GI	g2244732
BLAST score	551
E value	1.0e-56
Match length	105
% identity	100
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	231493
Seq. ID	LIB3197-029-Q1-M1-E11
Method	BLASTX
NCBI GI	g543905
BLAST score	453
E value	3.0e-45
Match length	110
% identity	81
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	231494
Seq. ID	LIB3197-029-Q1-M1-E12
Method	BLASTX
NCBI GI	g2702269
BLAST score	146
E value	2.0e-09
Match length	34
% identity	79
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231495
Seq. ID	LIB3197-029-Q1-M1-E2
Method	BLASTX
NCBI GI	g3461833
BLAST score	247
E value	3.0e-21
Match length	52
% identity	85
NCBI Description	(AC004138) putative expansin [Arabidopsis thaliana]

Seq. No.	231496
Seq. ID	LIB3197-029-Q1-M1-E4
Method	BLASTX
NCBI GI	g4240385
BLAST score	251
E value	1.0e-21
Match length	96
% identity	50
NCBI Description	(AF061027) omega-3 fatty acid desaturase precursor [Vernicia fordii]

Seq. No.	231497
Seq. ID	LIB3197-029-Q1-M1-E5
Method	BLASTX
NCBI GI	g4006900
BLAST score	429
E value	2.0e-42

Match length 134
% identity 63
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 231498
Seq. ID LIB3197-029-Q1-M1-E6
Method BLASTX
NCBI GI g4406819
BLAST score 209
E value 1.0e-16
Match length 107
% identity 48
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 231499
Seq. ID LIB3197-029-Q1-M1-E7
Method BLASTX
NCBI GI g1708236
BLAST score 145
E value 7.0e-11
Match length 59
% identity 68
NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No. 231500
Seq. ID LIB3197-029-Q1-M1-E8
Method BLASTX
NCBI GI g2497366
BLAST score 275
E value 3.0e-24
Match length 109
% identity 51
NCBI Description INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 >gi_2137851_pir__I49127 unknown intracellular protein - mouse >gi_558903 (U15635) unknown intracellular protein [Mus musculus]

Seq. No. 231501
Seq. ID LIB3197-029-Q1-M1-F10
Method BLASTX
NCBI GI g1465770
BLAST score 146
E value 4.0e-09
Match length 129
% identity 34
NCBI Description (U61233) cofactor D [Bos taurus]

Seq. No. 231502
Seq. ID LIB3197-029-Q1-M1-F12
Method BLASTX

NCBI GI	g2464905
BLAST score	195
E value	5.0e-15
Match length	85
% identity	51
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	231503
Seq. ID	LIB3197-029-Q1-M1-F4
Method	BLASTX
NCBI GI	g2052383
BLAST score	581
E value	4.0e-60
Match length	121
% identity	86
NCBI Description	(U66345) calreticulin [Arabidopsis thaliana]

Seq. No.	231504
Seq. ID	LIB3197-029-Q1-M1-F5
Method	BLASTX
NCBI GI	g1352664
BLAST score	483
E value	1.0e-48
Match length	97
% identity	93
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

Seq. No.	231505
Seq. ID	LIB3197-029-Q1-M1-F6
Method	BLASTX
NCBI GI	g4544443
BLAST score	417
E value	4.0e-41
Match length	113
% identity	43
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	231506
Seq. ID	LIB3197-029-Q1-M1-F7
Method	BLASTX
NCBI GI	g3337352
BLAST score	413
E value	1.0e-40
Match length	102
% identity	81
NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	231507
Seq. ID	LIB3197-029-Q1-M1-F9

Method	BLASTX
NCBI GI	g4128133
BLAST score	240
E value	3.0e-20
Match length	106
% identity	46
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	231508
Seq. ID	LIB3197-029-Q1-M1-G10
Method	BLASTX
NCBI GI	g3341681
BLAST score	448
E value	1.0e-44
Match length	90
% identity	99
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi_741994_prf__2008312A GTP-binding protein [Arabidopsis thaliana]

Seq. No.	231509
Seq. ID	LIB3197-029-Q1-M1-G11
Method	BLASTX
NCBI GI	g2384758
BLAST score	478
E value	4.0e-48
Match length	96
% identity	94
NCBI Description	(AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No.	231510
Seq. ID	LIB3197-029-Q1-M1-G3
Method	BLASTX
NCBI GI	g2828702
BLAST score	748
E value	1.0e-79
Match length	144
% identity	99
NCBI Description	(AF044414) alpha mannosidase 6A8B [Homo sapiens]

Seq. No.	231511
Seq. ID	LIB3197-029-Q1-M1-G4
Method	BLASTX
NCBI GI	g3548818
BLAST score	252
E value	1.0e-21
Match length	86
% identity	58
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	231512
Seq. ID	LIB3197-029-Q1-M1-G5
Method	BLASTX
NCBI GI	g3721864
BLAST score	176
E value	9.0e-13

Match length 124
% identity 37
NCBI Description (AB016068) Hs Ste24p [Homo sapiens]

Seq. No. 231513
Seq. ID LIB3197-029-Q1-M1-G6
Method BLASTX
NCBI GI g1644427
BLAST score 226
E value 1.0e-18
Match length 45
% identity 89
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 231514
Seq. ID LIB3197-029-Q1-M1-G7
Method BLASTX
NCBI GI g1737490
BLAST score 265
E value 3.0e-23
Match length 109
% identity 46
NCBI Description (U81006) p76 [Homo sapiens]

Seq. No. 231515
Seq. ID LIB3197-029-Q1-M1-G8
Method BLASTX
NCBI GI g3548805
BLAST score 273
E value 4.0e-24
Match length 111
% identity 50
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 231516
Seq. ID LIB3197-029-Q1-M1-G9
Method BLASTX
NCBI GI g1009712
BLAST score 614
E value 4.0e-64
Match length 131
% identity 86
NCBI Description (U27698) calreticulin [Arabidopsis thaliana]

Seq. No. 231517
Seq. ID LIB3197-029-Q1-M1-H1
Method BLASTX
NCBI GI g1706318
BLAST score 303
E value 1.0e-27
Match length 80
% identity 71
NCBI Description GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
>gi_1362098_pir__S56177 probable glutamate decarboxylase -
tomato >gi_995555_emb_CAA56812_ (X80840) homology to
pyroxidal-5'-phosphate-dependant glutamate decarboxylases;
putative start codon [Lycopersicon esculentum]

Seq. No.	231518
Seq. ID	LIB3197-029-Q1-M1-H10
Method	BLASTX
NCBI GI	g2431769
BLAST score	234
E value	1.0e-19
Match length	57
% identity	81
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	231519
Seq. ID	LIB3197-029-Q1-M1-H12
Method	BLASTX
NCBI GI	g1408471
BLAST score	515
E value	2.0e-52
Match length	132
% identity	76
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	231520
Seq. ID	LIB3197-029-Q1-M1-H4
Method	BLASTX
NCBI GI	g1351030
BLAST score	574
E value	2.0e-59
Match length	138
% identity	84
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_289365 (M35599) 60-kDa chaperonin-60 alpha-polypeptide precursor [Brassica napus]

Seq. No.	231521
Seq. ID	LIB3197-029-Q1-M1-H5
Method	BLASTX
NCBI GI	g267069
BLAST score	487
E value	3.0e-49
Match length	89
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231522
Seq. ID	LIB3197-029-Q1-M1-H6
Method	BLASTX
NCBI GI	g2511574
BLAST score	431
E value	9.0e-43
Match length	91
% identity	97

NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]
Seq. No.	231523
Seq. ID	LIB3197-029-Q1-M1-H7
Method	BLASTX
NCBI GI	g2129499
BLAST score	603
E value	7.0e-63
Match length	120
% identity	92
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	231524
Seq. ID	LIB3197-029-Q1-M1-H9
Method	BLASTX
NCBI GI	g1486472
BLAST score	441
E value	8.0e-44
Match length	101
% identity	84
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]
Seq. No.	231525
Seq. ID	LIB3197-030-Q1-M1-A10
Method	BLASTX
NCBI GI	g1778370
BLAST score	624
E value	3.0e-65
Match length	127
% identity	93
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]
Seq. No.	231526
Seq. ID	LIB3197-030-Q1-M1-A11
Method	BLASTX
NCBI GI	g2613143
BLAST score	189
E value	4.0e-16
Match length	79
% identity	55
NCBI Description	(AF030548) tubulin [Oryza sativa]
Seq. No.	231527
Seq. ID	LIB3197-030-Q1-M1-A12
Method	BLASTX
NCBI GI	g2651303
BLAST score	623
E value	4.0e-65
Match length	137
% identity	87
NCBI Description	(AC002336) putative potassium transporter [Arabidopsis thaliana]

Seq. No.	231528
Seq. ID	LIB3197-030-Q1-M1-A3
Method	BLASTX
NCBI GI	g3925363
BLAST score	431
E value	9.0e-43
Match length	112
% identity	68
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	231529
Seq. ID	LIB3197-030-Q1-M1-A4
Method	BLASTX
NCBI GI	g4558556
BLAST score	307
E value	4.0e-28
Match length	126
% identity	49
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	231530
Seq. ID	LIB3197-030-Q1-M1-A8
Method	BLASTX
NCBI GI	g4138722
BLAST score	239
E value	3.0e-20
Match length	81
% identity	62
NCBI Description	(Y09590) hexose transporter [Vitis vinifera]

Seq. No.	231531
Seq. ID	LIB3197-030-Q1-M1-A9
Method	BLASTX
NCBI GI	g120669
BLAST score	457
E value	1.0e-45
Match length	91
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231532
Seq. ID	LIB3197-030-Q1-M1-B1
Method	BLASTX
NCBI GI	g1587206
BLAST score	153
E value	1.0e-10
Match length	39
% identity	77
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	231533
Seq. ID	LIB3197-030-Q1-M1-B10

Method	BLASTX
NCBI GI	g2864624
BLAST score	335
E value	2.0e-31
Match length	137
% identity	53
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	231534
Seq. ID	LIB3197-030-Q1-M1-B2
Method	BLASTX
NCBI GI	g1587206
BLAST score	421
E value	2.0e-41
Match length	110
% identity	79
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	231535
Seq. ID	LIB3197-030-Q1-M1-B3
Method	BLASTX
NCBI GI	g1350956
BLAST score	490
E value	1.0e-49
Match length	105
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	231536
Seq. ID	LIB3197-030-Q1-M1-B5
Method	BLASTX
NCBI GI	g3097321
BLAST score	203
E value	7.0e-16
Match length	109
% identity	39
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	231537
Seq. ID	LIB3197-030-Q1-M1-B6
Method	BLASTX
NCBI GI	g3123271
BLAST score	164
E value	7.0e-12
Match length	31
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	231538
Seq. ID	LIB3197-030-Q1-M1-B8
Method	BLASTX
NCBI GI	g3421109
BLAST score	457
E value	1.0e-45
Match length	96
% identity	95

NCBI Description	(AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]
Seq. No.	231539
Seq. ID	LIB3197-030-Q1-M1-C1
Method	BLASTX
NCBI GI	g2811278
BLAST score	542
E value	1.0e-55
Match length	131
% identity	76
NCBI Description	(AF043284) expansin [Gossypium hirsutum]
Seq. No.	231540
Seq. ID	LIB3197-030-Q1-M1-C11
Method	BLASTX
NCBI GI	g2811278
BLAST score	753
E value	2.0e-80
Match length	139
% identity	97
NCBI Description	(AF043284) expansin [Gossypium hirsutum]
Seq. No.	231541
Seq. ID	LIB3197-030-Q1-M1-C6
Method	BLASTX
NCBI GI	g2498565
BLAST score	175
E value	1.0e-12
Match length	94
% identity	37
NCBI Description	C-MYC BINDING PROTEIN MM-1 >gi_1731809_dbj_BAA14006_ (D89667) c-myc binding protein [Homo sapiens] >gi_4505743_ref_NP_002615.1_pPFDN5_ prefoldin
Seq. No.	231542
Seq. ID	LIB3197-030-Q1-M1-C7
Method	BLASTX
NCBI GI	g3176690
BLAST score	169
E value	3.0e-12
Match length	91
% identity	46
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]
Seq. No.	231543
Seq. ID	LIB3197-030-Q1-M1-C8
Method	BLASTX
NCBI GI	g3334115
BLAST score	715
E value	6.0e-76
Match length	137
% identity	43
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664

(AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	231544
Seq. ID	LIB3197-030-Q1-M1-C9
Method	BLASTX
NCBI GI	g2811278
BLAST score	637
E value	9.0e-67
Match length	129
% identity	89
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231545
Seq. ID	LIB3197-030-Q1-M1-D10
Method	BLASTX
NCBI GI	g2245136
BLAST score	476
E value	6.0e-48
Match length	135
% identity	67
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	231546
Seq. ID	LIB3197-030-Q1-M1-D11
Method	BLASTX
NCBI GI	g4249386
BLAST score	280
E value	6.0e-25
Match length	106
% identity	58
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	231547
Seq. ID	LIB3197-030-Q1-M1-D5
Method	BLASTX
NCBI GI	g3080450
BLAST score	363
E value	1.0e-34
Match length	109
% identity	60
NCBI Description	(AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231548
Seq. ID	LIB3197-030-Q1-M1-D6
Method	BLASTX
NCBI GI	g4454012
BLAST score	175
E value	1.0e-12
Match length	49
% identity	65
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	231549
Seq. ID	LIB3197-030-Q1-M1-E10
Method	BLASTX
NCBI GI	g461987
BLAST score	638
E value	6.0e-67
Match length	133
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82042_pir__JS0719 translation elongation factor eEF-1 alpha chain - carrot >gi_217913_dbj_BAA02205_ (D12709) elongation factor 1-alpha [Daucus carota]

Seq. No.	231550
Seq. ID	LIB3197-030-Q1-M1-E11
Method	BLASTX
NCBI GI	g4510430
BLAST score	514
E value	2.0e-52
Match length	106
% identity	87
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	231551
Seq. ID	LIB3197-030-Q1-M1-E4
Method	BLASTX
NCBI GI	g3522945
BLAST score	242
E value	2.0e-20
Match length	117
% identity	41
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	231552
Seq. ID	LIB3197-030-Q1-M1-E5
Method	BLASTX
NCBI GI	g2129929
BLAST score	660
E value	2.0e-69
Match length	132
% identity	96
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 - tomato >gi_1049068 (U28403) RNA polymerase II subunit 2 [Solanum lycopersicum]

Seq. No.	231553
Seq. ID	LIB3197-030-Q1-M1-E6
Method	BLASTX
NCBI GI	g2062167
BLAST score	469
E value	4.0e-47
Match length	101
% identity	87
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	231554
Seq. ID	LIB3197-030-Q1-M1-F11
Method	BLASTX
NCBI GI	g1174592
BLAST score	598
E value	3.0e-62
Match length	111
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	231555
Seq. ID	LIB3197-030-Q1-M1-F12
Method	BLASTX
NCBI GI	g549063
BLAST score	357
E value	6.0e-34
Match length	110
% identity	65
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	231556
Seq. ID	LIB3197-030-Q1-M1-F5
Method	BLASTX
NCBI GI	g1174592
BLAST score	557
E value	2.0e-57
Match length	109
% identity	94
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	231557
Seq. ID	LIB3197-030-Q1-M1-G10
Method	BLASTX
NCBI GI	g267069
BLAST score	520
E value	4.0e-53
Match length	96
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231558
Seq. ID	LIB3197-030-Q1-M1-G11
Method	BLASTX
NCBI GI	g2811278
BLAST score	523
E value	2.0e-53
Match length	128

% identity	76
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231559
Seq. ID	LIB3197-030-Q1-M1-G4
Method	BLASTX
NCBI GI	g1174470
BLAST score	348
E value	7.0e-33
Match length	128
% identity	52
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	231560
Seq. ID	LIB3197-030-Q1-M1-G6
Method	BLASTX
NCBI GI	g1332579
BLAST score	550
E value	1.0e-56
Match length	112
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	231561
Seq. ID	LIB3197-030-Q1-M1-H10
Method	BLASTX
NCBI GI	g2146797
BLAST score	353
E value	3.0e-39
Match length	114
% identity	49
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	231562
Seq. ID	LIB3197-030-Q1-M1-H5
Method	BLASTX
NCBI GI	g2088654
BLAST score	398
E value	9.0e-39
Match length	120
% identity	71
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	231563
Seq. ID	LIB3197-031-Q1-M1-A5
Method	BLASTX
NCBI GI	g2132184
BLAST score	173
E value	2.0e-12
Match length	44

% identity	66
NCBI Description	hypothetical protein YPL093w - yeast (Saccharomyces cerevisiae) >gi_1151233 (U43281) Lpg15p [Saccharomyces cerevisiae]
Seq. No.	231564
Seq. ID	LIB3197-031-Q1-M1-A6
Method	BLASTX
NCBI GI	g3927825
BLAST score	239
E value	4.0e-20
Match length	56
% identity	77
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.	231565
Seq. ID	LIB3197-031-Q1-M1-B10
Method	BLASTX
NCBI GI	g4007792
BLAST score	251
E value	2.0e-21
Match length	65
% identity	72
NCBI Description	(AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]
Seq. No.	231566
Seq. ID	LIB3197-031-Q1-M1-B11
Method	BLASTX
NCBI GI	g4165018
BLAST score	364
E value	9.0e-35
Match length	134
% identity	54
NCBI Description	(D89053) Acyl-CoA synthetase 3 [Homo sapiens]
Seq. No.	231567
Seq. ID	LIB3197-031-Q1-M1-B4
Method	BLASTX
NCBI GI	g2980793
BLAST score	176
E value	1.0e-12
Match length	57
% identity	56
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	231568
Seq. ID	LIB3197-031-Q1-M1-B6
Method	BLASTX
NCBI GI	g2497753
BLAST score	190
E value	2.0e-14
Match length	49
% identity	63
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein

[Prunus dulcis]

Seq. No.	231569
Seq. ID	LIB3197-031-Q1-M1-C10
Method	BLASTX
NCBI GI	g2062167
BLAST score	402
E value	3.0e-39
Match length	85
% identity	88
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	231570
Seq. ID	LIB3197-031-Q1-M1-C11
Method	BLASTX
NCBI GI	g4098129
BLAST score	707
E value	6.0e-75
Match length	143
% identity	94
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	231571
Seq. ID	LIB3197-031-Q1-M1-C12
Method	BLASTX
NCBI GI	g1495251
BLAST score	466
E value	9.0e-47
Match length	97
% identity	91
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	231572
Seq. ID	LIB3197-031-Q1-M1-C2
Method	BLASTX
NCBI GI	g1899188
BLAST score	187
E value	2.0e-14
Match length	46
% identity	74
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	231573
Seq. ID	LIB3197-031-Q1-M1-C5
Method	BLASTX
NCBI GI	g2911052
BLAST score	563
E value	3.0e-58
Match length	124
% identity	88
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	231574
Seq. ID	LIB3197-031-Q1-M1-C9
Method	BLASTX
NCBI GI	g1730502

BLAST score 179
E value 5.0e-13
Match length 80
% identity 51
NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No. 231575
Seq. ID LIB3197-031-Q1-M1-D10
Method BLASTX
NCBI GI g2811278
BLAST score 555
E value 4.0e-57
Match length 133
% identity 77
NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 231576
Seq. ID LIB3197-031-Q1-M1-D11
Method BLASTX
NCBI GI g2924520
BLAST score 675
E value 3.0e-71
Match length 142
% identity 89
NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No. 231577
Seq. ID LIB3197-031-Q1-M1-D12
Method BLASTX
NCBI GI g2961300
BLAST score 520
E value 3.0e-53
Match length 118
% identity 92
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No. 231578
Seq. ID LIB3197-031-Q1-M1-D4
Method BLASTX
NCBI GI g2662341
BLAST score 717
E value 4.0e-76
Match length 145
% identity 95
NCBI Description (D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No. 231579
Seq. ID LIB3197-031-Q1-M1-D5
Method BLASTX
NCBI GI g728880
BLAST score 527

E value	7.0e-54
Match length	144
% identity	71
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]

Seq. No.	231580
Seq. ID	LIB3197-031-Q1-M1-D6
Method	BLASTX
NCBI GI	g2826884
BLAST score	155
E value	4.0e-10
Match length	41
% identity	71
NCBI Description	(AJ223635) transcription factor IIA large subunit [Arabidopsis thaliana]

Seq. No.	231581
Seq. ID	LIB3197-031-Q1-M1-D7
Method	BLASTX
NCBI GI	g2493133
BLAST score	214
E value	3.0e-17
Match length	83
% identity	49
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) >gi_2183244 (AF002134) Vma8p [Candida albicans]

Seq. No.	231582
Seq. ID	LIB3197-031-Q1-M1-D8
Method	BLASTX
NCBI GI	g3413170
BLAST score	287
E value	1.0e-25
Match length	91
% identity	68
NCBI Description	(AJ010227) 40S ribosomal protein S6 [Cicer arietinum]

Seq. No.	231583
Seq. ID	LIB3197-031-Q1-M1-D9
Method	BLASTX
NCBI GI	g3024020
BLAST score	655
E value	7.0e-69
Match length	131
% identity	93
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]

Seq. No.	231584
Seq. ID	LIB3197-031-Q1-M1-E10
Method	BLASTX
NCBI GI	g282980
BLAST score	414

E value	1.0e-40
Match length	115
% identity	68
NCBI Description	helix-loop-helix protein DEL - garden snapdragon >gi_166428 (M84913) DEL [Antirrhinum majus]

Seq. No.	231585
Seq. ID	LIB3197-031-Q1-M1-E12
Method	BLASTX
NCBI GI	g4217999
BLAST score	577
E value	1.0e-59
Match length	130
% identity	85
NCBI Description	(AC006135) putative ubiquitin--protein ligase (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No.	231586
Seq. ID	LIB3197-031-Q1-M1-E6
Method	BLASTX
NCBI GI	g2117700
BLAST score	512
E value	4.0e-52
Match length	101
% identity	91
NCBI Description	transketolase (EC 2.2.1.1) precursor - potato (fragment)

Seq. No.	231587
Seq. ID	LIB3197-031-Q1-M1-F10
Method	BLASTX
NCBI GI	g2811278
BLAST score	562
E value	6.0e-58
Match length	135
% identity	76
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231588
Seq. ID	LIB3197-031-Q1-M1-F12
Method	BLASTX
NCBI GI	g464986
BLAST score	370
E value	1.0e-35
Match length	69
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	231589
Seq. ID	LIB3197-031-Q1-M1-F4
Method	BLASTX
NCBI GI	g231503
BLAST score	704
E value	1.0e-74
Match length	152
% identity	96
NCBI Description	ACTIN 97 >gi_100417_pir__S20098 actin - potato >gi_21544_emb_CAA39280_ (X55751) actin [Solanum tuberosum]

Seq. No.	231590
Seq. ID	LIB3197-031-Q1-M1-F5
Method	BLASTX
NCBI GI	g3249081
BLAST score	323
E value	5.0e-30
Match length	124
% identity	27
NCBI Description	(AC004473) Strong similarity to AROGP2 gene gb_1762634 from Lycopersicon esculentum. [Arabidopsis thaliana]

Seq. No.	231591
Seq. ID	LIB3197-031-Q1-M1-F8
Method	BLASTX
NCBI GI	g2244734
BLAST score	534
E value	7.0e-55
Match length	106
% identity	98
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	231592
Seq. ID	LIB3197-031-Q1-M1-F9
Method	BLASTX
NCBI GI	g1170373
BLAST score	637
E value	8.0e-67
Match length	133
% identity	92
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	231593
Seq. ID	LIB3197-031-Q1-M1-G1
Method	BLASTX
NCBI GI	g2662343
BLAST score	647
E value	7.0e-68
Match length	124
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	231594
Seq. ID	LIB3197-031-Q1-M1-G10

Method	BLASTX
NCBI GI	g2984709
BLAST score	326
E value	2.0e-30
Match length	68
% identity	88
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No.	231595
Seq. ID	LIB3197-031-Q1-M1-G11
Method	BLASTX
NCBI GI	g2706450
BLAST score	481
E value	2.0e-48
Match length	111
% identity	84
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	231596
Seq. ID	LIB3197-031-Q1-M1-G2
Method	BLASTX
NCBI GI	g3860272
BLAST score	373
E value	8.0e-36
Match length	74
% identity	97
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	231597
Seq. ID	LIB3197-031-Q1-M1-G3
Method	BLASTX
NCBI GI	g4538911
BLAST score	186
E value	3.0e-16
Match length	114
% identity	43
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231598
Seq. ID	LIB3197-031-Q1-M1-G5
Method	BLASTX
NCBI GI	g3258576
BLAST score	375
E value	5.0e-36
Match length	121
% identity	60
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	231599
Seq. ID	LIB3197-031-Q1-M1-G6
Method	BLASTX
NCBI GI	g108513
BLAST score	150
E value	5.0e-10

Match length	53
% identity	57
NCBI Description	aldehyde reductase (EC 1.1.1.21) - bovine

Seq. No.	231600
Seq. ID	LIB3197-031-Q1-M1-G8
Method	BLASTX
NCBI GI	g2244749
BLAST score	628
E value	1.0e-65
Match length	127
% identity	92
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	231601
Seq. ID	LIB3197-031-Q1-M1-H1
Method	BLASTX
NCBI GI	g2462744
BLAST score	175
E value	9.0e-13
Match length	92
% identity	51
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	231602
Seq. ID	LIB3197-031-Q1-M1-H2
Method	BLASTX
NCBI GI	g1173198
BLAST score	401
E value	1.0e-41
Match length	97
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	231603
Seq. ID	LIB3197-031-Q1-M1-H5
Method	BLASTX
NCBI GI	g2654385
BLAST score	177
E value	2.0e-13
Match length	49
% identity	76
NCBI Description	(Z49852) alpha-tubulin [Loxodes striatus]

Seq. No.	231604
Seq. ID	LIB3197-031-Q1-M1-H7
Method	BLASTX
NCBI GI	g3702368
BLAST score	341
E value	3.0e-32
Match length	87
% identity	74
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No.	231605
Seq. ID	LIB3197-031-Q1-M1-H8
Method	BLASTX
NCBI GI	g1351722
BLAST score	275
E value	3.0e-24
Match length	136
% identity	42
NCBI Description	HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I >gi_1122371_emb_CAA92386_ (Z68198) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	231606
Seq. ID	LIB3197-033-Q1-M1-A10
Method	BLASTX
NCBI GI	g2493146
BLAST score	404
E value	2.0e-39
Match length	115
% identity	52
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No.	231607
Seq. ID	LIB3197-033-Q1-M1-A11
Method	BLASTX
NCBI GI	g3874228
BLAST score	182
E value	2.0e-13
Match length	123
% identity	21
NCBI Description	(Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST EMBL:D73546 comes from this gene; cDNA EST EMBL:D73669 comes from this gene; cDNA EST EMBL:D70979 comes from this gene; cDNA EST EMBL:D71075 comes from this gene; cDNA E

Seq. No.	231608
Seq. ID	LIB3197-033-Q1-M1-A5
Method	BLASTX
NCBI GI	g2244732
BLAST score	307
E value	3.0e-28
Match length	89
% identity	66
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	231609
Seq. ID	LIB3197-033-Q1-M1-A6
Method	BLASTX
NCBI GI	g1710521
BLAST score	148
E value	2.0e-13
Match length	46
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_

D0050460.1400

(X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No.	231610
Seq. ID	LIB3197-033-Q1-M1-A8
Method	BLASTX
NCBI GI	g2586127
BLAST score	237
E value	5.0e-20
Match length	95
% identity	51
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	231611
Seq. ID	LIB3197-033-Q1-M1-A9
Method	BLASTX
NCBI GI	g542052
BLAST score	375
E value	3.0e-36
Match length	85
% identity	79
NCBI Description	ethylene-forming enzyme EFE - common tobacco >gi_450357_emb_CAA82646_ (Z29529) ethylene forming enzyme (EFE) [Nicotiana tabacum]

Seq. No.	231612
Seq. ID	LIB3197-033-Q1-M1-B10
Method	BLASTX
NCBI GI	g100535
BLAST score	205
E value	3.0e-16
Match length	44
% identity	91
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	231613
Seq. ID	LIB3197-033-Q1-M1-B2
Method	BLASTX
NCBI GI	g3914999
BLAST score	278
E value	1.0e-24
Match length	75
% identity	80
NCBI Description	SUPEROXIDE DISMUTASE, CHLOROPLAST [CU-ZN] PRECURSOR >gi_1944326_dbj_BAA19675_ (D49486) copper/zinc-superoxide dismutase precursor [Solidago canadensis]

Seq. No.	231614
Seq. ID	LIB3197-033-Q1-M1-B6
Method	BLASTX
NCBI GI	g267069
BLAST score	336
E value	4.0e-45
Match length	95
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594

	tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	231615
Seq. ID	LIB3197-033-Q1-M1-B7
Method	BLASTX
NCBI GI	g3599491
BLAST score	228
E value	8.0e-19
Match length	57
% identity	75
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]
Seq. No.	231616
Seq. ID	LIB3197-033-Q1-M1-B8
Method	BLASTX
NCBI GI	g543905
BLAST score	464
E value	2.0e-46
Match length	110
% identity	82
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]
Seq. No.	231617
Seq. ID	LIB3197-033-Q1-M1-C1
Method	BLASTX
NCBI GI	g1762144
BLAST score	291
E value	3.0e-26
Match length	108
% identity	58
NCBI Description	(U48435) putative cytochrome P450 [Solanum chacoense]
Seq. No.	231618
Seq. ID	LIB3197-033-Q1-M1-C10
Method	BLASTX
NCBI GI	g4544399
BLAST score	564
E value	3.0e-58
Match length	128
% identity	86
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
Seq. No.	231619
Seq. ID	LIB3197-033-Q1-M1-C2
Method	BLASTX
NCBI GI	g125887
BLAST score	207
E value	2.0e-16
Match length	115
% identity	42
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No.	231620
Seq. ID	LIB3197-033-Q1-M1-C4
Method	BLASTX
NCBI GI	g2499535
BLAST score	360
E value	3.0e-38
Match length	111
% identity	65
NCBI Description	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]

Seq. No.	231621
Seq. ID	LIB3197-033-Q1-M1-C5
Method	BLASTX
NCBI GI	g2739382
BLAST score	540
E value	2.0e-55
Match length	148
% identity	31
NCBI Description	(AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	231622
Seq. ID	LIB3197-033-Q1-M1-C6
Method	BLASTX
NCBI GI	g1172977
BLAST score	514
E value	2.0e-52
Match length	120
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	231623
Seq. ID	LIB3197-033-Q1-M1-C8
Method	BLASTX
NCBI GI	g2384758
BLAST score	498
E value	2.0e-50
Match length	101
% identity	93
NCBI Description	(AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No.	231624
Seq. ID	LIB3197-033-Q1-M1-C9
Method	BLASTX
NCBI GI	g4098128
BLAST score	556
E value	3.0e-57
Match length	123
% identity	89
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	231625
Seq. ID	LIB3197-033-Q1-M1-D11
Method	BLASTX
NCBI GI	g3738257
BLAST score	500
E value	1.0e-50
Match length	105
% identity	93
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	231626
Seq. ID	LIB3197-033-Q1-M1-D2
Method	BLASTX
NCBI GI	g2267567
BLAST score	336
E value	1.0e-31
Match length	81
% identity	80
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	231627
Seq. ID	LIB3197-033-Q1-M1-D5
Method	BLASTX
NCBI GI	g120669
BLAST score	260
E value	4.0e-30
Match length	73
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231628
Seq. ID	LIB3197-033-Q1-M1-D8
Method	BLASTX
NCBI GI	g1814403
BLAST score	536
E value	6.0e-55
Match length	133
% identity	81
NCBI Description	(U84889) methionine synthase [Mesembryanthemum crystallinum]

Seq. No.	231629
Seq. ID	LIB3197-033-Q1-M1-D9
Method	BLASTX
NCBI GI	g4469023
BLAST score	175
E value	6.0e-13
Match length	45
% identity	73
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	231630
Seq. ID	LIB3197-033-Q1-M1-E1
Method	BLASTX
NCBI GI	g126041
BLAST score	344
E value	5.0e-33
Match length	71
% identity	99
NCBI Description	L-LACTATE DEHYDROGENASE H CHAIN (LDH-B) >gi_1070432_pir__DEHULH L-lactate dehydrogenase (EC 1.1.1.27) chain H - human >gi_34329_emb_CAA68701_ (Y00711) lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >gi_1200083_emb_CAA32033_ (X13794) lactate dehydrogenase B [Homo sapiens] >gi_4557032_ref_NP_002291.1_pLDHB_ lactate dehydrogenase B

Seq. No.	231631
Seq. ID	LIB3197-033-Q1-M1-E2
Method	BLASTX
NCBI GI	g3202042
BLAST score	192
E value	9.0e-15
Match length	112
% identity	43
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	231632
Seq. ID	LIB3197-033-Q1-M1-E4
Method	BLASTX
NCBI GI	g1071913
BLAST score	527
E value	6.0e-54
Match length	126
% identity	82
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	231633
Seq. ID	LIB3197-033-Q1-M1-E7
Method	BLASTX
NCBI GI	g1174867
BLAST score	163
E value	3.0e-17
Match length	68
% identity	69
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf__2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No.	231634
Seq. ID	LIB3197-033-Q1-M1-E9

Method	BLASTX
NCBI GI	g1245343
BLAST score	269
E value	1.0e-23
Match length	92
% identity	55
NCBI Description	(U50194) tripeptidylpeptidase II [Rattus norvegicus]

Seq. No.	231635
Seq. ID	LIB3197-033-Q1-M1-F10
Method	BLASTX
NCBI GI	g4454056
BLAST score	143
E value	7.0e-09
Match length	40
% identity	70
NCBI Description	(AJ000930) ClpP [Arabidopsis thaliana]

Seq. No.	231636
Seq. ID	LIB3197-033-Q1-M1-F5
Method	BLASTX
NCBI GI	g2078350
BLAST score	223
E value	3.0e-18
Match length	50
% identity	82
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	231637
Seq. ID	LIB3197-033-Q1-M1-F6
Method	BLASTX
NCBI GI	g3831444
BLAST score	149
E value	2.0e-09
Match length	105
% identity	51
NCBI Description	(AC005819) putative protein kinase [Arabidopsis thaliana]

Seq. No.	231638
Seq. ID	LIB3197-033-Q1-M1-G1
Method	BLASTX
NCBI GI	g117501
BLAST score	624
E value	3.0e-65
Match length	115
% identity	100
NCBI Description	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A) >gi_87015_pir__A37047 calreticulin precursor - human >gi_179882 (M84739) calreticulin [Homo sapiens] >gi_337487 (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A) precursor [Homo sapiens] >gi_1905911 (AD000092) calreticulin [Homo sapiens]

Seq. No.	231639
Seq. ID	LIB3197-033-Q1-M1-G3
Method	BLASTX

NCBI GI	g2827082
BLAST score	220
E value	6.0e-18
Match length	51
% identity	80
NCBI Description	(AF020272) malate dehydrogenase [Medicago sativa]

Seq. No.	231640
Seq. ID	LIB3197-033-Q1-M1-G4
Method	BLASTX
NCBI GI	g119350
BLAST score	253
E value	4.0e-37
Match length	102
% identity	79
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana]

Seq. No.	231641
Seq. ID	LIB3197-033-Q1-M1-G5
Method	BLASTX
NCBI GI	g4539335
BLAST score	547
E value	3.0e-56
Match length	151
% identity	68
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	231642
Seq. ID	LIB3197-033-Q1-M1-G6
Method	BLASTX
NCBI GI	g267073
BLAST score	452
E value	3.0e-52
Match length	108
% identity	93
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	231643
Seq. ID	LIB3197-033-Q1-M1-G7
Method	BLASTX
NCBI GI	g2961300
BLAST score	572
E value	3.0e-59
Match length	120
% identity	93
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	231644
Seq. ID	LIB3197-033-Q1-M1-G9
Method	BLASTX

NCBI GI	g2654559
BLAST score	253
E value	1.0e-21
Match length	140
% identity	36
NCBI Description	(AF006621) embryonic lung protein [Homo sapiens]

Seq. No.	231645
Seq. ID	LIB3197-033-Q1-M1-H1
Method	BLASTX
NCBI GI	g3236237
BLAST score	270
E value	8.0e-24
Match length	91
% identity	56
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	231646
Seq. ID	LIB3197-033-Q1-M1-H10
Method	BLASTX
NCBI GI	g3915031
BLAST score	693
E value	2.0e-73
Match length	137
% identity	96
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	231647
Seq. ID	LIB3197-033-Q1-M1-H12
Method	BLASTX
NCBI GI	g1419088
BLAST score	668
E value	2.0e-70
Match length	127
% identity	94
NCBI Description	(Z71395) calreticulin [Nicotiana plumbaginifolia]

Seq. No.	231648
Seq. ID	LIB3197-033-Q1-M1-H7
Method	BLASTX
NCBI GI	g4406780
BLAST score	512
E value	4.0e-52
Match length	130
% identity	74
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	231649
Seq. ID	LIB3197-033-Q1-M1-H8
Method	BLASTX
NCBI GI	g3461833
BLAST score	453

E value 3.0e-45
Match length 108
% identity 74
NCBI Description (AC004138) putative expansin [Arabidopsis thaliana]

Seq. No. 231650
Seq. ID LIB3197-034-Q1-M1-A10
Method BLASTX
NCBI GI g1841464
BLAST score 165
E value 2.0e-11
Match length 38
% identity 45
NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 231651
Seq. ID LIB3197-034-Q1-M1-A11
Method BLASTX
NCBI GI g1841464
BLAST score 223
E value 3.0e-18
Match length 41
% identity 51
NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 231652
Seq. ID LIB3197-034-Q1-M1-A12
Method BLASTX
NCBI GI g1408471
BLAST score 426
E value 5.0e-42
Match length 97
% identity 77
NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 231653
Seq. ID LIB3197-034-Q1-M1-A5
Method BLASTX
NCBI GI g3377797
BLAST score 305
E value 2.0e-50
Match length 132
% identity 76
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No. 231654
Seq. ID LIB3197-034-Q1-M1-A7
Method BLASTX
NCBI GI g3420239
BLAST score 236
E value 2.0e-20

Match length	46
% identity	96
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	231655
Seq. ID	LIB3197-034-Q1-M1-A9
Method	BLASTX
NCBI GI	g2286153
BLAST score	554
E value	4.0e-57
Match length	112
% identity	99
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	231656
Seq. ID	LIB3197-034-Q1-M1-B11
Method	BLASTX
NCBI GI	g3395432
BLAST score	179
E value	4.0e-13
Match length	74
% identity	55
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	231657
Seq. ID	LIB3197-034-Q1-M1-B12
Method	BLASTX
NCBI GI	g3668089
BLAST score	262
E value	8.0e-23
Match length	98
% identity	49
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	231658
Seq. ID	LIB3197-034-Q1-M1-B2
Method	BLASTX
NCBI GI	g1890281
BLAST score	365
E value	6.0e-35
Match length	117
% identity	22
NCBI Description	(U89984) transformation-sensitive protein homolog [Acanthamoeba castellanii]

Seq. No.	231659
Seq. ID	LIB3197-034-Q1-M1-B4
Method	BLASTX
NCBI GI	g3021348
BLAST score	183
E value	8.0e-14
Match length	38
% identity	87
NCBI Description	(AJ004961) ribosomal protein L18 [Cicer arietinum]

Seq. No.	231660
Seq. ID	LIB3197-034-Q1-M1-B5

Method	BLASTX
NCBI GI	g267069
BLAST score	658
E value	3.0e-69
Match length	122
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231661
Seq. ID	LIB3197-034-Q1-M1-B6
Method	BLASTX
NCBI GI	g2911050
BLAST score	141
E value	1.0e-08
Match length	97
% identity	40
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	231662
Seq. ID	LIB3197-034-Q1-M1-B9
Method	BLASTX
NCBI GI	g133959
BLAST score	242
E value	2.0e-20
Match length	50
% identity	94
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_81526_pir__A30833 ribosomal protein S4 - spinach chloroplast >gi_343377 (M16878) ribosomal protein S4 [Spinacia oleracea] >gi_225464_prf__1303355A ribosomal protein S4 [Spinacia oleracea]

Seq. No.	231663
Seq. ID	LIB3197-034-Q1-M1-C1
Method	BLASTX
NCBI GI	g464981
BLAST score	274
E value	2.0e-24
Match length	55
% identity	93
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	231664
Seq. ID	LIB3197-034-Q1-M1-C10
Method	BLASTX
NCBI GI	g4544384
BLAST score	243
E value	4.0e-21
Match length	66
% identity	92
NCBI Description	(AC007047) unknown protein [Arabidopsis thaliana]

Seq. No.	231665
Seq. ID	LIB3197-034-Q1-M1-C11
Method	BLASTX
NCBI GI	g2739046
BLAST score	194
E value	8.0e-15
Match length	102
% identity	38
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	231666
Seq. ID	LIB3197-034-Q1-M1-C2
Method	BLASTX
NCBI GI	g3157932
BLAST score	150
E value	1.0e-09
Match length	131
% identity	33
NCBI Description	(AC002131) Similar to hypothetical protein HYP1 gb_Z97338 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	231667
Seq. ID	LIB3197-034-Q1-M1-C4
Method	BLASTX
NCBI GI	g3334115
BLAST score	438
E value	2.0e-44
Match length	117
% identity	81
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	231668
Seq. ID	LIB3197-034-Q1-M1-C5
Method	BLASTX
NCBI GI	g135406
BLAST score	647
E value	7.0e-68
Match length	126
% identity	96
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	231669
Seq. ID	LIB3197-034-Q1-M1-C6
Method	BLASTX
NCBI GI	g3819164
BLAST score	660
E value	2.0e-69
Match length	144
% identity	90
NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine

max]

Seq. No.	231670
Seq. ID	LIB3197-034-Q1-M1-C8
Method	BLASTX
NCBI GI	g3023190
BLAST score	521
E value	4.0e-53
Match length	129
% identity	79
NCBI Description	14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685) 14-3-3 protein [Solanum tuberosum]

Seq. No.	231671
Seq. ID	LIB3197-034-Q1-M1-D1
Method	BLASTX
NCBI GI	g1922251
BLAST score	496
E value	3.0e-50
Match length	97
% identity	98
NCBI Description	(Y12072) farnesyl pyrophosphate synthase [Gossypium arboreum]

Seq. No.	231672
Seq. ID	LIB3197-034-Q1-M1-D10
Method	BLASTX
NCBI GI	g2129758
BLAST score	535
E value	8.0e-55
Match length	112
% identity	82
NCBI Description	ubiquitin conjugating enzyme E2 protein - Arabidopsis thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No.	231673
Seq. ID	LIB3197-034-Q1-M1-D6
Method	BLASTX
NCBI GI	g2688830
BLAST score	574
E value	2.0e-59
Match length	150
% identity	76
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	231674
Seq. ID	LIB3197-034-Q1-M1-D8
Method	BLASTX
NCBI GI	g475048
BLAST score	630
E value	6.0e-66
Match length	134
% identity	64
NCBI Description	(X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]

Seq. No. 231675

Seq. ID	LIB3197-034-Q1-M1-D9
Method	BLASTX
NCBI GI	g2894592
BLAST score	329
E value	1.0e-30
Match length	87
% identity	71
NCBI Description	(AL021889) predicted protein [Arabidopsis thaliana]

Seq. No.	231676
Seq. ID	LIB3197-034-Q1-M1-E2
Method	BLASTX
NCBI GI	g2894612
BLAST score	302
E value	1.0e-27
Match length	94
% identity	63
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	231677
Seq. ID	LIB3197-034-Q1-M1-E7
Method	BLASTX
NCBI GI	g2791834
BLAST score	527
E value	7.0e-54
Match length	103
% identity	98
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	231678
Seq. ID	LIB3197-034-Q1-M1-E8
Method	BLASTX
NCBI GI	g1620898
BLAST score	333
E value	4.0e-31
Match length	88
% identity	73
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]

Seq. No.	231679
Seq. ID	LIB3197-034-Q1-M1-F1
Method	BLASTX
NCBI GI	g1945611
BLAST score	265
E value	3.0e-23
Match length	120
% identity	44
NCBI Description	(AB003103) 26S proteasome subunit p55 [Homo sapiens] >gi_4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome, macropain) 26S subunit, non-ATPase,

Seq. No.	231680
Seq. ID	LIB3197-034-Q1-M1-F10
Method	BLASTX
NCBI GI	g2497543
BLAST score	536

E value	4.0e-55
Match length	117
% identity	91
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	231681
Seq. ID	LIB3197-034-Q1-M1-F12
Method	BLASTX
NCBI GI	g479386
BLAST score	407
E value	9.0e-40
Match length	89
% identity	90
NCBI Description	isocitrate dehydrogenase - soybean

Seq. No.	231682
Seq. ID	LIB3197-034-Q1-M1-F2
Method	BLASTX
NCBI GI	g464849
BLAST score	804
E value	3.0e-86
Match length	152
% identity	99
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	231683
Seq. ID	LIB3197-034-Q1-M1-F3
Method	BLASTX
NCBI GI	g4193388
BLAST score	424
E value	9.0e-42
Match length	125
% identity	70
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	231684
Seq. ID	LIB3197-034-Q1-M1-F4
Method	BLASTX
NCBI GI	g81857
BLAST score	340
E value	6.0e-32
Match length	71
% identity	90
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No.	231685
Seq. ID	LIB3197-034-Q1-M1-F5
Method	BLASTX
NCBI GI	g4193388
BLAST score	259

E value	1.0e-22
Match length	69
% identity	72
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	231686
Seq. ID	LIB3197-034-Q1-M1-F6
Method	BLASTX
NCBI GI	g312179
BLAST score	558
E value	2.0e-57
Match length	130
% identity	82
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	231687
Seq. ID	LIB3197-034-Q1-M1-F9
Method	BLASTX
NCBI GI	g4193388
BLAST score	292
E value	2.0e-26
Match length	82
% identity	74
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	231688
Seq. ID	LIB3197-034-Q1-M1-G11
Method	BLASTX
NCBI GI	g4049349
BLAST score	423
E value	1.0e-41
Match length	122
% identity	67
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	231689
Seq. ID	LIB3197-034-Q1-M1-G2
Method	BLASTX
NCBI GI	g3334299
BLAST score	584
E value	1.0e-60
Match length	122
% identity	93
NCBI Description	PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) >gi_2315211_emb_CAA74725_ (Y14339) proteasome alpha subunit [Lycopersicon esculentum]

Seq. No.	231690
Seq. ID	LIB3197-034-Q1-M1-G3
Method	BLASTX

NCBI GI	g2661840
BLAST score	147
E value	2.0e-09
Match length	51
% identity	55
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	231691
Seq. ID	LIB3197-034-Q1-M1-G5
Method	BLASTX
NCBI GI	g4006924
BLAST score	482
E value	1.0e-48
Match length	108
% identity	79
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	231692
Seq. ID	LIB3197-034-Q1-M1-G7
Method	BLASTX
NCBI GI	g3219766
BLAST score	737
E value	2.0e-78
Match length	150
% identity	97
NCBI Description	ACTIN 82 >gi_1498370 (U60483) actin [Solanum tuberosum]

Seq. No.	231693
Seq. ID	LIB3197-034-Q1-M1-G8
Method	BLASTX
NCBI GI	g3913366
BLAST score	202
E value	8.0e-16
Match length	120
% identity	36
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi_1597723 (U67422) CRINKLY4 precursor [Zea mays]

Seq. No.	231694
Seq. ID	LIB3197-034-Q1-M1-G9
Method	BLASTX
NCBI GI	g2811278
BLAST score	567
E value	1.0e-58
Match length	135
% identity	77
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231695
Seq. ID	LIB3197-034-Q1-M1-H10
Method	BLASTX
NCBI GI	g3122673
BLAST score	521
E value	4.0e-53
Match length	129
% identity	79

NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.	231696
Seq. ID	LIB3197-034-Q1-M1-H2
Method	BLASTX
NCBI GI	g3860247
BLAST score	539
E value	3.0e-55
Match length	112
% identity	87
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.	231697
Seq. ID	LIB3197-034-Q1-M1-H4
Method	BLASTX
NCBI GI	g2760326
BLAST score	250
E value	3.0e-21
Match length	81
% identity	56
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]
Seq. No.	231698
Seq. ID	LIB3197-035-Q1-M1-A11
Method	BLASTX
NCBI GI	g2118231
BLAST score	582
E value	2.0e-60
Match length	130
% identity	85
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) AHA10 - Arabidopsis thaliana >gi_765354_bbs_157347 (S74033) plasma membrane H(+)-ATPase isoform AHA10=P-type ATPase [Arabidopsis thaliana, cv. Columbia, Peptide, 946 aa] [Arabidopsis thaliana]
Seq. No.	231699
Seq. ID	LIB3197-035-Q1-M1-A12
Method	BLASTX
NCBI GI	g4559322
BLAST score	303
E value	9.0e-28
Match length	107
% identity	62
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.	231700
Seq. ID	LIB3197-035-Q1-M1-A3
Method	BLASTX
NCBI GI	g2642450
BLAST score	328
E value	1.0e-30
Match length	102
% identity	63
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative

metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	231701
Seq. ID	LIB3197-035-Q1-M1-A5
Method	BLASTX
NCBI GI	g2129753
BLAST score	381
E value	1.0e-36
Match length	95
% identity	67
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	231702
Seq. ID	LIB3197-035-Q1-M1-A6
Method	BLASTX
NCBI GI	g1076282
BLAST score	542
E value	6.0e-59
Match length	130
% identity	87
NCBI Description	aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana (fragment) >gi_599625_emb_CAA58046_ (X82839) aconitase [Arabidopsis thaliana]

Seq. No.	231703
Seq. ID	LIB3197-035-Q1-M1-B1
Method	BLASTX
NCBI GI	g3450889
BLAST score	350
E value	4.0e-33
Match length	102
% identity	73
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	231704
Seq. ID	LIB3197-035-Q1-M1-B10
Method	BLASTX
NCBI GI	g3834310
BLAST score	473
E value	1.0e-47
Match length	91
% identity	99
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	231705
Seq. ID	LIB3197-035-Q1-M1-B11
Method	BLASTX
NCBI GI	g3608171
BLAST score	303
E value	8.0e-28
Match length	81
% identity	75

NCBI Description	(D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]
Seq. No.	231706
Seq. ID	LIB3197-035-Q1-M1-B12
Method	BLASTX
NCBI GI	g42356
BLAST score	270
E value	9.0e-24
Match length	132
% identity	45
NCBI Description	(X03709) aminopeptidase N (aa 1-176) [Escherichia coli]
Seq. No.	231707
Seq. ID	LIB3197-035-Q1-M1-B2
Method	BLASTX
NCBI GI	g462137
BLAST score	308
E value	3.0e-53
Match length	126
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
Seq. No.	231708
Seq. ID	LIB3197-035-Q1-M1-B3
Method	BLASTX
NCBI GI	g3420055
BLAST score	426
E value	5.0e-42
Match length	106
% identity	76
NCBI Description	(AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.	231709
Seq. ID	LIB3197-035-Q1-M1-B4
Method	BLASTX
NCBI GI	g1710521
BLAST score	583
E value	2.0e-60
Match length	125
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_ (X94296) L24 ribosomal protein [Hordeum vulgare]
Seq. No.	231710
Seq. ID	LIB3197-035-Q1-M1-B6
Method	BLASTX
NCBI GI	g1617274
BLAST score	668
E value	2.0e-70
Match length	145
% identity	83
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]
Seq. No.	231711
Seq. ID	LIB3197-035-Q1-M1-B8
Method	BLASTX

NCBI GI	g4490737
BLAST score	281
E value	4.0e-25
Match length	123
% identity	53
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	231712
Seq. ID	LIB3197-035-Q1-M1-B9
Method	BLASTX
NCBI GI	g1350944
BLAST score	391
E value	5.0e-38
Match length	80
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	231713
Seq. ID	LIB3197-035-Q1-M1-C10
Method	BLASTX
NCBI GI	g4469025
BLAST score	222
E value	3.0e-18
Match length	49
% identity	80
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	231714
Seq. ID	LIB3197-035-Q1-M1-C11
Method	BLASTX
NCBI GI	g467698
BLAST score	185
E value	9.0e-14
Match length	125
% identity	34
NCBI Description	(X78326) SUR4 [Saccharomyces cerevisiae]

Seq. No.	231715
Seq. ID	LIB3197-035-Q1-M1-C12
Method	BLASTX
NCBI GI	g2341034
BLAST score	547
E value	3.0e-56
Match length	111
% identity	97
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	231716
Seq. ID	LIB3197-035-Q1-M1-C2
Method	BLASTX
NCBI GI	g2088651
BLAST score	217
E value	1.0e-17
Match length	87
% identity	44
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	231717
Seq. ID	LIB3197-035-Q1-M1-C4
Method	BLASTX
NCBI GI	g2388689
BLAST score	271
E value	7.0e-24
Match length	92
% identity	65
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	231718
Seq. ID	LIB3197-035-Q1-M1-C8
Method	BLASTX
NCBI GI	g1843527
BLAST score	569
E value	7.0e-59
Match length	116
% identity	56
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	231719
Seq. ID	LIB3197-035-Q1-M1-D1
Method	BLASTX
NCBI GI	g4206210
BLAST score	256
E value	8.0e-40
Match length	136
% identity	69
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	231720
Seq. ID	LIB3197-035-Q1-M1-D11
Method	BLASTX
NCBI GI	g4544399
BLAST score	478
E value	4.0e-48
Match length	140
% identity	63
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	231721
Seq. ID	LIB3197-035-Q1-M1-D2
Method	BLASTX
NCBI GI	g2815246
BLAST score	144
E value	2.0e-14
Match length	55
% identity	69
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	231722
Seq. ID	LIB3197-035-Q1-M1-D3
Method	BLASTX

NCBI GI	g1174470
BLAST score	254
E value	6.0e-22
Match length	72
% identity	61
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	231723
Seq. ID	LIB3197-035-Q1-M1-D4
Method	BLASTX
NCBI GI	g4454051
BLAST score	353
E value	2.0e-33
Match length	74
% identity	88
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	231724
Seq. ID	LIB3197-035-Q1-M1-D5
Method	BLASTX
NCBI GI	g1335862
BLAST score	659
E value	2.0e-69
Match length	141
% identity	94
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	231725
Seq. ID	LIB3197-035-Q1-M1-D6
Method	BLASTX
NCBI GI	g2662341
BLAST score	752
E value	3.0e-80
Match length	145
% identity	97
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	231726
Seq. ID	LIB3197-035-Q1-M1-D8
Method	BLASTX
NCBI GI	g3914394
BLAST score	360
E value	2.0e-34
Match length	80
% identity	82
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	231727
Seq. ID	LIB3197-035-Q1-M1-E1
Method	BLASTX
NCBI GI	g3123745
BLAST score	232
E value	3.0e-19
Match length	115
% identity	43
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	231728
Seq. ID	LIB3197-035-Q1-M1-E11
Method	BLASTX
NCBI GI	g3757514
BLAST score	583
E value	2.0e-60
Match length	128
% identity	88
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	231729
Seq. ID	LIB3197-035-Q1-M1-E6
Method	BLASTX
NCBI GI	g2570047
BLAST score	174
E value	2.0e-12
Match length	118
% identity	28
NCBI Description	(Y09234) MSTK2S kinase-like protein [Mus musculus]

Seq. No.	231730
Seq. ID	LIB3197-035-Q1-M1-E9
Method	BLASTX
NCBI GI	g547753
BLAST score	196
E value	4.0e-15
Match length	67
% identity	61
NCBI Description	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

Seq. No.	231731
Seq. ID	LIB3197-035-Q1-M1-F2
Method	BLASTX
NCBI GI	g1710551
BLAST score	281
E value	5.0e-25
Match length	51
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_ (X95458) ribosomal protein L39 [Zea mays]

Seq. No.	231732
Seq. ID	LIB3197-035-Q1-M1-F7
Method	BLASTX
NCBI GI	g2444178

BLAST score	265
E value	2.0e-25
Match length	82
% identity	72
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	231733
Seq. ID	LIB3197-035-Q1-M1-F9
Method	BLASTX
NCBI GI	g2827753
BLAST score	364
E value	1.0e-44
Match length	102
% identity	93
NCBI Description	TUBULIN BETA CHAIN >gi_1490665 (U64029) beta-tubulin 1 [Daucus carota]

Seq. No.	231734
Seq. ID	LIB3197-035-Q1-M1-G2
Method	BLASTX
NCBI GI	g120669
BLAST score	458
E value	7.0e-46
Match length	92
% identity	91
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231735
Seq. ID	LIB3197-035-Q1-M1-G3
Method	BLASTX
NCBI GI	g120669
BLAST score	225
E value	1.0e-18
Match length	77
% identity	57
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231736
Seq. ID	LIB3197-035-Q1-M1-G8
Method	BLASTX
NCBI GI	g135406
BLAST score	507
E value	1.0e-51
Match length	99
% identity	96
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	231737
Seq. ID	LIB3197-035-Q1-M1-H1
Method	BLASTX
NCBI GI	g1172872
BLAST score	261
E value	7.0e-23
Match length	102
% identity	59
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	231738
Seq. ID	LIB3197-035-Q1-M1-H2
Method	BLASTX
NCBI GI	g70644
BLAST score	410
E value	4.0e-40
Match length	82
% identity	18
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	231739
Seq. ID	LIB3197-035-Q1-M1-H3
Method	BLASTX
NCBI GI	g2500341
BLAST score	166
E value	2.0e-11
Match length	38
% identity	76
NCBI Description	50S RIBOSOMAL PROTEIN L36 >gi_1652406_dbj_BAA17328_ (D90905) 50S ribosomal protein L36 [Synechocystis sp.]

Seq. No.	231740
Seq. ID	LIB3197-035-Q1-M1-H7
Method	BLASTX
NCBI GI	g267069
BLAST score	416
E value	4.0e-41
Match length	76
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231741
Seq. ID	LIB3197-035-Q1-M1-H9
Method	BLASTX
NCBI GI	g2529677
BLAST score	225
E value	1.0e-18
Match length	49

% identity	84
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No.	231742
Seq. ID	LIB3197-037-Q1-M1-A10
Method	BLASTX
NCBI GI	g3122326
BLAST score	230
E value	1.0e-19
Match length	56
% identity	77
NCBI Description	LEC14B PROTEIN >gi_1181604_dbj_BAA11768_ (D83074) LEC14B protein [Lithospermum erythrorhizon]

Seq. No.	231743
Seq. ID	LIB3197-037-Q1-M1-A3
Method	BLASTX
NCBI GI	g3420239
BLAST score	309
E value	1.0e-28
Match length	61
% identity	95
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	231744
Seq. ID	LIB3197-037-Q1-M1-A4
Method	BLASTX
NCBI GI	g2088651
BLAST score	164
E value	1.0e-11
Match length	80
% identity	40
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	231745
Seq. ID	LIB3197-037-Q1-M1-A9
Method	BLASTX
NCBI GI	g4006848
BLAST score	184
E value	1.0e-23
Match length	77
% identity	74
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	231746
Seq. ID	LIB3197-037-Q1-M1-B12
Method	BLASTX
NCBI GI	g2435522
BLAST score	267
E value	2.0e-23
Match length	105
% identity	59
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No. 231747
Seq. ID LIB3197-037-Q1-M1-B4
Method BLASTX
NCBI GI g3097321
BLAST score 164
E value 2.0e-11
Match length 83
% identity 41
NCBI Description (AB013289) Bd 30K [Glycine max]

Seq. No. 231748
Seq. ID LIB3197-037-Q1-M1-B7
Method BLASTX
NCBI GI g4512651
BLAST score 198
E value 2.0e-15
Match length 95
% identity 39
NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 231749
Seq. ID LIB3197-037-Q1-M1-B9
Method BLASTX
NCBI GI g4539010
BLAST score 228
E value 7.0e-19
Match length 134
% identity 18
NCBI Description (AL049481) putative DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No. 231750
Seq. ID LIB3197-037-Q1-M1-C4
Method BLASTX
NCBI GI g730583
BLAST score 247
E value 4.0e-21
Match length 113
% identity 50
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No. 231751
Seq. ID LIB3197-037-Q1-M1-C5
Method BLASTX
NCBI GI g3128176
BLAST score 123
E value 3.0e-10
Match length 103
% identity 39
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 231752
Seq. ID LIB3197-037-Q1-M1-C7

Method	BLASTX
NCBI GI	g3549669
BLAST score	348
E value	7.0e-33
Match length	81
% identity	84
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	231753
Seq. ID	LIB3197-037-Q1-M1-C9
Method	BLASTX
NCBI GI	g4115377
BLAST score	383
E value	6.0e-37
Match length	111
% identity	71
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	231754
Seq. ID	LIB3197-037-Q1-M1-D1
Method	BLASTX
NCBI GI	g4249388
BLAST score	153
E value	3.0e-10
Match length	74
% identity	46
NCBI Description	(AC005966) Similar to gb_AF025438 Opa-interacting protein (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	231755
Seq. ID	LIB3197-037-Q1-M1-D8
Method	BLASTX
NCBI GI	g1174718
BLAST score	146
E value	2.0e-09
Match length	99
% identity	37
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	231756
Seq. ID	LIB3197-037-Q1-M1-E1
Method	BLASTX
NCBI GI	g1335862
BLAST score	175
E value	6.0e-13
Match length	73
% identity	49
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	231757
Seq. ID	LIB3197-037-Q1-M1-E7
Method	BLASTX
NCBI GI	g2129471
BLAST score	251

E value	2.0e-21
Match length	72
% identity	64
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	231758
Seq. ID	LIB3197-037-Q1-M1-E8
Method	BLASTX
NCBI GI	g3128176
BLAST score	146
E value	2.0e-09
Match length	113
% identity	31
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	231759
Seq. ID	LIB3197-037-Q1-M1-E9
Method	BLASTX
NCBI GI	g120470
BLAST score	189
E value	1.0e-14
Match length	51
% identity	71
NCBI Description	P55-C-FOS PROTO-ONCOGENE PROTEIN (G0S7 PROTEIN) >gi_68869_pir__TVHUF1 transforming protein fos - human >gi_29904_emb_CAA24756_ (V01512) c-fos [Homo sapiens] >gi_182735 (K00650) c-fos protein [Homo sapiens] >gi_4063509_gb_AAC98315.1_ (AF111167) cfos [Homo sapiens]

Seq. No.	231760
Seq. ID	LIB3197-037-Q1-M1-F1
Method	BLASTX
NCBI GI	g4512711
BLAST score	383
E value	5.0e-37
Match length	138
% identity	57
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	231761
Seq. ID	LIB3197-037-Q1-M1-F3
Method	BLASTX
NCBI GI	g3046731
BLAST score	227
E value	1.0e-34
Match length	86
% identity	93
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	231762
Seq. ID	LIB3197-037-Q1-M1-F7
Method	BLASTX
NCBI GI	g2789660
BLAST score	368
E value	2.0e-35

Match length	96
% identity	74
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	231763
Seq. ID	LIB3197-037-Q1-M1-F9
Method	BLASTX
NCBI GI	g4567273
BLAST score	238
E value	3.0e-23
Match length	69
% identity	81
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No.	231764
Seq. ID	LIB3197-037-Q1-M1-G3
Method	BLASTX
NCBI GI	g2811278
BLAST score	409
E value	4.0e-40
Match length	115
% identity	69
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231765
Seq. ID	LIB3197-037-Q1-M1-G8
Method	BLASTX
NCBI GI	g462013
BLAST score	316
E value	3.0e-29
Match length	108
% identity	61
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	231766
Seq. ID	LIB3197-037-Q1-M1-H2
Method	BLASTX
NCBI GI	g3869088
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	231767
Seq. ID	LIB3197-038-Q1-M1-H11
Method	BLASTX
NCBI GI	g730241
BLAST score	316
E value	4.0e-29
Match length	123
% identity	50
NCBI Description	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN

GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) >gi_473947_dbj_BAA06126_ (D29643) similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392). [Homo sapiens]

Seq. No.	231768
Seq. ID	LIB3197-038-Q1-M1-H12
Method	BLASTX
NCBI GI	g2829902
BLAST score	505
E value	2.0e-51
Match length	110
% identity	88
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	231769
Seq. ID	LIB3197-038-Q1-M1-H6
Method	BLASTX
NCBI GI	g401322
BLAST score	230
E value	4.0e-19
Match length	58
% identity	79
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	231770
Seq. ID	LIB3197-039-Q1-M1-A1
Method	BLASTX
NCBI GI	g464734
BLAST score	608
E value	2.0e-63
Match length	126
% identity	94
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]

Seq. No.	231771
Seq. ID	LIB3197-039-Q1-M1-A12
Method	BLASTX
NCBI GI	g119350
BLAST score	611
E value	1.0e-63
Match length	136
% identity	88
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana]

Seq. No.	231772
Seq. ID	LIB3197-039-Q1-M1-A8
Method	BLASTX
NCBI GI	g4217999
BLAST score	391
E value	4.0e-38
Match length	95
% identity	80
NCBI Description	(AC006135) putative ubiquitin--protein ligase (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No.	231773
Seq. ID	LIB3197-039-Q1-M1-B1
Method	BLASTX
NCBI GI	g3608137
BLAST score	192
E value	1.0e-14
Match length	100
% identity	44
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	231774
Seq. ID	LIB3197-039-Q1-M1-B11
Method	BLASTX
NCBI GI	g1737492
BLAST score	393
E value	4.0e-38
Match length	111
% identity	19
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	231775
Seq. ID	LIB3197-039-Q1-M1-B2
Method	BLASTX
NCBI GI	g114682
BLAST score	345
E value	2.0e-32
Match length	113
% identity	65
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No.	231776
Seq. ID	LIB3197-039-Q1-M1-B3
Method	BLASTX
NCBI GI	g3319682
BLAST score	545
E value	6.0e-56
Match length	114
% identity	85
NCBI Description	(Y17720) SPINDLY protein [Petunia x hybrida]

Seq. No.	231777

Seq. ID	LIB3197-039-Q1-M1-B5
Method	BLASTX
NCBI GI	g3360289
BLAST score	180
E value	3.0e-13
Match length	50
% identity	62
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	231778
Seq. ID	LIB3197-039-Q1-M1-C1
Method	BLASTX
NCBI GI	g267069
BLAST score	649
E value	3.0e-68
Match length	120
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231779
Seq. ID	LIB3197-039-Q1-M1-C12
Method	BLASTX
NCBI GI	g4490308
BLAST score	232
E value	3.0e-19
Match length	56
% identity	86
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	231780
Seq. ID	LIB3197-039-Q1-M1-C3
Method	BLASTX
NCBI GI	g2827537
BLAST score	437
E value	2.0e-43
Match length	120
% identity	69
NCBI Description	(AL021633) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	231781
Seq. ID	LIB3197-039-Q1-M1-C6
Method	BLASTX
NCBI GI	g2499710
BLAST score	535
E value	9.0e-55
Match length	125
% identity	77
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No.	231782

09604605.100600

Seq. ID	LIB3197-039-Q1-M1-C7
Method	BLASTX
NCBI GI	g267069
BLAST score	668
E value	2.0e-70
Match length	124
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231783
Seq. ID	LIB3197-039-Q1-M1-C8
Method	BLASTX
NCBI GI	g2507281
BLAST score	666
E value	3.0e-70
Match length	119
% identity	100
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	231784
Seq. ID	LIB3197-039-Q1-M1-C9
Method	BLASTX
NCBI GI	g120669
BLAST score	556
E value	2.0e-57
Match length	107
% identity	95
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	231785
Seq. ID	LIB3197-039-Q1-M1-D10
Method	BLASTX
NCBI GI	g3776578
BLAST score	300
E value	3.0e-27
Match length	118
% identity	46
NCBI Description	(AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	231786
Seq. ID	LIB3197-039-Q1-M1-D11
Method	BLASTX
NCBI GI	g2130442
BLAST score	315
E value	5.0e-29
Match length	142
% identity	47
NCBI Description	hypothetical protein SPAC8A4.01c - fission yeast

	(Schizosaccharomyces pombe) (fragment) >gi_1052534_emb_CAA91511_ (Z66569) unknown [Schizosaccharomyces pombe]
Seq. No.	231787
Seq. ID	LIB3197-039-Q1-M1-D12
Method	BLASTX
NCBI GI	g2281649
BLAST score	165
E value	2.0e-11
Match length	82
% identity	51
NCBI Description	(AF003105) AP2 domain containing protein RAP2.12 [Arabidopsis thaliana]
Seq. No.	231788
Seq. ID	LIB3197-039-Q1-M1-D4
Method	BLASTX
NCBI GI	g2809232
BLAST score	399
E value	7.0e-39
Match length	121
% identity	67
NCBI Description	(AC002560) F21B7.1 [Arabidopsis thaliana]
Seq. No.	231789
Seq. ID	LIB3197-039-Q1-M1-D5
Method	BLASTX
NCBI GI	g2065019
BLAST score	333
E value	4.0e-31
Match length	121
% identity	27
NCBI Description	(Y09823) hypothetical protein [Arabidopsis thaliana]
Seq. No.	231790
Seq. ID	LIB3197-039-Q1-M1-D6
Method	BLASTX
NCBI GI	g231496
BLAST score	633
E value	3.0e-66
Match length	143
% identity	87
NCBI Description	ACTIN 58 >gi_100421_pir__S20094 actin - potato >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]
Seq. No.	231791
Seq. ID	LIB3197-039-Q1-M1-D7
Method	BLASTX
NCBI GI	g4220474
BLAST score	496
E value	2.0e-50
Match length	110
% identity	91
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	231792
Seq. ID	LIB3197-039-Q1-M1-D8
Method	BLASTX
NCBI GI	g2281092
BLAST score	216
E value	2.0e-17
Match length	66
% identity	70
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231793
Seq. ID	LIB3197-039-Q1-M1-E10
Method	BLASTX
NCBI GI	g1173218
BLAST score	622
E value	6.0e-65
Match length	124
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	231794
Seq. ID	LIB3197-039-Q1-M1-E4
Method	BLASTX
NCBI GI	g2494626
BLAST score	169
E value	7.0e-12
Match length	121
% identity	35
NCBI Description	HYPOTHETICAL 47.6 KD PROTEIN F49C12.8 IN CHROMOSOME IV >gi_3877366_emb_CAA92512_ (Z68227) cDNA EST EMBL:Z14827 comes from this gene; cDNA EST EMBL:C13370 comes from this gene; cDNA EST EMBL:C11280 comes from this gene; cDNA EST yk336d8.3 comes from this gene; cDNA EST yk336d8.5 comes from this gene; cDNA ES

Seq. No.	231795
Seq. ID	LIB3197-039-Q1-M1-E5
Method	BLASTX
NCBI GI	g2642443
BLAST score	307
E value	5.0e-28
Match length	150
% identity	36
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	231796
Seq. ID	LIB3197-039-Q1-M1-E6
Method	BLASTX
NCBI GI	g2982463
BLAST score	316
E value	6.0e-32
Match length	109
% identity	72
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	231797
Seq. ID	LIB3197-039-Q1-M1-F10
Method	BLASTX
NCBI GI	g232024
BLAST score	350
E value	4.0e-33
Match length	120
% identity	61
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	231798
Seq. ID	LIB3197-039-Q1-M1-F11
Method	BLASTX
NCBI GI	g4406780
BLAST score	361
E value	2.0e-41
Match length	118
% identity	73
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	231799
Seq. ID	LIB3197-039-Q1-M1-F12
Method	BLASTX
NCBI GI	g4490332
BLAST score	268
E value	2.0e-23
Match length	99
% identity	56
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	231800
Seq. ID	LIB3197-039-Q1-M1-F4
Method	BLASTX
NCBI GI	g3738257
BLAST score	464
E value	1.0e-46
Match length	97
% identity	94
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	231801
Seq. ID	LIB3197-039-Q1-M1-F6
Method	BLASTX
NCBI GI	g495866
BLAST score	588
E value	4.0e-61
Match length	107
% identity	2
NCBI Description	(L23982) collagen type VII [Homo sapiens]

Seq. No.	231802

Seq. ID	LIB3197-039-Q1-M1-G10
Method	BLASTX
NCBI GI	g2633727
BLAST score	170
E value	5.0e-12
Match length	93
% identity	44
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	231803
Seq. ID	LIB3197-039-Q1-M1-G11
Method	BLASTX
NCBI GI	g3914996
BLAST score	258
E value	2.0e-22
Match length	95
% identity	60
NCBI Description	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine aminotransferase [Arabidopsis thaliana]

Seq. No.	231804
Seq. ID	LIB3197-039-Q1-M1-G5
Method	BLASTX
NCBI GI	g3249084
BLAST score	466
E value	1.0e-46
Match length	127
% identity	24
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	231805
Seq. ID	LIB3197-039-Q1-M1-G6
Method	BLASTX
NCBI GI	g4454014
BLAST score	278
E value	1.0e-24
Match length	141
% identity	45
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	231806
Seq. ID	LIB3197-039-Q1-M1-H10
Method	BLASTX
NCBI GI	g2829902
BLAST score	538
E value	3.0e-55
Match length	116
% identity	89
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	231807
Seq. ID	LIB3197-039-Q1-M1-H12
Method	BLASTX
NCBI GI	g1706377
BLAST score	495
E value	3.0e-50
Match length	117
% identity	78
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_499018_emb_CAA53578_ (X75964) dihydroflavonol reductase [Vitis vinifera]

Seq. No.	231808
Seq. ID	LIB3197-039-Q1-M1-H5
Method	BLASTX
NCBI GI	g4098129
BLAST score	582
E value	2.0e-60
Match length	129
% identity	88
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	231809
Seq. ID	LIB3197-039-Q1-M1-H9
Method	BLASTX
NCBI GI	g2340050
BLAST score	226
E value	9.0e-19
Match length	66
% identity	71
NCBI Description	(L48989) troponin T [Mus musculus]

Seq. No.	231810
Seq. ID	LIB3197-040-Q1-M1-A10
Method	BLASTX
NCBI GI	g1911166
BLAST score	607
E value	3.0e-63
Match length	142
% identity	74
NCBI Description	(X94400) soluble-starch-synthase [Solanum tuberosum]

Seq. No.	231811
Seq. ID	LIB3197-040-Q1-M1-A11
Method	BLASTX
NCBI GI	g3292830
BLAST score	278
E value	1.0e-24
Match length	139
% identity	50
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	231812
Seq. ID	LIB3197-040-Q1-M1-A12
Method	BLASTX
NCBI GI	g2129499

BLAST score	175
E value	4.0e-13
Match length	72
% identity	57
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	231813
Seq. ID	LIB3197-040-Q1-M1-A2
Method	BLASTX
NCBI GI	g1800147
BLAST score	362
E value	1.0e-34
Match length	106
% identity	69
NCBI Description	(U83655) membrane associated protein [Arabidopsis thaliana]

Seq. No.	231814
Seq. ID	LIB3197-040-Q1-M1-A3
Method	BLASTX
NCBI GI	g1724102
BLAST score	471
E value	2.0e-47
Match length	94
% identity	96
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	231815
Seq. ID	LIB3197-040-Q1-M1-A6
Method	BLASTX
NCBI GI	g3786001
BLAST score	302
E value	2.0e-27
Match length	74
% identity	74
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	231816
Seq. ID	LIB3197-040-Q1-M1-A8
Method	BLASTX
NCBI GI	g267069
BLAST score	441
E value	5.0e-44
Match length	81
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231817
Seq. ID	LIB3197-040-Q1-M1-B10
Method	BLASTX
NCBI GI	g4204695
BLAST score	405
E value	1.0e-39

Match length	143
% identity	60
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No.	231818
Seq. ID	LIB3197-040-Q1-M1-B3
Method	BLASTX
NCBI GI	g2811278
BLAST score	491
E value	1.0e-49
Match length	124
% identity	75
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231819
Seq. ID	LIB3197-040-Q1-M1-B4
Method	BLASTX
NCBI GI	g4567260
BLAST score	520
E value	4.0e-53
Match length	131
% identity	73
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	231820
Seq. ID	LIB3197-040-Q1-M1-B5
Method	BLASTX
NCBI GI	g4204695
BLAST score	423
E value	1.0e-41
Match length	152
% identity	59
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No.	231821
Seq. ID	LIB3197-040-Q1-M1-B6
Method	BLASTX
NCBI GI	g2642448
BLAST score	602
E value	1.0e-62
Match length	142
% identity	36
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231822
Seq. ID	LIB3197-040-Q1-M1-B7
Method	BLASTX
NCBI GI	g2147165
BLAST score	487
E value	3.0e-49
Match length	96
% identity	55

NCBI Description	calmodulin - Bidens pilosa >gi_939860_emb_CAA61980_ (X89890) Calmodulin [Bidens pilosa]
Seq. No.	231823
Seq. ID	LIB3197-040-Q1-M1-B8
Method	BLASTX
NCBI GI	g2687726
BLAST score	142
E value	7.0e-09
Match length	85
% identity	39
NCBI Description	(AJ003246) 2'-hydroxydihydrodaidzein reductase [Glycine max]
Seq. No.	231824
Seq. ID	LIB3197-040-Q1-M1-B9
Method	BLASTX
NCBI GI	g3212869
BLAST score	481
E value	1.0e-48
Match length	106
% identity	84
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	231825
Seq. ID	LIB3197-040-Q1-M1-C10
Method	BLASTX
NCBI GI	g3360289
BLAST score	285
E value	2.0e-25
Match length	103
% identity	27
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]
Seq. No.	231826
Seq. ID	LIB3197-040-Q1-M1-C12
Method	BLASTX
NCBI GI	g120669
BLAST score	457
E value	1.0e-45
Match length	91
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	231827
Seq. ID	LIB3197-040-Q1-M1-C2
Method	BLASTX
NCBI GI	g4417283
BLAST score	196
E value	3.0e-15
Match length	104
% identity	40

NCBI Description (AC007019) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No. 231828
Seq. ID LIB3197-040-Q1-M1-C6
Method BLASTX
NCBI GI g1839188
BLAST score 264
E value 5.0e-23
Match length 65
% identity 77
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 231829
Seq. ID LIB3197-040-Q1-M1-C8
Method BLASTX
NCBI GI g4103324
BLAST score 601
E value 1.0e-62
Match length 129
% identity 91
NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No. 231830
Seq. ID LIB3197-040-Q1-M1-C9
Method BLASTX
NCBI GI g2706450
BLAST score 287
E value 1.0e-25
Match length 85
% identity 71
NCBI Description (AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No. 231831
Seq. ID LIB3197-040-Q1-M1-D11
Method BLASTX
NCBI GI g1945611
BLAST score 352
E value 2.0e-33
Match length 134
% identity 52
NCBI Description (AB003103) 26S proteasome subunit p55 [Homo sapiens] >gi_4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome, macropain) 26S subunit, non-ATPase,

Seq. No. 231832
Seq. ID LIB3197-040-Q1-M1-D12
Method BLASTX
NCBI GI g4469023
BLAST score 558
E value 2.0e-57
Match length 124
% identity 85
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 231833

Seq. ID LIB3197-040-Q1-M1-D2
Method BLASTX
NCBI GI g3068705
BLAST score 183
E value 2.0e-13
Match length 116
% identity 39
NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 231834
Seq. ID LIB3197-040-Q1-M1-D3
Method BLASTX
NCBI GI g2190992
BLAST score 340
E value 4.0e-32
Match length 103
% identity 64
NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No. 231835
Seq. ID LIB3197-040-Q1-M1-D5
Method BLASTX
NCBI GI g2791834
BLAST score 643
E value 2.0e-67
Match length 125
% identity 98
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No. 231836
Seq. ID LIB3197-040-Q1-M1-D7
Method BLASTX
NCBI GI g4056503
BLAST score 151
E value 5.0e-10
Match length 36
% identity 81
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 231837
Seq. ID LIB3197-040-Q1-M1-D9
Method BLASTX
NCBI GI g4538897
BLAST score 375
E value 4.0e-36
Match length 101
% identity 68
NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No. 231838
Seq. ID LIB3197-040-Q1-M1-E1
Method BLASTX
NCBI GI g2677828
BLAST score 407
E value 9.0e-40
Match length 119

% identity	66
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	231839
Seq. ID	LIB3197-040-Q1-M1-E11
Method	BLASTX
NCBI GI	g2662343
BLAST score	667
E value	3.0e-70
Match length	128
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	231840
Seq. ID	LIB3197-040-Q1-M1-E12
Method	BLASTX
NCBI GI	g4314370
BLAST score	344
E value	2.0e-39
Match length	122
% identity	62
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231841
Seq. ID	LIB3197-040-Q1-M1-E2
Method	BLASTX
NCBI GI	g2564112
BLAST score	278
E value	1.0e-24
Match length	140
% identity	39
NCBI Description	(AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]

Seq. No.	231842
Seq. ID	LIB3197-040-Q1-M1-E3
Method	BLASTX
NCBI GI	g2832623
BLAST score	309
E value	3.0e-28
Match length	76
% identity	74
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	231843
Seq. ID	LIB3197-040-Q1-M1-E4
Method	BLASTX
NCBI GI	g3080427
BLAST score	672
E value	7.0e-71
Match length	139
% identity	90
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	231844
Seq. ID	LIB3197-040-Q1-M1-E5

Method	BLASTX
NCBI GI	g1220196
BLAST score	682
E value	5.0e-72
Match length	146
% identity	87
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	231845
Seq. ID	LIB3197-040-Q1-M1-E6
Method	BLASTX
NCBI GI	g2501578
BLAST score	465
E value	1.0e-46
Match length	104
% identity	93
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	231846
Seq. ID	LIB3197-040-Q1-M1-E7
Method	BLASTX
NCBI GI	g2832625
BLAST score	560
E value	9.0e-58
Match length	142
% identity	74
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	231847
Seq. ID	LIB3197-040-Q1-M1-E8
Method	BLASTX
NCBI GI	g2832623
BLAST score	156
E value	2.0e-10
Match length	56
% identity	59
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	231848
Seq. ID	LIB3197-040-Q1-M1-E9
Method	BLASTX
NCBI GI	g2501578
BLAST score	487
E value	4.0e-49
Match length	109
% identity	94
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	231849
Seq. ID	LIB3197-040-Q1-M1-F1

Method	BLASTX
NCBI GI	g1304227
BLAST score	307
E value	5.0e-28
Match length	69
% identity	75
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	231850
Seq. ID	LIB3197-040-Q1-M1-F5
Method	BLASTX
NCBI GI	g417060
BLAST score	551
E value	1.0e-56
Match length	108
% identity	94
NCBI Description	GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi_1094850_prf__2106409A Gln synthetase [Vigna aconitifolia]

Seq. No.	231851
Seq. ID	LIB3197-040-Q1-M1-F6
Method	BLASTX
NCBI GI	g464734
BLAST score	366
E value	3.0e-35
Match length	79
% identity	92
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]

Seq. No.	231852
Seq. ID	LIB3197-040-Q1-M1-F7
Method	BLASTX
NCBI GI	g1707857
BLAST score	574
E value	2.0e-59
Match length	134
% identity	79
NCBI Description	(Y09291) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No.	231853
Seq. ID	LIB3197-040-Q1-M1-F9
Method	BLASTX
NCBI GI	g2827529
BLAST score	255
E value	6.0e-22
Match length	125
% identity	45
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	231854
Seq. ID	LIB3197-040-Q1-M1-G10
Method	BLASTX
NCBI GI	g3334138
BLAST score	151
E value	1.0e-14
Match length	82
% identity	54
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	231855
Seq. ID	LIB3197-040-Q1-M1-G11
Method	BLASTX
NCBI GI	g464849
BLAST score	590
E value	2.0e-61
Match length	118
% identity	99
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	231856
Seq. ID	LIB3197-040-Q1-M1-G12
Method	BLASTX
NCBI GI	g4539543
BLAST score	638
E value	6.0e-67
Match length	130
% identity	97
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	231857
Seq. ID	LIB3197-040-Q1-M1-G3
Method	BLASTX
NCBI GI	g4063751
BLAST score	284
E value	2.0e-25
Match length	152
% identity	39
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	231858
Seq. ID	LIB3197-040-Q1-M1-G5
Method	BLASTX
NCBI GI	g3927825
BLAST score	346
E value	1.0e-32
Match length	70
% identity	91
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	231859
Seq. ID	LIB3197-040-Q1-M1-G8
Method	BLASTX
NCBI GI	g1345882
BLAST score	561
E value	8.0e-58
Match length	134
% identity	77
NCBI Description	CYTOCHROME B5

Seq. No.	231860
Seq. ID	LIB3197-040-Q1-M1-H1
Method	BLASTX
NCBI GI	g322750
BLAST score	502
E value	1.0e-62
Match length	128
% identity	89
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	231861
Seq. ID	LIB3197-040-Q1-M1-H10
Method	BLASTX
NCBI GI	g2462746
BLAST score	539
E value	2.0e-55
Match length	119
% identity	84
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	231862
Seq. ID	LIB3197-040-Q1-M1-H11
Method	BLASTX
NCBI GI	g2583125
BLAST score	627
E value	1.0e-65
Match length	134
% identity	90
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	231863
Seq. ID	LIB3197-040-Q1-M1-H12
Method	BLASTX
NCBI GI	g2262170
BLAST score	183
E value	1.0e-13
Match length	62
% identity	58
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	231864

Seq. ID	LIB3197-040-Q1-M1-H2
Method	BLASTX
NCBI GI	g2811278
BLAST score	654
E value	9.0e-69
Match length	132
% identity	89
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231865
Seq. ID	LIB3197-040-Q1-M1-H3
Method	BLASTX
NCBI GI	g1703375
BLAST score	578
E value	7.0e-60
Match length	117
% identity	96
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	231866
Seq. ID	LIB3197-040-Q1-M1-H6
Method	BLASTX
NCBI GI	g3451075
BLAST score	221
E value	3.0e-18
Match length	62
% identity	65
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	231867
Seq. ID	LIB3197-040-Q1-M1-H7
Method	BLASTX
NCBI GI	g2347198
BLAST score	368
E value	3.0e-35
Match length	86
% identity	80
NCBI Description	(AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231868
Seq. ID	LIB3197-040-Q1-M1-H9
Method	BLASTX
NCBI GI	g1486472
BLAST score	344
E value	1.0e-32
Match length	78
% identity	85
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	231869
Seq. ID	LIB3197-041-Q1-M1-A1
Method	BLASTX
NCBI GI	g541847
BLAST score	379
E value	1.0e-36

Match length	111
% identity	65
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No.	231870
Seq. ID	LIB3197-041-Q1-M1-A10
Method	BLASTX
NCBI GI	g4455209
BLAST score	581
E value	3.0e-60
Match length	145
% identity	77
NCBI Description	(AL035440) putative Proline synthetase associated protein [Arabidopsis thaliana]

Seq. No.	231871
Seq. ID	LIB3197-041-Q1-M1-A12
Method	BLASTX
NCBI GI	g132944
BLAST score	542
E value	1.0e-55
Match length	137
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	231872
Seq. ID	LIB3197-041-Q1-M1-A3
Method	BLASTX
NCBI GI	g231587
BLAST score	145
E value	4.0e-12
Match length	70
% identity	61
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase [Oryza sativa]

Seq. No.	231873
Seq. ID	LIB3197-041-Q1-M1-A4
Method	BLASTX
NCBI GI	g1703108
BLAST score	339
E value	5.0e-49
Match length	95
% identity	94
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	231874
Seq. ID	LIB3197-041-Q1-M1-A5

Method	BLASTX
NCBI GI	g4263507
BLAST score	211
E value	1.0e-19
Match length	97
% identity	49
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231875
Seq. ID	LIB3197-041-Q1-M1-A7
Method	BLASTX
NCBI GI	g2501490
BLAST score	331
E value	7.0e-31
Match length	124
% identity	51
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) >gi_1620013_dbj_BAA12737_ (D85186) UDP-glucose:flavonoid-3-glucosyltransferase [Gentiana triflora]

Seq. No.	231876
Seq. ID	LIB3197-041-Q1-M1-A8
Method	BLASTX
NCBI GI	g2827559
BLAST score	205
E value	3.0e-16
Match length	70
% identity	59
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	231877
Seq. ID	LIB3197-041-Q1-M1-B12
Method	BLASTX
NCBI GI	g3201627
BLAST score	152
E value	7.0e-10
Match length	44
% identity	61
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	231878
Seq. ID	LIB3197-041-Q1-M1-B3
Method	BLASTX
NCBI GI	g2811278
BLAST score	561
E value	8.0e-58
Match length	134
% identity	77
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231879
Seq. ID	LIB3197-041-Q1-M1-B5
Method	BLASTX
NCBI GI	g2738949

BLAST score 522
E value 2.0e-53
Match length 109
% identity 90
NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No. 231880
Seq. ID LIB3197-041-Q1-M1-B7
Method BLASTX
NCBI GI g3309243
BLAST score 704
E value 1.0e-74
Match length 147
% identity 90
NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No. 231881
Seq. ID LIB3197-041-Q1-M1-B8
Method BLASTX
NCBI GI g3834321
BLAST score 632
E value 3.0e-66
Match length 135
% identity 92
NCBI Description (AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No. 231882
Seq. ID LIB3197-041-Q1-M1-B9
Method BLASTX
NCBI GI g4325282
BLAST score 604
E value 7.0e-63
Match length 135
% identity 81
NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No. 231883
Seq. ID LIB3197-041-Q1-M1-C1
Method BLASTX
NCBI GI g4544399
BLAST score 380
E value 1.0e-36
Match length 146
% identity 50
NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 231884
Seq. ID LIB3197-041-Q1-M1-C10
Method BLASTX

NCBI GI	g2058456
BLAST score	577
E value	1.0e-59
Match length	115
% identity	97
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	231885
Seq. ID	LIB3197-041-Q1-M1-C11
Method	BLASTX
NCBI GI	g4107343
BLAST score	173
E value	2.0e-12
Match length	97
% identity	38
NCBI Description	(AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq. No.	231886
Seq. ID	LIB3197-041-Q1-M1-C12
Method	BLASTX
NCBI GI	g2078350
BLAST score	275
E value	3.0e-24
Match length	120
% identity	51
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	231887
Seq. ID	LIB3197-041-Q1-M1-C2
Method	BLASTX
NCBI GI	g2160166
BLAST score	352
E value	2.0e-33
Match length	142
% identity	57
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	231888
Seq. ID	LIB3197-041-Q1-M1-C5
Method	BLASTX
NCBI GI	g4455293
BLAST score	378
E value	2.0e-36
Match length	87
% identity	91
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	231889
Seq. ID	LIB3197-041-Q1-M1-C6
Method	BLASTX
NCBI GI	g3080400
BLAST score	373
E value	8.0e-36
Match length	80
% identity	88

NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]
Seq. No.	231890
Seq. ID	LIB3197-041-Q1-M1-C7
Method	BLASTX
NCBI GI	g3334115
BLAST score	301
E value	2.0e-27
Match length	80
% identity	75
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]
Seq. No.	231891
Seq. ID	LIB3197-041-Q1-M1-C9
Method	BLASTX
NCBI GI	g1724102
BLAST score	443
E value	4.0e-44
Match length	89
% identity	96
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]
Seq. No.	231892
Seq. ID	LIB3197-041-Q1-M1-D1
Method	BLASTX
NCBI GI	g3182981
BLAST score	525
E value	1.0e-53
Match length	127
% identity	78
NCBI Description	CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_ (D86494) diminuto [Pisum sativum]
Seq. No.	231893
Seq. ID	LIB3197-041-Q1-M1-D10
Method	BLASTX
NCBI GI	g1724102
BLAST score	519
E value	6.0e-53
Match length	117
% identity	85
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]
Seq. No.	231894
Seq. ID	LIB3197-041-Q1-M1-D12
Method	BLASTX
NCBI GI	g729475
BLAST score	389
E value	1.0e-37
Match length	119

% identity	65
NCBI Description	FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) >gi_1362788_pir__A56531 DNA structure-specific endonuclease FEN1 - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda 5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa] >gi_642090 (L37374) endonuclease [Homo sapiens] >gi_3169155 (AC004770) FEN1_HUMAN; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_ (X76771) flap endonuclease-1 [Homo sapiens]

Seq. No.	231895
Seq. ID	LIB3197-041-Q1-M1-D5
Method	BLASTX
NCBI GI	g3790102
BLAST score	732
E value	7.0e-78
Match length	146
% identity	88
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	231896
Seq. ID	LIB3197-041-Q1-M1-D8
Method	BLASTX
NCBI GI	g3122386
BLAST score	506
E value	2.0e-51
Match length	113
% identity	82
NCBI Description	WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum]

Seq. No.	231897
Seq. ID	LIB3197-041-Q1-M1-E1
Method	BLASTX
NCBI GI	g2407790
BLAST score	422
E value	1.0e-41
Match length	139
% identity	18
NCBI Description	(AF019910) grr1 [Glycine max]

Seq. No.	231898
Seq. ID	LIB3197-041-Q1-M1-E11
Method	BLASTX
NCBI GI	g2655008
BLAST score	319
E value	2.0e-29
Match length	112
% identity	54
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	231899
Seq. ID	LIB3197-041-Q1-M1-E12
Method	BLASTX
NCBI GI	g3108053

BLAST score	752
E value	3.0e-80
Match length	150
% identity	96
NCBI Description	(AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea mays]

Seq. No.	231900
Seq. ID	LIB3197-041-Q1-M1-E2
Method	BLASTX
NCBI GI	g2493046
BLAST score	404
E value	2.0e-39
Match length	112
% identity	72
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_82297_pir__A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	231901
Seq. ID	LIB3197-041-Q1-M1-E5
Method	BLASTX
NCBI GI	g401322
BLAST score	384
E value	4.0e-37
Match length	88
% identity	86
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	231902
Seq. ID	LIB3197-041-Q1-M1-E6
Method	BLASTX
NCBI GI	g1082766
BLAST score	212
E value	6.0e-17
Match length	52
% identity	73
NCBI Description	ribosomal protein L29 - human >gi_793843_emb_CAA89008_ (Z49148) ribosomal protein L29 [Homo sapiens]

Seq. No.	231903
Seq. ID	LIB3197-041-Q1-M1-F1
Method	BLASTX
NCBI GI	g4335750
BLAST score	271
E value	7.0e-24
Match length	84
% identity	54
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	231904
Seq. ID	LIB3197-041-Q1-M1-F10

Method	BLASTX
NCBI GI	g232024
BLAST score	768
E value	4.0e-82
Match length	144
% identity	100
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	231905
Seq. ID	LIB3197-041-Q1-M1-F11
Method	BLASTX
NCBI GI	g2252824
BLAST score	340
E value	6.0e-32
Match length	126
% identity	58
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	231906
Seq. ID	LIB3197-041-Q1-M1-F12
Method	BLASTX
NCBI GI	g1703129
BLAST score	524
E value	1.0e-53
Match length	97
% identity	99
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	231907
Seq. ID	LIB3197-041-Q1-M1-F2
Method	BLASTX
NCBI GI	g3183454
BLAST score	207
E value	2.0e-16
Match length	94
% identity	43
NCBI Description	HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No.	231908
Seq. ID	LIB3197-041-Q1-M1-F4
Method	BLASTX
NCBI GI	g3360289
BLAST score	439
E value	2.0e-43
Match length	102
% identity	83
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	231909
Seq. ID	LIB3197-041-Q1-M1-F5
Method	BLASTX
NCBI GI	g1041706
BLAST score	448
E value	1.0e-44
Match length	103
% identity	75
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	231910
Seq. ID	LIB3197-041-Q1-M1-F7
Method	BLASTX
NCBI GI	g543905
BLAST score	357
E value	9.0e-51
Match length	127
% identity	83
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	231911
Seq. ID	LIB3197-041-Q1-M1-F8
Method	BLASTX
NCBI GI	g2275210
BLAST score	156
E value	2.0e-10
Match length	81
% identity	43
NCBI Description	(AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No.	231912
Seq. ID	LIB3197-041-Q1-M1-G1
Method	BLASTX
NCBI GI	g3395427
BLAST score	205
E value	4.0e-16
Match length	110
% identity	45
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	231913
Seq. ID	LIB3197-041-Q1-M1-G10
Method	BLASTX
NCBI GI	g2833380
BLAST score	299
E value	3.0e-27
Match length	120
% identity	56
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2) (PRS II) >gi_2146772_pir__S71262 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) II - Arabidopsis thaliana (fragment) >gi_1064885_emb_CAA63552_ (X92974) phosphoribosyl pyrophosphate synthetase II [Arabidopsis thaliana]

Seq. No.	231914
Seq. ID	LIB3197-041-Q1-M1-G12
Method	BLASTX
NCBI GI	g1220196
BLAST score	807
E value	1.0e-86
Match length	150
% identity	100
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	231915
Seq. ID	LIB3197-041-Q1-M1-G2
Method	BLASTX
NCBI GI	g2558654
BLAST score	391
E value	6.0e-38
Match length	141
% identity	56
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	231916
Seq. ID	LIB3197-041-Q1-M1-G3
Method	BLASTX
NCBI GI	g2119937
BLAST score	378
E value	2.0e-36
Match length	79
% identity	91
NCBI Description	translation initiation factor eIF-4A.13 - common tobacco (fragment)

Seq. No.	231917
Seq. ID	LIB3197-041-Q1-M1-G4
Method	BLASTX
NCBI GI	g2213610
BLAST score	165
E value	3.0e-20
Match length	81
% identity	50
NCBI Description	(AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No.	231918
Seq. ID	LIB3197-041-Q1-M1-G5
Method	BLASTX
NCBI GI	g2980788
BLAST score	257
E value	3.0e-22
Match length	136
% identity	46
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	231919
Seq. ID	LIB3197-041-Q1-M1-G7
Method	BLASTX
NCBI GI	g2827713
BLAST score	376

E value	3.0e-36
Match length	126
% identity	63
NCBI Description	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]

Seq. No.	231920
Seq. ID	LIB3197-041-Q1-M1-G9
Method	BLASTX
NCBI GI	g1170898
BLAST score	507
E value	1.0e-51
Match length	122
% identity	84
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial - cider tree >gi_473206_emb_CAA55383_ (X78800) mitochondrial malate dehydrogenase [Eucalyptus gunnii]

Seq. No.	231921
Seq. ID	LIB3197-041-Q1-M1-H1
Method	BLASTX
NCBI GI	g1617036
BLAST score	370
E value	2.0e-35
Match length	89
% identity	75
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]

Seq. No.	231922
Seq. ID	LIB3197-041-Q1-M1-H10
Method	BLASTX
NCBI GI	g3128175
BLAST score	181
E value	3.0e-13
Match length	100
% identity	39
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	231923
Seq. ID	LIB3197-041-Q1-M1-H11
Method	BLASTX
NCBI GI	g1848212
BLAST score	536
E value	4.0e-55
Match length	116
% identity	49
NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]

Seq. No.	231924
Seq. ID	LIB3197-041-Q1-M1-H12
Method	BLASTX
NCBI GI	g541950
BLAST score	245
E value	2.0e-21
Match length	52

% identity	90
NCBI Description	SPCP1 protein - soybean >gi_310576 (L12257) nodulin-26 [Glycine max]

Seq. No.	231925
Seq. ID	LIB3197-041-Q1-M1-H3
Method	BLASTX
NCBI GI	g729623
BLAST score	454
E value	3.0e-45
Match length	106
% identity	85
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP 78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 5) (BIP 5) >gi_100340_pir__S21880 heat shock protein BiP homolog blp5 - common tobacco >gi_19813_emb_CAA42660_ (X60058) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	231926
Seq. ID	LIB3197-041-Q1-M1-H5
Method	BLASTX
NCBI GI	g1170507
BLAST score	727
E value	3.0e-77
Match length	144
% identity	97
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Seq. No.	231927
Seq. ID	LIB3197-041-Q1-M1-H8
Method	BLASTX
NCBI GI	g3650037
BLAST score	433
E value	7.0e-43
Match length	103
% identity	82
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	231928
Seq. ID	LIB3197-041-Q1-M1-H9
Method	BLASTX
NCBI GI	g2811278
BLAST score	479
E value	3.0e-48
Match length	102
% identity	86
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	231929
Seq. ID	LIB3197-042-Q1-M1-A7
Method	BLASTX
NCBI GI	g416758

BLAST score	166
E value	9.0e-12
Match length	77
% identity	45
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	231930
Seq. ID	LIB3197-042-Q1-M1-A9
Method	BLASTX
NCBI GI	g2984709
BLAST score	357
E value	3.0e-34
Match length	71
% identity	96
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No.	231931
Seq. ID	LIB3197-042-Q1-M1-B1
Method	BLASTX
NCBI GI	g4432830
BLAST score	482
E value	1.0e-48
Match length	121
% identity	71
NCBI Description	(AC006283) similar to pheromone receptor deficient mutant [Arabidopsis thaliana]

Seq. No.	231932
Seq. ID	LIB3197-042-Q1-M1-B2
Method	BLASTX
NCBI GI	g1483150
BLAST score	371
E value	1.0e-35
Match length	84
% identity	80
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]

Seq. No.	231933
Seq. ID	LIB3197-042-Q1-M1-B3
Method	BLASTX
NCBI GI	g112972
BLAST score	568
E value	1.0e-58
Match length	128
% identity	85
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi_167546 (M92660) aspartate aminotransferase [Daucus carota] >gi_445587_prf__1909339A Asp aminotransferase [Daucus carota]

Seq. No.	231934
Seq. ID	LIB3197-042-Q1-M1-B9
Method	BLASTX

NCBI GI g2194118
BLAST score 195
E value 6.0e-15
Match length 68
% identity 54
NCBI Description (AC002062) F20P5.4 gene product [Arabidopsis thaliana]

Seq. No. 231935
Seq. ID LIB3197-042-Q1-M1-C1
Method BLASTX
NCBI GI g4097579
BLAST score 583
E value 2.0e-60
Match length 121
% identity 88
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 231936
Seq. ID LIB3197-042-Q1-M1-C2
Method BLASTX
NCBI GI g2507422
BLAST score 446
E value 2.0e-44
Match length 107
% identity 86
NCBI Description CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No. 231937
Seq. ID LIB3197-042-Q1-M1-C7
Method BLASTX
NCBI GI g2246442
BLAST score 166
E value 2.0e-11
Match length 70
% identity 46
NCBI Description (U63298) farnesyltransferase alpha subunit [Pisum sativum]

Seq. No. 231938
Seq. ID LIB3197-042-Q1-M1-F10
Method BLASTX
NCBI GI g2749939
BLAST score 169
E value 7.0e-12
Match length 55
% identity 56
NCBI Description (U70999) CCS1 [Chlamydomonas reinhardtii] >gi_2749941 (U71000) CCS1 [Chlamydomonas reinhardtii]

Seq. No. 231939
Seq. ID LIB3197-042-Q1-M1-F11
Method BLASTX
NCBI GI g267069
BLAST score 626
E value 2.0e-65

Match length	116
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231940
Seq. ID	LIB3197-042-Q1-M1-F4
Method	BLASTX
NCBI GI	g4490736
BLAST score	459
E value	7.0e-46
Match length	140
% identity	39
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	231941
Seq. ID	LIB3197-042-Q1-M1-G10
Method	BLASTX
NCBI GI	g3121853
BLAST score	159
E value	1.0e-10
Match length	132
% identity	32
NCBI Description	CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) >gi_2584785_emb_CAA73228_ (Y12696) p64 bovine chloride channel-like protein [Homo sapiens]

Seq. No.	231942
Seq. ID	LIB3197-042-Q1-M1-G11
Method	BLASTX
NCBI GI	g4512671
BLAST score	189
E value	6.0e-15
Match length	59
% identity	73
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	231943
Seq. ID	LIB3197-042-Q1-M1-G12
Method	BLASTX
NCBI GI	g4406372
BLAST score	278
E value	1.0e-24
Match length	99
% identity	57
NCBI Description	(AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No.	231944
Seq. ID	LIB3197-042-Q1-M1-G5
Method	BLASTX
NCBI GI	g3646373
BLAST score	340
E value	2.0e-32
Match length	69

% identity	91
NCBI Description	(AJ011078) RGP1 protein [Oryza sativa]

Seq. No.	231945
Seq. ID	LIB3197-042-Q1-M1-H10
Method	BLASTX
NCBI GI	g2146731
BLAST score	568
E value	1.0e-58
Match length	141
% identity	31
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	231946
Seq. ID	LIB3197-042-Q1-M1-H11
Method	BLASTX
NCBI GI	g2623300
BLAST score	167
E value	1.0e-11
Match length	74
% identity	66
NCBI Description	(AC002409) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	231947
Seq. ID	LIB3197-042-Q1-M1-H12
Method	BLASTX
NCBI GI	g2911047
BLAST score	400
E value	5.0e-39
Match length	113
% identity	70
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	231948
Seq. ID	LIB3197-042-Q1-M1-H4
Method	BLASTX
NCBI GI	g3249105
BLAST score	265
E value	4.0e-23
Match length	146
% identity	40
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	231949
Seq. ID	LIB3197-042-Q1-M1-H5
Method	BLASTX
NCBI GI	g169989
BLAST score	515
E value	2.0e-52
Match length	111
% identity	90
NCBI Description	(L12157) NADPH-specific isocitrate dehydrogenase [Glycine max]

Seq. No.	231950
Seq. ID	LIB3197-043-Q1-M1-A10
Method	BLASTX
NCBI GI	g2244839
BLAST score	355
E value	1.0e-33
Match length	153
% identity	15
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	231951
Seq. ID	LIB3197-043-Q1-M1-A5
Method	BLASTX
NCBI GI	g1657617
BLAST score	486
E value	5.0e-49
Match length	110
% identity	85
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	231952
Seq. ID	LIB3197-043-Q1-M1-A6
Method	BLASTX
NCBI GI	g1418990
BLAST score	283
E value	3.0e-25
Match length	71
% identity	75
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	231953
Seq. ID	LIB3197-043-Q1-M1-B10
Method	BLASTX
NCBI GI	g3402279
BLAST score	622
E value	5.0e-65
Match length	127
% identity	91
NCBI Description	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

Seq. No.	231954
Seq. ID	LIB3197-043-Q1-M1-B11
Method	BLASTX
NCBI GI	g3236248
BLAST score	476
E value	6.0e-48
Match length	131
% identity	72
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	231955
Seq. ID	LIB3197-043-Q1-M1-B5
Method	BLASTX
NCBI GI	g2832658

BLAST score 175
E value 1.0e-12
Match length 114
% identity 34
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 231956
Seq. ID LIB3197-043-Q1-M1-F2
Method BLASTX
NCBI GI g4455365
BLAST score 153
E value 5.0e-10
Match length 31
% identity 87
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 231957
Seq. ID LIB3197-043-Q1-M1-G1
Method BLASTX
NCBI GI g4510395
BLAST score 545
E value 5.0e-56
Match length 133
% identity 73
NCBI Description (AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No. 231958
Seq. ID LIB3197-043-Q1-M1-G3
Method BLASTX
NCBI GI g4521249
BLAST score 523
E value 2.0e-53
Match length 133
% identity 77
NCBI Description (AB013912) DNA helicase [Mus musculus]

Seq. No. 231959
Seq. ID LIB3197-043-Q1-M1-G7
Method BLASTX
NCBI GI g2335098
BLAST score 481
E value 2.0e-48
Match length 146
% identity 63
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 231960
Seq. ID LIB3197-043-Q1-M1-G8
Method BLASTX
NCBI GI g2498329
BLAST score 367
E value 4.0e-43
Match length 131
% identity 71
NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana

	>gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]
Seq. No.	231961
Seq. ID	LIB3197-043-Q1-M1-G9
Method	BLASTX
NCBI GI	g3150402
BLAST score	99
E value	3.0e-10
Match length	48
% identity	85
NCBI Description	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]
Seq. No.	231962
Seq. ID	LIB3197-043-Q1-M1-H1
Method	BLASTX
NCBI GI	g2129499
BLAST score	607
E value	3.0e-63
Match length	125
% identity	91
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.	231963
Seq. ID	LIB3197-043-Q1-M1-H2
Method	BLASTX
NCBI GI	g2160322
BLAST score	517
E value	1.0e-52
Match length	101
% identity	95
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]
Seq. No.	231964
Seq. ID	LIB3197-043-Q1-M1-H3
Method	BLASTX
NCBI GI	g1345132
BLAST score	698
E value	7.0e-74
Match length	155
% identity	86
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
Seq. No.	231965
Seq. ID	LIB3197-043-Q1-M1-H7
Method	BLASTX
NCBI GI	g267069

BLAST score	363
E value	6.0e-40
Match length	90
% identity	92
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231966
Seq. ID	LIB3197-043-Q1-M1-H8
Method	BLASTX
NCBI GI	g606942
BLAST score	293
E value	2.0e-26
Match length	111
% identity	59
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	231967
Seq. ID	LIB3197-044-Q1-M1-A1
Method	BLASTX
NCBI GI	g1703115
BLAST score	439
E value	8.0e-44
Match length	83
% identity	99
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	231968
Seq. ID	LIB3197-044-Q1-M1-A11
Method	BLASTX
NCBI GI	g730125
BLAST score	147
E value	2.0e-09
Match length	54
% identity	59
NCBI Description	NADPH-CYTOCHROME P450 REDUCTASE >gi_322739_pir__S31502 NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Madagascar periwinkle >gi_18139_emb_CAA49446_ (X69791) NADPH--ferrihemoprotein reductase [Catharanthus roseus]

Seq. No.	231969
Seq. ID	LIB3197-044-Q1-M1-A12
Method	BLASTX
NCBI GI	g2642238
BLAST score	368
E value	2.0e-35
Match length	84
% identity	89
NCBI Description	(AF031241) endoplasmic reticulum HSC70-cognate binding protein precursor [Glycine max]

Seq. No.	231970

Seq. ID	LIB3197-044-Q1-M1-A3
Method	BLASTX
NCBI GI	g3337366
BLAST score	299
E value	2.0e-27
Match length	108
% identity	57
NCBI Description	(AC004481) unknown protein [Arabidopsis thaliana]

Seq. No.	231971
Seq. ID	LIB3197-044-Q1-M1-A5
Method	BLASTX
NCBI GI	g267069
BLAST score	453
E value	2.0e-45
Match length	88
% identity	95
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	231972
Seq. ID	LIB3197-044-Q1-M1-A6
Method	BLASTX
NCBI GI	g1527172
BLAST score	191
E value	5.0e-19
Match length	76
% identity	55
NCBI Description	(U67676) alpha-2 tubulin [Hirudo medicinalis] >gi_1532193_gb_AAB07891_ (U67678) alpha-2 tubulin [Hirudo medicinalis]

Seq. No.	231973
Seq. ID	LIB3197-044-Q1-M1-B1
Method	BLASTX
NCBI GI	g3158376
BLAST score	162
E value	1.0e-13
Match length	80
% identity	54
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	231974
Seq. ID	LIB3197-044-Q1-M1-B12
Method	BLASTX
NCBI GI	g2245394
BLAST score	247
E value	4.0e-21
Match length	75
% identity	64
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No.	231975
Seq. ID	LIB3197-044-Q1-M1-B3
Method	BLASTX

09604704.0000

NCBI GI	g4512712
BLAST score	144
E value	4.0e-09
Match length	97
% identity	30
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	231976
Seq. ID	LIB3197-044-Q1-M1-B5
Method	BLASTX
NCBI GI	g3540178
BLAST score	320
E value	1.0e-29
Match length	116
% identity	58
NCBI Description	(AC004122) calcium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	231977
Seq. ID	LIB3197-044-Q1-M1-B7
Method	BLASTX
NCBI GI	g1174613
BLAST score	509
E value	5.0e-52
Match length	100
% identity	98
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	231978
Seq. ID	LIB3197-044-Q1-M1-C11
Method	BLASTX
NCBI GI	g2580440
BLAST score	236
E value	6.0e-20
Match length	115
% identity	48
NCBI Description	(D87261) PCF2 [Oryza sativa]

Seq. No.	231979
Seq. ID	LIB3197-044-Q1-M1-C12
Method	BLASTX
NCBI GI	g1762142
BLAST score	396
E value	2.0e-38
Match length	142
% identity	55
NCBI Description	(U48434) putative cytochrome P450 [Solanum chacoense]

Seq. No.	231980
Seq. ID	LIB3197-044-Q1-M1-C6
Method	BLASTX
NCBI GI	g2191128
BLAST score	384
E value	4.0e-37

Match length	135
% identity	64
NCBI Description	(AF007269) belongs to the L5P family of ribosomal proteins [Arabidopsis thaliana]

Seq. No.	231981
Seq. ID	LIB3197-044-Q1-M1-C7
Method	BLASTX
NCBI GI	g2801536
BLAST score	435
E value	4.0e-43
Match length	141
% identity	60
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	231982
Seq. ID	LIB3197-044-Q1-M1-D11
Method	BLASTX
NCBI GI	g3021506
BLAST score	499
E value	7.0e-51
Match length	119
% identity	86
NCBI Description	(X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	231983
Seq. ID	LIB3197-044-Q1-M1-D12
Method	BLASTX
NCBI GI	g731097
BLAST score	300
E value	3.0e-27
Match length	124
% identity	52
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN) >gi_1083086_pir__A55910 subunit D vacuolar H(+)-ATPase - bovine >gi_517446 (U11927) vacuolar H-ATPase subunit D [Bos gaurus]

Seq. No.	231984
Seq. ID	LIB3197-044-Q1-M1-D2
Method	BLASTX
NCBI GI	g2982303
BLAST score	419
E value	3.0e-41
Match length	94
% identity	82
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	231985
Seq. ID	LIB3197-044-Q1-M1-D3
Method	BLASTX
NCBI GI	g1174592
BLAST score	527
E value	5.0e-54
Match length	98
% identity	99

NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	231986
Seq. ID	LIB3197-044-Q1-M1-D5
Method	BLASTX
NCBI GI	g541951
BLAST score	404
E value	2.0e-39
Match length	128
% identity	63
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	231987
Seq. ID	LIB3197-044-Q1-M1-D6
Method	BLASTX
NCBI GI	g2398807
BLAST score	354
E value	1.0e-33
Match length	107
% identity	64
NCBI Description	(Z99091) succinate dehydrogenase [Schizosaccharomyces pombe]

Seq. No.	231988
Seq. ID	LIB3197-044-Q1-M1-E1
Method	BLASTX
NCBI GI	g2738949
BLAST score	491
E value	1.0e-49
Match length	102
% identity	90
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	231989
Seq. ID	LIB3197-044-Q1-M1-E10
Method	BLASTX
NCBI GI	g3953470
BLAST score	251
E value	2.0e-21
Match length	90
% identity	60
NCBI Description	(AC002328) F20N2.15 [Arabidopsis thaliana]

Seq. No.	231990
Seq. ID	LIB3197-044-Q1-M1-E11
Method	BLASTX
NCBI GI	g1928981
BLAST score	503
E value	4.0e-51
Match length	107
% identity	93
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	231991
Seq. ID	LIB3197-044-Q1-M1-E3
Method	BLASTX
NCBI GI	g464846
BLAST score	340
E value	4.0e-32
Match length	73
% identity	84
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	231992
Seq. ID	LIB3197-044-Q1-M1-E8
Method	BLASTX
NCBI GI	g3063396
BLAST score	553
E value	5.0e-57
Match length	109
% identity	94
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	231993
Seq. ID	LIB3197-044-Q1-M1-E9
Method	BLASTX
NCBI GI	g1174718
BLAST score	191
E value	2.0e-14
Match length	130
% identity	16
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	231994
Seq. ID	LIB3197-044-Q1-M1-F10
Method	BLASTX
NCBI GI	g3024017
BLAST score	414
E value	8.0e-41
Match length	81
% identity	95
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	231995
Seq. ID	LIB3197-044-Q1-M1-F11
Method	BLASTX
NCBI GI	g4165861
BLAST score	284
E value	2.0e-25
Match length	136
% identity	24
NCBI Description	(AF006603) histone deacetylase mHDA2 [Mus musculus]

Seq. No.	231996
Seq. ID	LIB3197-044-Q1-M1-F12
Method	BLASTX
NCBI GI	g2583123
BLAST score	340
E value	4.0e-32
Match length	94
% identity	70
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	231997
Seq. ID	LIB3197-044-Q1-M1-F4
Method	BLASTX
NCBI GI	g3618343
BLAST score	195
E value	6.0e-15
Match length	104
% identity	41
NCBI Description	(AB009398) 26S proteasome subunit p40.5 [Homo sapiens] >gi_4506223_ref_NP_002808.1_pPSMD13_ proteasome (prosome, macropain) 26S subunit, non-ATPase,

Seq. No.	231998
Seq. ID	LIB3197-044-Q1-M1-F7
Method	BLASTX
NCBI GI	g2935298
BLAST score	323
E value	4.0e-30
Match length	83
% identity	75
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	231999
Seq. ID	LIB3197-044-Q1-M1-F9
Method	BLASTX
NCBI GI	g2062167
BLAST score	329
E value	7.0e-31
Match length	93
% identity	67
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	232000
Seq. ID	LIB3197-044-Q1-M1-G10
Method	BLASTX
NCBI GI	g4204260
BLAST score	197
E value	4.0e-15
Match length	61
% identity	61
NCBI Description	(AC005223) 25568 [Arabidopsis thaliana]

Seq. No.	232001

Seq. ID	LIB3197-044-Q1-M1-G11
Method	BLASTX
NCBI GI	g3551960
BLAST score	426
E value	4.0e-44
Match length	139
% identity	65
NCBI Description	(AF082033) senescence-associated protein 15 [Hemerocallis hybrid cultivar]

Seq. No.	232002
Seq. ID	LIB3197-044-Q1-M1-G2
Method	BLASTX
NCBI GI	g3176098
BLAST score	411
E value	2.0e-44
Match length	141
% identity	42
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	232003
Seq. ID	LIB3197-044-Q1-M1-G4
Method	BLASTX
NCBI GI	g1724102
BLAST score	560
E value	1.0e-57
Match length	122
% identity	85
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	232004
Seq. ID	LIB3197-044-Q1-M1-G5
Method	BLASTX
NCBI GI	g3600054
BLAST score	192
E value	1.0e-14
Match length	106
% identity	40
NCBI Description	(AF080120) No definition line found [Arabidopsis thaliana]

Seq. No.	232005
Seq. ID	LIB3197-044-Q1-M1-G6
Method	BLASTX
NCBI GI	g1724102
BLAST score	509
E value	9.0e-52
Match length	117
% identity	83
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	232006
Seq. ID	LIB3197-044-Q1-M1-H2
Method	BLASTX
NCBI GI	g1361974
BLAST score	192